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OM nucleic - nucleic search, using sw model

Run on: August 30, 2003, 18:46:00 ; Search time 1971.58 seconds
(without alignments)
9026.108 Million cell updates/sec

Title: US-08-836-455-1

Perfect score: 435

Sequence: 1 ATGGGGGCCCTGCTCAGAT.....CACCATCCAGTAAGCTTGGG 435

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.:

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_cm.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
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- 27: em_sts.*
- 28: em_un.*
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- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	435	100.0	435	6	AR164505	AR164505 Sequence
2	435	100.0	435	6	BD085737	BD085737 Methods o
3	377	86.7	381	10	AF124721	AF124721 Mus muscu
4	117	26.9	321	10	AF163749	AF163749 Mus muscu
5	108	24.8	303	10	MUSIGLAF	M36246 Mouse Ig ka
6	108	24.8	324	6	AX722008	AX722008 Sequence
7	107	24.6	302	10	MMU55588	U55588 Mus musculu
8	107	24.6	756	6	AX256284	AX256284 Sequence
9	107	24.6	771	6	AX256296	AX256296 Sequence
10	107	24.6	1497	6	AX256302	AX256302 Sequence
11	100	23.4	387	6	AR169918	AR169918 Sequence
12	100	23.0	269	10	MMVJIG7	X54760 Mouse rearr
13	100	23.0	273	10	MMU21066	U21066 Mus musculu
14	100	23.0	276	6	AR026090	AR026090 Sequence
15	100	23.0	276	6	AR026094	AR026094 Sequence
16	100	23.0	276	10	MMVJIG12	X54765 Mouse rearr
17	100	23.0	279	10	MMVKMRB11	X63811 M.musculus
18	100	23.0	283	10	AF144956	AF144956 Mus muscu
19	100	23.0	285	10	MMU29617	U29617 Mus musculu
20	100	23.0	323	10	AY229938	AY229938 Mus muscu
21	100	23.0	324	6	I03643	I03643 Sequence 4
22	100	23.0	324	6	I07835	I07835 Sequence 4
23	100	23.0	326	10	MMVJIG3	X54756 Mouse rearr
24	100	23.0	348	10	MMVJIG	X54755 Mouse rearr
25	100	23.0	354	10	AB089681	AB089681 Mus muscu
26	100	23.0	381	10	AF045495	AF045495 Mus muscu
27	100	23.0	381	10	AF045508	AF045508 Mus muscu
28	100	23.0	443	10	MMU88675	U88675 Mus musculu
29	100	23.0	684	10	MUSIGKAC1	J00565 Mus musculu
30	100	23.0	685	10	MMIGK7	V00808 Part of the
31	100	23.0	203877	10	AC122260	AC122260 Mus muscu
32	99	22.8	390	10	MUSIKCC	L41880 Mus musculu
33	97	22.3	640	10	MMU242670	AJ242670 Mus muscu
34	96	22.1	218	10	MMVJIG4	X54757 Mouse rearr
35	93	21.4	535	6	BD021878	BD021878 Humanized
36	91	20.9	452	10	AB050077	AB050077 Mus muscu
37	91	20.9	453	10	AB050084	AB050084 Mus muscu
38	91	20.9	456	10	MUSIGKCNK	M1914 Mouse Ig re
39	90	20.7	438	6	E09035	E09035 cDNA encodi
40	90	20.7	438	6	I32991	I32991 Sequence 45
41	89	20.5	321	10	MUSIGKAA3	M59920 Mouse Ig ge
42	89	20.5	324	10	MUSX	L48667 Mus musculu
43	89	20.5	381	10	AF045510	AF045510 Mus muscu
44	88	20.2	290	10	AF144902	AF144902 Mus muscu
45	86	19.8	308	10	AF139248	AF139248 Mus muscu

ALIGNMENTS

RESULT 1	AR164505	AR164505	435 bp	DNA	linear	PAT 17-OCT-2001
LOCUS	Sequence 1	from patent US 6274143.				
DEFINITION	Sequence 1	from patent US 6274143.				
ACCESSION	AR164505					
VERSION	AR164505.1	GI:16237555				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 435)					
AUTHORS	Chatterjee, M. and Foon, K. A.					
TITLE	Methods of delaying development of HMFG-associated tumors using anti-idiotypic antibody 11D10					
JOURNAL	Patent: US 6274143-A 1 14-AUG-2001;					

6/11/98

FEATURES source Location/Qualifiers
 1. .435
 /organism="unknown"
 BASE COUNT 100 a 111 c 102 g 122 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 2.6e-258;
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGCCCTCTGCTCAGATCTCTGGGCTCTTGTGCTCTGTGTTCCAGGTACAGATGT 60
 DB 1 ATGGGGCCCTCTGCTCAGATCTCTGGGCTCTTGTGCTCTGTGTTCCAGGTACAGATGT 60

QY 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGATCAGT 120
 DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGATCAGT 120

QY 121 CTCACCTTGTGGGCAAGTCAGGACATGGTATTAACCTTACATTTGGCTTCAGCAGGAACCA 180
 DB 121 CTCACCTTGTGGGCAAGTCAGGACATGGTATTAACCTTACATTTGGCTTCAGCAGGAACCA 180

QY 181 GATGGAACCTTAAACCCCTGATCTACGCCACATCCAGTTAGTCTGTGTCGCCAAA 240
 DB 181 GATGGAACCTTAAACCCCTGATCTACGCCACATCCAGTTAGTCTGTGTCGCCAAA 240

QY 241 AGGTTTCAGTGGCAGTCTGGGTCAGATTAATCTCCACATCAGCAGCCTTGTAGTCT 300
 DB 241 AGGTTTCAGTGGCAGTCTGGGTCAGATTAATCTCCACATCAGCAGCCTTGTAGTCT 300

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 DB 361 GGGACCAAGCTGGAAATAAAGCGGCTGATGCTCACCACATGATCCATCTTCCACCA 420

QY 421 TCCAGTAAGCTTGGG 435
 DB 421 TCCAGTAAGCTTGGG 435

RESULT 2
 BD085737
 LOCUS 435 bp DNA linear PAT 27-AUG-2002
 DEFINITION Methods of delaying development of HMFG-associated tumors using anti-idiotypic antibody 11D10.
 ACCESSION BD085737
 VERSION BD085737.1 GI:22631347
 KEYWORDS JP 2001523269-A/1.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 435)
 AUTHORS Chatterjee, M. and Foon, K.A.
 TITLE Methods of delaying development of HMFG-associated tumors using anti-idiotypic antibody 11D10
 JOURNAL Patent: JP 2001523269-A 1 20-NOV-2001;
 COMMENT THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
 OS Unidentified
 PN JP 2001523269-A/1
 PD 20-NOV-2001
 PF 12-JUN-1998 JP 1999503252
 PR 13-JUN-1997 US 60/049540, 11-JUN-1998 US 09/096244 PI
 PC MALAYA CHATTERJEE, KENNETH A. FOON
 CC A61K39/395, A61K39/39//C07K16/42
 CC Strandedness: Single;
 CC Topology: Linear;
 CC Methods of delaying development of HMFG-associated tumors CC
 CC anti-idiotypic antibody 11D10
 FH Key Location/Qualifiers

FT CDS 1. .435
 FT mat peptide
 Location/Qualifiers
 1. .435
 /organism="unidentified"
 /mol_type="genomic DNA"
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 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGCCCTCTGCTCAGATCTCTGGGCTCTTGTGCTCTGTGTTCCAGGTACAGATGT 60
 DB 1 ATGGGGCCCTCTGCTCAGATCTCTGGGCTCTTGTGCTCTGTGTTCCAGGTACAGATGT 60

QY 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGATCAGT 120
 DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGATCAGT 120

QY 121 CTCACCTTGTGGGCAAGTCAGGACATGGTATTAACCTTACATTTGGCTTCAGCAGGAACCA 180
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QY 181 GATGGAACCTTAAACCCCTGATCTACGCCACATCCAGTTAGTCTGTGTCGCCAAA 240
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QY 241 AGGTTTCAGTGGCAGTCTGGGTCAGATTAATCTCCACATCAGCAGCCTTGTAGTCT 300
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QY 301 GAAGATTTTGTAGCTTATCTGCTACATAATGCTAGTCTCGGTACACGTTCCGGAGGG 360
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QY 361 GGGACCAAGCTGGAAATAAAGCGGCTGATGCTCACCACATGATCCATCTTCCACCA 420
 DB 361 GGGACCAAGCTGGAAATAAAGCGGCTGATGCTCACCACATGATCCATCTTCCACCA 420

QY 421 TCCAGTAAGCTTGGG 435
 DB 421 TCCAGTAAGCTTGGG 435

RESULT 3
 AF124721
 LOCUS 381 bp mRNA linear ROD 22-MAY-2001
 DEFINITION Mus musculus immunoglobulin light chain mRNA, partial cds.
 ACCESSION AF124721
 VERSION AF124721.1 GI:14164546
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 381)
 AUTHORS Tripathi, P.K., Qin, H., Bhattacharya-Chatterjee, M., Ceriani, R.L., Foon, K.A. and Chatterjee, S.K.
 TITLE Construction and characterization of a chimeric fusion protein consisting of an anti-idiotypic antibody mimicking a breast cancer-associated antigen and the cytokine GM-CSF
 JOURNAL Hybridoma 18 (2), 193-202 (1999)
 MEDLINE 9305687
 PUBMED 10380019
 REFERENCE 2 (bases 1 to 381)
 AUTHORS Chatterjee, S.K. and Tripathi, P.K.
 TITLE Direct Submission
 JOURNAL Submitted (29-JAN-1999) Internal Medicine, University of Kentucky, 800 Rose Street, Lexington, KY 40536, USA
 FEATURES Location/Qualifiers

JOURNAL	Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma University Health Sciences Center, 940 St. Young Blvd, Oklahoma City, OK 73190, USA
FEATURES	Location/Qualifiers
SOURCE	1. 321
	/organism="Mus musculus"
	/mol_type="mRNA"
	/strain="BALB/c"
	/db_xref="taxon:10090"
	/note="mab 49.8.9"
	<1. >321
	/note="V-J segments"
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	/protein_id="AAD47028.1"
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	KLEIK"
BASE COUNT	84 a 77 c 75 g 85 t
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Query Match	26.9%; Score 117; DB 10; Length 321;
Best Local Similarity	99.1%; Pred. No. 1.5e-60;
Matches	217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	163 TGGCTTCAGCAGGACCAACAGATGGAACATATTAAACGCTGTACGCACATCCAGTTTA 222
DB	103 TGGCTTCAGCAGGACCAACAGATGGAACATATTAAACGCTGTACGCACATCCAGTTTA 162
QY	223 GGTTCGTGTGTCCTCCCAAAAGGTTTCAGTGGCAGTAGGTCCTGGTGCAGATTATCTCTCACC 282
DB	163 GATTCTGTGTGTCCTCCCAAAAGGTTTCAGTGGCAGTAGGTCCTGGTGCAGATTATCTCTCACC 222
QY	283 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGTCTACAAATATGCTAGTTCT 342
DB	223 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGTCTACAAATATGCTAGTTCT 282
QY	343 CCGTACAGCTTCGGAGGGGGACCAAGCTGGAATAAAA 381
DB	283 CCGTACAGCTTCGGAGGGGGACCAAGCTGGAATAAAA 321
RESULT 5	
MUSIGLAF	303 bp mRNA linear ROD 27-APR-1993
LOCUS	
DEFINITION	Mouse Ig kappa-chain mRNA V region, partial cds, from hybridoma H220-23.
ACCESSION	M36246.1
VERSION	GI:197631
KEYWORDS	V-region; immunoglobulin kappa-chain; immunoglobulin light chain; processed gene.
SOURCE	Mus musculus (house mouse)
ORGANISM	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 303)
AUTHORS	Kavaler, J., Caton, A. J., Staudt, L. M., Schwartz, D. and Gerhard, W.
TITLE	A set of closely related antibodies dominates the primary antibody response to the antigenic site CB of the A/P/8/34 Influenza virus hemagglutinin
JOURNAL	J. Immunol. 145 (7), 2312-2321 (1990)
MEDLINE	90375932
PUBMED	2118933
COMMENT	Original source text: Mouse (strain BALB/c), cDNA to mRNA, from hybridoma H220-23. Draft entry and computer-readable sequence for [J. Immunol. (1990) in press] kindly submitted by J.Kavaler, 06-JUL-1990.
FEATURES	Location/Qualifiers
SOURCE	1. 303
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	/db_xref="taxon:10090"
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	/note="anti-idiotypic antibody 11D10; mimics a breast cancer-associated antigen, human fat globule (HMFG)"
	/codon_start=1
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	/protein_id="AAK55120.1"
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	/translation="MRAPQILGLFLLPFTGRCDIQMTQSPSSLSASLGRVSLTCSR
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BASE COUNT	90 a 93 c 89 g 109 t
ORIGIN	
Query Match	86.7%; Score 377; DB 10; Length 381;
Best Local Similarity	100.0%; Pred. No. 3e-222;
Matches	377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	5 GGGCCCTGCTCAGATTCCTGGTCTCTGTGCTCTGTTTCCAGGTACCAGATGTGACA 64
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QY	65 TCCAGATGACCCAGTCTCCATCCCTCTATCTGCTCTCTGGGACAAAGAGTCAGTCTCA 124
DB	65 TCCAGATGACCCAGTCTCCATCCCTCTATCTGCTCTCTGGGACAAAGAGTCAGTCTCA 124
QY	125 CTTGTGCGGCAAGTCAGGACATTCGGTATTAACCTTACATTTGCTTCAGCAGAACCCAGATG 184
DB	125 CTTGTGCGGCAAGTCAGGACATTCGGTATTAACCTTACATTTGCTTCAGCAGAACCCAGATG 184
QY	185 GAACATTAAAGCCTGTATACGCCACATCCAGTTAGTCTGGTCTCCCAAAAGGT 244
DB	185 GAACATTAAAGCCTGTATACGCCACATCCAGTTAGTCTGGTCTCCCAAAAGGT 244
QY	245 TCAGTGGCAGTAGGTCTGGTGCAGATTATCTTCACCATCAGCAGCCTTGAGTCTGAAG 304
DB	245 TCAGTGGCAGTAGGTCTGGTGCAGATTATCTTCACCATCAGCAGCCTTGAGTCTGAAG 304
QY	305 ATTTGTAGCCTATTACTGTCTACAATATGCTAGTCTCCGTACACCTTCGGAGGGGGA 364
DB	305 ATTTGTAGCCTATTACTGTCTACAATATGCTAGTCTCCGTACACCTTCGGAGGGGGA 364
QY	365 CCAAGCTGGAATAAAA 381
DB	365 CCAAGCTGGAATAAAA 381
RESULT 4	
AF163749	321 bp mRNA linear ROD 20-JUL-2001
LOCUS	
DEFINITION	Mus musculus mab 49.8.9 immunoglobulin light chain variable region mRNA, partial cds.
ACCESSION	AF163749
VERSION	GI:5690304
KEYWORDS	
SOURCE	Mus musculus (house mouse)
ORGANISM	
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 321)
AUTHORS	Mertens, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.
TITLE	Molecular analysis of cross-reactive anti-myosin/anti-streptococcal mouse monoclonal antibodies
JOURNAL	Mol. Immunol. 37 (15), 901-913 (2000)
MEDLINE	21179651
PUBMED	11282394
COMMENT	2 (bases 1 to 321)
AUTHORS	Mertens, N.M. and Cunningham, M.W.
TITLE	Direct Submission

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/strain="BALB/c"
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Query Match      24.8%; Score 108; DB 10; Length 303;
Best Local Similarity 99.0%; Pred. No. 5.8e-55;
Matches 208; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 163 TGGCTTCAGCAGGACCAAGTGGACACTATTAAACGCCTGATCTACGCCACATCCAGTTTA 222
Db 85 TGGCTTCAGCAGGACCAAGTGGACACTATTAAACGCCTGATCTACGCCACATCCAGTTTA 144
QY 223 GGTTCGTGTGCCCAAAAGGTTTCAGTGGCAGTAGGTCGTGGTCAGATTATTCCTCACC 282
Db 145 GATTCTGTGTGCCCAAAAGGTTTCAGTGGCAGTAGGTCGTGGTCAGATTATTCCTCACC 204
QY 283 ATCAGCAGCCTTGAGTCTGAAGATTTGTAGCCCTATTACTGTCTACAAATATGCTAGTTCT 342
Db 205 ATCAGCAGCCTTGAGTCTGAAGATTTGTAGCTATTACTGTCTACAAATATGCTAGTTCT 264
QY 343 CCGTACACGTTCCGAGGGGGGACCAAGCTG 372
Db 265 CCGTACACGTTCCGAGGGGGGACCAAGCTG 294
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RESULT 6
AX722008 LOCUS      324 bp      DNA      linear      PAT 07-MAY-2003
DEFINITION      Sequence 2 from Patent WO03025181.
ACCESSION      AX722008
VERSION      AX722008.1 GI:30422583
KEYWORDS      synthetic construct
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1
AUTHORS      Moser,M. and Oesch,B.
TITLE      Dna sequences that encode variable regions of antibodies that bind
JOURNAL      to the prion protein (prp), and prp-binding polypeptides
Prionics AG (CH) Patent: WO 03025181-A 2 27-MAR-2003;
FEATURES      source
BASE COUNT      82 a  79 c  77 g  86 t
ORIGIN
Query Match      24.8%; Score 108; DB 6; Length 324;
Best Local Similarity 99.4%; Pred. No. 5.8e-55;
Matches 158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 225 TTCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGGTCGTGGTCAGATTATTCCTCACCAT 284
Db 165 TTCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGGTCGTGGTCAGATTATTCCTCACCAT 224
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285 CAGCAGCCTTCAGTCTCAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCC 344
225 CAGCAGCCTTCAGTCTCAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCC 284
345 GTACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAACG 383
285 GTACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAACG 323
RESULT 7
MMU55588 LOCUS      302 bp      mRNA      linear      ROD 14-SEP-2001
DEFINITION      Mus musculus anti-DNA immunoglobulin light chain IgG, antibody
363s.62, partial cds.
ACCESSION      U55588
VERSION      U55588.1 GI:1870291
KEYWORDS      Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 302)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Krishnan,M.R., Jou,N.T. and Marion,T.N.
TITLE      Correlation between the amino acid position of arginine in VH-CDR3
and specificity for native DNA among autoimmune antibodies
JOURNAL      J. Immunol. 157 (6), 2430-2439 (1996)
MEDLINE      96399071
PUBMED      8805642
REFERENCE      2 (bases 1 to 302)
AUTHORS      Marion,T.N.
TITLE      Direct Submission
JOURNAL      Submitted (18-APR-1996) Tony N. Marion, Dept. of
Microbiology/Immunology, University of Tennessee, 858 Madison Ave.,
Memphis, TN 38163, USA
FEATURES      source
BASE COUNT      74 a  72 c  71 g  84 t  1 others
ORIGIN
Query Match      24.6%; Score 107; DB 10; Length 302;
Best Local Similarity 99.0%; Pred. No. 2.4e-54;
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QY 283 ATCAGCAGCCTTCAGTCTGAAGATTTTGTAGCCCTATTACTGTCTACAATATGCTAGTTCT 342
Db 214 ATCAGCAGCCTTCAGTCTGAAGATTTTGTAGCATTACTGTCTACAATATGCTAGTTCT 273
QY 343 CCGTACACGTTCCGAGGGGGGACCAAGCT 371
Db 274 CCGTACACGTTCCGAGGGGGGACCAAGCT 302
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RESULT 8	AX256284	756 bp	DNA	linear	PAT 10-OCT-2001
LOCUS	AX256284	Sequence 54 from Patent WO0171005.			
DEFINITION	AX256284				
ACCESSION	AX256284.1	GI:16075160			
VERSION					
KEYWORDS		synthetic construct			
SOURCE		synthetic construct			
ORGANISM		artificial sequences.			
REFERENCE	1				
AUTHORS		Kufer, P., Rietmuller, G., Lutterbuese, R., Borschert, K., Kischel, R., Mayer, M. and Hofmeister, R.			
TITLE		Multifunctional polypeptides comprising a binding site to an epitope of the nkx2d receptor complex			
JOURNAL		Patent: WO 0171005-A 54 27-SEP-2001;			
		Kufer, Peter (DE)			

BASE COUNT		184 a		180 c		204 g		188 t	
ORIGIN									
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Best Local Similarity	99.0%;	Pred. No. 2.5e-54;							
Matches 207;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;					
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Db	502	TGGCTTCAGCAGGAAC	CAGATGGAAC	TATTAAACGCCTGATCTACGCCACATCCAGTTTA	561				
QY	223	GGTCTGGTCTCCCCAAAGGTT	CAGTGGGCAGTAGGTC	TGGGTGAGATTATTCCTCACC	282				
Db	562	GATTCTGGTGTCCCCAAAGGTT	CAGTGGGCAGTAGGTC	TGGGTGAGATTATTCCTCACC	621				
QY	283	ATCAGCAGCCTTCGAGTCTGAAGATTTTGTAGCCCTATTAC	TGCTACAAATATGCTAGTTCT	342					
Db	622	ATCAGCAGCCTTCGAGTCTGAAGATTTTGTAGACTATTAC	TGCTACAAATATGCTAGTTCT	681					
QY	343	CCGTACACGTTCCGAGGGGGACCAAGCT	371						
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[illegible]

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KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 387)
AUTHORS       Anand,N.N., Barber,B.H., Cates,G.C., Caterini,J.E. and Klein,M.H.
TITLE        Chimeric antibodies for delivery of antigens to selected cells of
              the immune system
JOURNAL      Patent: US 6291208-A 1 18-SEP-2001;
FEATURES     Location/Qualifiers
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Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 102 TCTGGGCAAGAGTCACTCTCACTTCTCGGGCAAGTCAGGA 143
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Db 108 TCTGGGCAAGAGTCACTCTCACTTCTCGGGCAAGTCAGGA 149
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RESULT 12
MMVJIG7      269 bp DNA linear ROD 25-JUL-2002
LOCUS       Mouse rearranged kappa immunoglobulin light chain (V.J).
ACCESSION   X54760
VERSION     X54760.1 GI:21998644
KEYWORDS    Ig light chain; immunoglobulin.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   Harada,K. and Yamagishi,H.
AUTHORS     Harada,K. and Yamagishi,H.
TITLE       Lack of feedback inhibition of V kappa gene rearrangement by
            productively rearranged alleles
JOURNAL     J. Exp. Med. 173 (2), 409-415 (1991)
MEDLINE     91108338
PUBMED      1988542
REFERENCE   2 (bases 1 to 269)
AUTHORS     Yamagishi,H.
TITLE       Direct Submission
JOURNAL     Submitted (02-OCT-1990) Yamagishi H., Dept of Biophysics Faculty of
            Science Kyoto University, Sakyo-ku Kyoto 606, Japan
FEATURES    Location/Qualifiers
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74 t

misc_feature  69 a 61 c 65 g 74 t
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Best Local Similarity 99.3%; Pred. No. 5.5e-50;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 163 TGGCTTCAGCAGGAACCAAGATGGAACATATTAAACGCCCTGATCTACGCCACATCCAGTTTA 222
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Db 47 TGGCTTCAGCAGGAACCAAGATGGAACATATTAAACGCCCTGATCTACGCCACATCCAGTTTA 106
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QY 223 GGTTCCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGGTACAGATTATTTCTTCACC 282
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Db 107 GATTCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGGTACAGATTATTTCTTCACC 166
      |||||||
QY 283 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 313
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Db 167 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 197
      |||||||
RESULT 13
MMU21066     273 bp mRNA linear ROD 14-FEB-1996
LOCUS       Mus musculus immunoglobulin kappa chain V-J regions mRNA, clone
DEFINITION  MRL3-7, partial cds.
ACCESSION   U21066
VERSION     U21066.1 GI:699556
KEYWORDS    Mus musculus (house mouse)
SOURCE      Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 273)
AUTHORS     Roark,J.H., Kuntz,C.L., Nguyen,K.A., Mandik,L., Cattermole,M. and
            Erikson,J.
TITLE       B cell selection and allelic exclusion of an anti-DNA Ig transgene
            in MRL-lpr/lpr mice
JOURNAL     J. Immunol. 154 (9), 4444-4455 (1995)
MEDLINE     95238942
PUBMED      772301
REFERENCE   2 (bases 1 to 273)
AUTHORS     Roark,J.H.
TITLE       Direct Submission
JOURNAL     Submitted (15-FEB-1995) Jessica H. Roark, Wistar Institute, 3601
            Spruce St., Philadelphia, PA 19104, USA
FEATURES    Location/Qualifiers
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BASE COUNT   68 a 63 c 66 g 76 t
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Query Match  23.0%; Score 100; DB 10; Length 273;
Best Local Similarity 99.3%; Pred. No. 5.5e-50;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 66 TGGCTTCAGCAGAACCCAGATGGAACACTATTAAACGCGCTGATCTAGCCACATCCAGTTTA 125
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QY 223 GGTTCCTGGTGTCCTCCCAAGGTTTCAGTGGCAGTAGGCTCGGCTCAGATTATTCTCTCACC 282
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Db 126 GATTCTGGTGTCCTCCCAAGGTTTCAGTGGCAGTAGGCTCGGCTCAGATTATTCTCTCACC 185
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QY 283 ATCAGCAGCCTTGAGCTCTGAAGATTTTGTAG 313
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RESULT 14
AR026090

LOCUS AR026090 276 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 44 from patent US 5855885.
ACCESSION AR026090
VERSION AR026090.1 GI:5936930
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 276)

AUTHORS Smith, R., McCafferty, J., Chiswell, D., Darsley, M. J., Fitzgerald, K.,
Kenten, J. H., Martin, M. T., Titmas, R. C. and Williams, R. O.

TITLE Isolation and production of catalytic antibodies using phage

technology

JOURNAL Patent: US 5855885-A 44 05-JAN-1999;

FEATURES Location/Qualifiers

source

1..276

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BASE COUNT 68 a 65 c 63 g 80 t

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Query Match 23.0%; Score 100; DB 6; Length 276;
Best Local Similarity 99.3%; Pred. No. 5.5e-50;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 79 TGGCTTCAGCAGAACCCAGATGGAACACTATTAAACGCGCTGATCTAGCCACATCCAGTTTA 138
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QY 223 GGTTCCTGGTGTCCTCCCAAGGTTTCAGTGGCAGTAGGCTCGGCTCAGATTATTCTCTCACC 282
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QY 283 ATCAGCAGCCTTGAGCTCTGAAGATTTTGTAG 313
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Db 199 ATCAGCAGCCTTGAGCTCTGAAGATTTTGTAG 229
|||||

RESULT 15

AR026094

LOCUS AR026094 276 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 52 from patent US 5855885.
ACCESSION AR026094
VERSION AR026094.1 GI:5936934
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE

1 (bases 1 to 276)

AUTHORS Smith, R., McCafferty, J., Chiswell, D., Darsley, M. J., Fitzgerald, K.,
Kenten, J. H., Martin, M. T., Titmas, R. C. and Williams, R. O.

TITLE Isolation and production of catalytic antibodies using phage

technology

JOURNAL Patent: US 5855885-A 52 05-JAN-1999;

FEATURES Location/Qualifiers

source

1..276

/organism="unknown"

BASE COUNT 67 a 65 c 64 g 80 t

ORIGIN

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Best Local Similarity 99.3%; Pred. No. 5.5e-50;
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QY 223 GGTTCCTGGTGTCCTCCCAAGGTTTCAGTGGCAGTAGGCTCGGCTCAGATTATTCTCTCACC 282
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QY 283 ATCAGCAGCCTTGAGCTCTGAAGATTTTGTAG 313
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Searched: 2552736 seqs, 1349719017 residues

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	435	100.0	435	18 AAT85149	Murine monoclonal
2	435	100.0	435	20 AAV83772	Antibody 11D10 lig
3	435	100.0	435	25 AAL51273	Mouse 11D10 antibo
4	107	24.6	756	24 AAS97136	P4-3 single chain
5	107	24.6	771	24 AAS97142	P5-10 single chain
6	107	24.6	1497	24 AAS97145	3B10xP4-3 bispecif
7	102	23.4	387	18 AAT77851	Murine anti-human
8	102	23.4	387	24 AAD32138	Murine 44H104 mab

9	100	23.0	276	20 AAX00879	Mouse derived RT3
10	100	23.0	276	20 AAX00875	Mouse derived RT3
11	100	23.0	450	4 AAN30165	Sequence encoding
12	93	21.4	535	19 AAV20086	Consensus DNA sequ
13	90	20.7	438	16 AAO90431	DNA encoding anti-bo
14	86	19.8	979	24 ABE52791	Murine m166 antibo
15	85	19.5	642	18 AAT85091	Mouse monoclonal a
16	85	19.5	651	21 AAA44346	Human secreted exp
17	85	19.5	652	17 AAT87818	Antibody 3G2 light
18	85	19.5	654	25 ACC44908	TSH receptor antib
19	85	19.5	654	25 ACC44909	TSH receptor antib
20	85	19.5	678	21 AAA27849	WOW-1 Fab light ch
21	85	19.5	698	25 ABE16574	Mouse DNA encoding
22	85	19.5	723	16 AAO92503	Mouse antibody F4-
23	85	19.5	738	21 AAZ61037	Nucleotide sequenc
24	84	19.3	639	10 AAN91657	Chimeric antibody
25	83	19.1	465	16 AAO85387	MAB 4197X light ch
26	82	18.9	324	21 AAZ49534	Mouse anti-IL-18 a
27	82	18.9	407	21 AAZ49548	Mouse light chain
28	82	18.9	711	21 AAZ49542	PEscFv#125-2H reco
29	82	18.9	729	21 AAZ49543	PEscFv#125-2H HT r
30	81	18.6	882	14 AAQ48038	Monoclonal antibod
31	80	18.4	654	25 ACC44928	TSH receptor antib
32	80	18.4	654	25 ACC44929	TSH receptor antib
33	80	18.4	729	25 ABE16570	Mouse DNA encoding
34	79	18.2	426	22 AAD13177	Murine antibody 1D
35	79	18.2	438	18 AAT70809	Mouse anti-idiotyp
36	79	18.2	537	12 AAQ14801	Encodes murine ant
37	79	18.2	537	12 AAQ14651	R6-5-D6 anti-ICAM-
38	78	17.9	366	13 AAQ27140	ICAM-1 inhibiting
39	78	17.9	451	21 AAA43470	Mouse secreted exp
40	77	17.7	504	25 ABE16572	Mouse DNA encoding
41	73	16.8	321	21 AAA38909	650E2 hybridoma VL
42	73	16.8	456	22 AAC66996	Filamentous phage
43	73	16.8	867	22 AAC67002	Filamentous phage
44	70	16.1	360	18 AAT96344	cDNA for Ig light
45	70	16.1	1848	18 AAT96346	Chimeric gene cont

ALIGNMENTS

RESULT 1
AAT85149
ID AAT85149 standard; cDNA; 435 BP.
XX
AC AAT85149;
XX
XX
DT 25-MAR-2003 (updated)
DT 04-JAN-1998 (first entry)
XX
DE Murine monoclonal anti-idiotyp antibody 11D10 VL cDNA.
XX
KW Monoclonal antibody 11D10; anti-idiotyp antibody; mucin;
KW human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss.
XX
OS Mus musculus.
XX
FH Key
FT sig_peptide Location/Qualifiers
FT mat_peptide 1..60
FT 61..435 /*tag= a
FT /*tag= b

WO9722699-A2.

XX
XX
PD 26-JUN-1997.
XX
XX
PF 19-DEC-1996; 96WO-US20757.
XX
XX
PR 20-DEC-1995; 95US-0575762.
PR 26-JAN-1996; 96US-0591965.
PR 13-DEC-1996; 96US-0766350.

XX PA (KENT) UNIV KENTUCKY.
 XX PI Chatterjee M, Chatterjee SK, Foon KA;
 XX DE WPI; 1997-341690/31.
 DR DR P-PSDB; AAW27119.
 XX Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
 PT against human milk fat globule disease associated tumours,
 PT especially breast cancer
 XX
 PS Claim 11; Page 94; 130pp; English.
 XX
 CC This cDNA sequence encodes the light chain variable region VL
 CC (AAW85149) of monoclonal anti-idiotypic antibody 11D10 produced by
 CC hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
 CC naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotypic
 CC response. It elicits an immune response against a specific epitope
 CC of a high mol.wt. mucin of human milk fat globule (HMFG). It
 CC induces an immunological response to HMFG in mice, rabbits, monkeys
 CC and patients with advanced HMFG-associated tumours. Pharmaceutical
 CC compositions and vaccines comprising 11D10, 11D10 polypeptides
 CC and/or 11D10 polynucleotides are claimed. Also claimed are
 CC diagnostic kits and methods of using 11D10, 11D10 polypeptides
 CC and/or 11D10 polynucleotides, including methods of treating HMFG-
 CC associated tumours.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;

Query Match 100.0%; Score 435; DB 18; Length 435;
 Best Local Similarity 100.0%; Pred. No. 6.5e-210;
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGCCCCCTGCTCAGATCTTGGGTTCTTGTGCTCTTGTTCAGGTACACAGTGT 60
 DB 1 ATGGGGCCCCCTGCTCAGATCTTGGGTTCTTGTGCTCTTGTTCAGGTACACAGTGT 60
 QY 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCCCTCTCTGGGACAAAGAGTCAGT 120
 DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCCCTCTCTGGGACAAAGAGTCAGT 120
 QY 121 CTCACCTGTGCGGCAAGTCAGGACATGGTATTAACTTACATTGCTTCCAGGTACACCA 180
 DB 121 CTCACCTGTGCGGCAAGTCAGGACATGGTATTAACTTACATTGCTTCCAGGTACACCA 180
 QY 181 GATGGAACTATTAAACCCCTGATCTAGCCACATCCAGTTAGTGTCTGCTGCCCAAA 240
 DB 181 GATGGAACTATTAAACCCCTGATCTAGCCACATCCAGTTAGTGTCTGCTGCCCAAA 240
 QY 241 AGGTTTCAGTGGCAGTAGGCTTGGGTCAGATTTATCTCTACCATCAGCAGCCTTGAGTCT 300
 DB 241 AGGTTTCAGTGGCAGTAGGCTTGGGTCAGATTTATCTCTACCATCAGCAGCCTTGAGTCT 300
 QY 301 GAGATTTTGTAGCTATTACTGTCTACATATAGTGTCTCGGTACAGTTCCGGAGG 360
 DB 301 GAGATTTTGTAGCTATTACTGTCTACATATAGTGTCTCGGTACAGTTCCGGAGG 360
 QY 361 GGGACCAAGCTGGAAATAAACGGGCTGATGCTGTCACCAACTGTATCCATCTTCCACCA 420
 DB 361 GGGACCAAGCTGGAAATAAACGGGCTGATGCTGTCACCAACTGTATCCATCTTCCACCA 420
 QY 421 TCCAGTAAGCTTGGG 435
 DB 421 TCCAGTAAGCTTGGG 435

RESULT 2
 AAW83772
 ID AAW83772 standard; cDNA; 435 BP.
 XX
 AC AAW83772;

XX 16-MAR-1999 (first entry)
 XX DT Antibody 11D10 light chain variable region coding sequence.
 XX DE Murine; mouse; antibody; light chain; variable region; anti-idiotypic; ss;
 KW human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
 XX
 XX Mus sp.
 XX OS
 PH Key Location/Qualifiers
 FT CDS 1..435
 FT /tag= a
 FT /product= "antibody 11D10 light chain variable region"
 FT /transl_except= (pos:163..165, aa:Thr)
 FT /note= "no stop codon is given at the 3' end of the
 FT sequence"
 FT sig_peptide 1..60
 FT /tag= b
 FT mat_peptide 61..435
 FT /tag= c
 XX WO9856419-A1.
 PN
 XX 17-DEC-1998.
 PD
 XX 12-JUN-1998; 98WO-US12250.
 XX
 XX 11-JUN-1998; 98US-0096244.
 PR 13-JUN-1997; 97US-0049540.
 XX
 XX (KENT) UNIV KENTUCKY RES FOUND.
 PA
 XX Chatterjee M, Foon KA;
 PI
 XX WPI; 1999-060029/05.
 DR P-PSDB; AAW87593.
 XX
 PT Delaying development of, or treating, HMFG-associated tumours -
 PT using anti-idiotypic antibody 11D10 raised against antibodies to
 PT human milk fat globule protein
 XX
 PS Disclosure; Fig 1; 54pp; English.
 XX
 CC This sequence represents the coding sequence for the murine antibody
 CC 11D10 light chain variable region. This anti-idiotypic antibody is used
 CC to delay the development of, or treat, a human milk fat globule (HMFG)
 CC associated tumour in an individual having low tumour burden.
 CC The antibody 11D10 is used to prevent the recurrence of HMFG-associated
 CC tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma,
 CC especially for treating breast tumours.
 XX
 SQ Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;

Query Match 100.0%; Score 435; DB 20; Length 435;
 Best Local Similarity 100.0%; Pred. No. 6.5e-210;
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGCCCCCTGCTCAGATCTTGGGTTCTTGTGCTCTTGTTCAGGTACACAGTGT 60
 DB 1 ATGGGGCCCCCTGCTCAGATCTTGGGTTCTTGTGCTCTTGTTCAGGTACACAGTGT 60
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 DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCCCTCTCTGGGACAAAGAGTCAGT 120
 QY 121 CTCACCTGTGCGGCAAGTCAGGACATGGTATTAACTTACATTGCTTCCAGGTACACCA 180
 DB 121 CTCACCTGTGCGGCAAGTCAGGACATGGTATTAACTTACATTGCTTCCAGGTACACCA 180
 QY 181 GATGGAACTATTAAACCCCTGATCTAGCCACATCCAGTTAGTGTCTGCTGCCCAAA 240
 DB 181 GATGGAACTATTAAACCCCTGATCTAGCCACATCCAGTTAGTGTCTGCTGCCCAAA 240

QY 241 AGGTTACAGTGGCAGTAGCTGGGTCAGATTATCTCTCACCATCAGCAGCCTTGAGTCT 300
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 Db 241 AGGTTACAGTGGCAGTAGCTGGGTCAGATTATCTCTCACCATCAGCAGCCTTGAGTCT 300
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 Db 361 GGGACCAAGCTGGAATAAAAGGGGCTGATGCTGACCAACGTATCCATCTTCCACCA 420
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 QY 421 TCCAGTAAGCTTGGG 435
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 Db 421 TCCAGTAAGCTTGGG 435
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RESULT 3

AAL51273
 ID AAL51273 standard; cDNA; 435 BP.

AC AAL51273;

DT 20-MAR-2003 (first entry)

DE Mouse l1d10 antibody light chain variable region coding sequence.

KW Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; HMFG;
 KW carcinoembryonic antigen; CEA; l1d10; 3H1; HMFG-associated tumour;
 KW CEA-associated tumour; anti-idiotype antibody.

OS Mus musculus.

FH Key Location/Qualifiers

FT 1..435

FT /*tag- a

FT /partial

FT /product- "Mouse l1d10 anti-idiotype antibody light chain

FT variable region"

FT /note- "No stop codon is given"

FT sig_peptide 1..60

FT /*tag- b

FT mat_peptide 61..435

FT /*tag- c

PN WO200292012-A2.

PD 21-NOV-2002.

PF 17-MAY-2002; 2002WO-US15840.

PR 17-MAY-2001; 2001US-0861294.

PA (KENT) UNIV KENTUCKY RES FOUND.

PI Chatterjee M, Foon KA;

PI WPI: 2003-129216/12.

DR P-PSDB; AA016292.

XX Use of anti-idiotypic antibodies for human milk fat globules (HMFG) - or

PT carcinoembryonic antigen (CEA)-associated tumor for delaying the

PT development of, or treating a HMFG- or CEA-associated tumor (e.g.

PT breast tumor) in humans

XX Disclosure; Fig 1; 98pp; English.

XX The invention comprises a method for delaying the development of, or

CC treating a tumour that is associated with human milk fat globules (HMFG)

CC or carcinoembryonic antigen (CEA). The method of the invention involves

CC administering an anti-idiotypic antibody for HMFG (e.g. l1d10), and an

CC anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for

CC delaying the development, of or treating HMFG/CEA-associated tumours. The
 CC present cDNA sequence encodes the light chain variable region of the
 CC mouse l1d10 anti-idiotype antibody.

SQ Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;

Query Match 100.0%; Score 435; DB 25; Length 435;
 Best Local Similarity 100.0%; Pred. No. 6.5e-210;
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGGCCCCGCTCAGATTCTTGGGTTCTTGTGCTCTTGTTCACAGTACCAGATGT 60
 |||||
 Db 1 ATGGGGGGCCCCGCTCAGATTCTTGGGTTCTTGTGCTCTTGTTCACAGTACCAGATGT 60
 |||||

QY 61 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCTCTCTGGGACAAAGAGTCACT 120
 |||||
 Db 61 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCTCTCTGGGACAAAGAGTCACT 120
 |||||

QY 121 CTCACCTTGTGGGCAAGTCAGGACATTTGGTATTAACCTTACATTTGCTTCAGCAGGAACCA 180
 |||||
 Db 121 CTCACCTTGTGGGCAAGTCAGGACATTTGGTATTAACCTTACATTTGCTTCAGCAGGAACCA 180
 |||||

QY 181 GATGGAACCTATTAAACGGCTGATCTACGCCACATCCAGTTTAGTGTCTGCTCCCAAA 240
 |||||
 Db 181 GATGGAACCTATTAAACGGCTGATCTACGCCACATCCAGTTTAGTGTCTGCTCCCAAA 240
 |||||

QY 241 AGGTTACAGTGGCAGTAGGTCCTGGGTCAGATTATCTCTCACCATCAGCAGCCTTGAGTCT 300
 |||||
 Db 241 AGGTTACAGTGGCAGTAGGTCCTGGGTCAGATTATCTCTCACCATCAGCAGCCTTGAGTCT 300
 |||||

QY 301 GAAGATTTGTAGCCTATTACTGTCTACAATATGCTTCTCCGTCACAGTTTCGGAGGG 360
 |||||
 Db 301 GAAGATTTGTAGCCTATTACTGTCTACAATATGCTTCTCCGTCACAGTTTCGGAGGG 360
 |||||

QY 361 GGGACCAAGCTGGAATAAAAGGGGCTGATGCTGACCAACGTATCCATCTTCCACCA 420
 |||||
 Db 361 GGGACCAAGCTGGAATAAAAGGGGCTGATGCTGACCAACGTATCCATCTTCCACCA 420
 |||||

QY 421 TCCAGTAAGCTTGGG 435

Db 421 TCCAGTAAGCTTGGG 435

RESULT 4

AAS97136

ID AAS97136 standard; DNA; 756 BP.

AC AAS97136;

DT 26-FEB-2002 (first entry)

DE P4-3 single chain Fv DNA.

KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
 KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
 KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
 KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
 KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; ds;
 KW helminth; cytostatic; antimicrobial; immunomodulatory; P4-2; P4-3; P4-14;
 KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
 KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.

OS Homo sapiens.

PN WO200171005-A2.

XX 27-SEP-2001.

XX 26-MAR-2001; 2001WO-EP03414.

XX 24-MAR-2000; 2000EP-0106467.

XX (KUFE/) KUFER P.

```
XX Kufer P, Rietmueller G, Lutterbuese R, Borschert K, Kischel R;
PI Mayer M, Hofmeiester R;
XX WPI; 2002-055119/07.
DR P-PSDB; AAU/2862.
XX
XX Multifunctional polypeptides comprising binding sites that specifically
PT recognise extracellular groups of the NKG2D receptor complex and
PT domains which function as receptors or ligands, useful for treating
PT cancers and infectious diseases -
XX
XX Example 7; Fig 16; 114pp; English.
XX
XX The invention relates to a multifunctional polypeptide comprising a
XX domain with a binding site that specifically recognises an extracellular
XX group of the NKG2D receptor complex and a second domain which functions
XX as a receptor or ligand. The polypeptide and its associated
XX polynucleotide are used for the preparation of a pharmaceutical
XX composition for the treatment of cancer, infections and/or autoimmune
XX conditions. The cancer may be a tumour of the head and neck, stomach,
XX oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
XX larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
XX bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
XX The infectious diseases can be caused by viruses, bacteria, fungi,
XX protozoa or helminths. The autoimmune diseases include multiple
XX sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
XX uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
XX diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
XX autoimmune hepatitis. The sequences represent DNA encoding the
XX polypeptides of the invention.
XX
XX Sequence 756 BP; 184 A; 180 C; 204 G; 188 T; 0 other;
XX
XX Query Match 24.6%; Score 107; DB 24; Length 756;
XX Best Local Similarity 99.0%; Pred. No. 5.5e-44;
XX Matches 207; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 163 TGGCTTCAGCAGGAACACAGATGGAAGTATTTAAACGGCTGATCTACGCCATCCAGTTTA 222
XX 502 TGGCTTCAGCAGGAACACAGATGGAAGTATTTAAACGGCTGATCTACGCCATCCAGTTTA 561
XX 223 GGTTCCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGTCTGGGTCAGATTATTCCTCACC 282
XX 562 GATTCCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGTCTGGGTCAGATTATTCCTCACC 621
XX 283 ATCAGCAGCCTTCAGTCTGAAGATTTTGTAGCCCTATTACTGTCTACAATATGCTAGTTCT 342
XX 622 ATCAGCAGCCTTCAGTCTGAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCT 681
XX
XX 343 CCGTACACGTTCCGAGGGGGGACCAAGCT 371
XX 682 CCGTACACGTTCCGAGGGGGGACCAAGCT 710
XX
XX RESULT 5
XX ID AAS97142
XX AC AAS97142;
XX
XX 26-FEB-2002 (first entry)
XX
XX p5-10 single chain Fv DNA.
XX
XX Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
XX autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
XX intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
XX prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
XX sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; ds;
XX helminth; cytostatic; antimicrobial; immunomodulatory; p4-2; p4-3; p4-14;
XX p4-15; p5-2; p5-3; p5-9; p5-10; p5-11; p5-23; 3B10xp4-3; 3B10xp4-14;
XX p53 tetramerisation domain; 3B10xp5-2; 3B10xp5-23.
```

```
XX Homo sapiens.
XX OS
XX PN WO200171005-A2.
XX XX
XX PD 27-SEP-2001.
XX
XX 26-MAR-2001; 2001WO-EP03414.
XX PF
XX 24-MAR-2000; 2000EP-0106467.
XX PR
XX (KUFE/) KUFER P.
XX
XX Kufer P, Rietmueller G, Lutterbuese R, Borschert K, Kischel R;
XX Mayer M, Hofmeiester R;
XX WPI; 2002-055119/07.
XX P-PSDB; AAU/2868.
XX
XX Multifunctional polypeptides comprising binding sites that specifically
XX recognise extracellular groups of the NKG2D receptor complex and
XX domains which function as receptors or ligands, useful for treating
XX cancers and infectious diseases -
XX
XX Example 7; Fig 16; 114pp; English.
XX
XX The invention relates to a multifunctional polypeptide comprising a
XX domain with a binding site that specifically recognises an extracellular
XX group of the NKG2D receptor complex and a second domain which functions
XX as a receptor or ligand. The polypeptide and its associated
XX polynucleotide are used for the preparation of a pharmaceutical
XX composition for the treatment of cancer, infections and/or autoimmune
XX conditions. The cancer may be a tumour of the head and neck, stomach,
XX oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
XX larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
XX bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
XX The infectious diseases can be caused by viruses, bacteria, fungi,
XX protozoa or helminths. The autoimmune diseases include multiple
XX sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
XX uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
XX diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
XX autoimmune hepatitis. The sequences represent DNA encoding the
XX polypeptides of the invention.
XX
XX Sequence 771 BP; 181 A; 190 C; 206 G; 194 T; 0 other;
XX
XX Query Match 24.6%; Score 107; DB 24; Length 771;
XX Best Local Similarity 99.0%; Pred. No. 5.5e-44;
XX Matches 207; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 163 TGGCTTCAGCAGGAACACAGATGGAAGTATTTAAACGGCTGATCTACGCCATCCAGTTTA 222
XX 517 TGGCTTCAGCAGGAACACAGATGGAAGTATTTAAACGGCTGATCTACGCCATCCAGTTTA 576
XX 223 GGTTCCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGTCTGGGTCAGATTATTCCTCACC 282
XX 577 GATTCCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGTCTGGGTCAGATTATTCCTCACC 636
XX 283 ATCAGCAGCCTTCAGTCTGAAGATTTTGTAGCCCTATTACTGTCTACAATATGCTAGTTCT 342
XX 637 ATCAGCAGCCTTCAGTCTGAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCT 696
XX 343 CCGTACACGTTCCGAGGGGGGACCAAGCT 371
XX 697 CCGTACACGTTCCGAGGGGGGACCAAGCT 725
XX
XX RESULT 6
XX ID AAS97145
XX AC AAS97145 standard; DNA; 1497 BP.
XX XX
XX AAS97145;
XX
```


DT 26-FEB-2002 (first entry)
DE 3B10xP4-3 bispecific single chain Fv DNA.
XX Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; ds;
KW helminth; cytotoxic; antimicrobial; immunomodulatory; P4-2; P4-3; P4-14;
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
XX Homo sapiens.
OS
XX
XX WO200171005-A2.
XX
XX 27-SEP-2001.
XX
XX 26-MAR-2001; 2001WO-EP03414.
XX
XX 24-MAR-2000; 2000EP-0106467.
XX (KUFE/) KUFER P.
XX
XX Kufer P, Riethmuller G, Lutterbuese R, Borschert K, Kischel R;
PI Mayer M, Hofmeister R;
XX
XX WPI: 2002-055119/07.
XX P-PSDB; AAU72871.
XX
XX Multifunctional polypeptides comprising binding sites that specifically
PT recognise extracellular groups of the NKG2D receptor complex and
PT domains which function as receptors or ligands, useful for treating
PT cancers and infectious diseases.
XX
XX Example 5; Fig 16; 114pp; English.
XX
XX The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NKG2D receptor complex and a second domain which functions
CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. The sequences represent DNA encoding the
XX polypeptides of the invention.
SQ Sequence 1497 BP; 364 A; 358 C; 407 G; 368 T; 0 other;
Query Match 24.6%; Score 107; DB 24; Length 1497;
Best Local Similarity 99.0%; Pred. No. 5.4e-44;
Matches 207; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 163 TGGCTTCAGCAGGACACAGATGGAACTATTAACGCCCTGATCTAGCCACATCCAGTTTA 222
DB TTTT
1243 TGGCTTCAGCAGGACACAGATGGAACTATTAACGCCCTGATCTAGCCACATCCAGTTTA 1302
QY 223 GGTTCGTGTCCTCCCAAGGTTTCAGTGGCAGATGGTCTGGGTGATGATTCTCTCACC 282
DB TTTT
1303 GATTCGTGTCCTCCCAAGGTTTCAGTGGCAGATGGTCTGGGTGATGATTCTCTCACC 1362
QY 283 ATCAGCAGCCTTGAGTCTGAAGATTTTCTAGCCTATTACTGCTACATATGCTAGTCT 342-
DB TTTT
1363 ATCAGCAGCCTTGAGTCTGAAGATTTTCTAGCCTATTACTGCTACATATGCTAGTCT 1422

QY 343 CCGTACAGTTCGGAGGGGGGACCAAGCT 371
DB 1423 CCGTACAGTTCGGAGGGGGGACCAAGCT 1451
RESULT 7
AAT77851
ID AAT77851 standard; cDNA; 387 BP.
XX
AC AAT77851;
XX
DT 03-NOV-1997 (first entry)
XX
DE Murine anti-human class II monoclonal antibody 44H104 VL chain cDNA.
XX
KW Antibody; light chain; variable region; hybridoma cell line 44H104;
KW immune response; enhance; stimulate; vaccine; immunodiagnosis;
KW antigen delivery; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 1..387
FT /*tag= a
FT /note= "Encodes 44H104 light chain variable region,
FT including secretion signal; termination
FT codon not given"
XX
PN WO9640941-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-CA00400.
XX
XX 07-JUN-1995; 95US-0483576.
XX
XX (CONN-) CONNAUGHT LAB LTD.
XX
XX Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH;
XX
XX WPI: 1997-077271/07.
XX P-PSDB; AAW22537.
XX
XX Recombinant conjugate antibody mol., modified for delivering an
PT antigen - elicits enhanced immune response without the use of
PT adjuvant to generate antibodies which are useful in vaccines or
PT immuno:diagnosis
XX
XX Example 1; Fig 1A; 64pp; English.
XX
XX Novel recombinant conjugate antibody molecules comprise a monoclonal
CC antibody specific for a surface structure of antigen presenting
CC cells (APC), genetically modified to contain at least one antigen
CC of delivering at one or more preselcted sites. The conjugate is capable
CC of delivering the antigen to APC and eliciting an immune response to
CC the antigen. The new conjugates are useful as vaccines and are able
CC to elicit an enhanced immune response without the use of an adjuvant.
CC In a specific example, a conjugate was constructed using the murine
CC anti-human class II monoclonal antibody secreted by hybridoma
CC 44H104. The peptide CLTB36 was chosen as antigen; it consists of
CC a tandemly linked T and B cell epitope derived from HIV MN strain.
CC The present sequence encodes the light chain variable region which
CC was PCR amplified from 44H104 and used in the preparation of a
CC conjugate with antigen CLTB36.
XX
SQ Sequence 387 BP; 90 A; 95 C; 90 G; 112 T; 0 other;
Query Match 23.4%; Score 102; DB 18; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.9e-41;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GTTCCAGGTACAGATGTCATCCAGATGACCATCCAGATGACCATCTCTTATCTGCTC 101

```

Db      48 GTTTCAGGTACCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCTTATCTGCCTC 107
      102 TCTGGGACAAAGAGTCAGTCTCACTTGTCTGGGCAAGTCAGGA 143
      108 TCTGGGACAAAGAGTCAGTCTCACTTGTCTGGGCAAGTCAGGA 149

RESULT 8
AAD32138
ID AAD32138 standard; DNA; 387 BP.
XX
AC AAD32138;
XX
DT 18-JUN-2002 (first entry)
XX
DE Murine 44H104 mab variable light chain (VL) DNA.
XX
KW Murine; mab; light chain; VL; conjugate antibody; antigen delivery;
KW immune system; vaccine; detecting agent; antibacterial; gene; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..387
FT /product= "Murine 44H104 mab VL"
FT /tag= a
FT /trans_except= (pos:277..279, aa:Thr)
FT /note= "this translation exception occurs while
FT decoding for murine mab VL alternative version
FT (AAE20204); CDS does not include stop codon"
FT /partial
XX
PN US2002025315-A1.
XX
XX
XX
PD 28-FEB-2002.
XX
XX
PF 14-JAN-1998; 98US-0007093.
XX
XX
PR 14-JAN-1998; 98US-0007093.
XX
XX
PA (ANAN/) ANAND N N.
PA (BARB/) BARBER B H.
PA (CATE/) CATES G A.
PA (CATE/) CATERINI J E.
PA (KLEI/) KLEIN M H.
XX
XX
PI Anand NN, Barber BH, Cates GA, Caterini JE, Klein MH;
XX
XX
WPI: 2002-267519/31.
DR P-PSDB; AAE20200, AAE20204.
XX
XX
Novel recombinant conjugate antibody, useful as a vaccine against
pathogens having a specific antigen, comprises a monoclonal antibody
specific for an antigen presenting cell surface structure -
XX
XX
Example 1; Fig 1A; 28pp; English.
XX
XX
The invention relates to a recombinant conjugate antibody, comprising
a monoclonal antibody specific for a surface structure of antigen
presenting cells genetically modified to contain an antigen moiety
for the purpose of delivery of the antigen moiety to antigen-
presenting cells of the immune system. The conjugate antibody is
formulated as a vaccine to protect a host against a disease caused
by a pathogen expressing the antigen. The antibody is useful as a
detecting agent. The present sequence is murine 44H104 mab variable
light chain (VL) DNA.
XX
SQ Sequence 387 BP; 90 A; 95 C; 90 G; 112 T; 0 other;
Query Match 23.4%; Score 102; DB 24; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.9e-41;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      42 GTTTCAGGTACCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCTTATCTGCCTC 101
      48 GTTTCAGGTACCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCTTATCTGCCTC 107
QY      102 TCTGGGACAAAGAGTCAGTCTCACTTGTCTGGGCAAGTCAGGA 143
      108 TCTGGGACAAAGAGTCAGTCTCACTTGTCTGGGCAAGTCAGGA 149
Db

RESULT 9
AAX00879
ID AAX00879 standard; DNA; 276 BP.
XX
AC AAX00879;
XX
DT 29-MAR-1999 (first entry)
XX
DE Mouse derived RT3 phage antibody light chain pattern C genetic sequence.
XX
KW Catalytic; antibody; phage display; immunising; phage expression vector;
KW produg; scfv; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..276
FT /tag= a
FT /note= "the start and stop codons are not indicated"
XX
PN US9855885-A.
XX
XX
XX
PD 05-JAN-1999.
XX
XX
PF 14-JUL-1994; 94US-0273146.
XX
XX
PR 22-JAN-1993; 93US-0007684.
PR 14-JUL-1994; 94US-0273146.
XX
XX
PA (CHIS/) CHISWELL D.
PA (DARS/) DARSLEY M J.
PA (FITZ/) FITZGERALD K.
PA (KENT/) KENTEN J H.
PA (MART/) MARTIN M T.
PA (MCCA/) MCCAFFERTY J.
PA (SMIT/) SMITH R.
PA (TITM/) TITMAS R C.
PA (WILL/) WILLIAMS R O.
XX
XX
PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;
XX
XX
WPI: 1999-105036/09.
DR P-PSDB; AAW95480.
XX
XX
Production of catalytic antibodies displayed on bacteriophages -
comprises generating a gene library of antibody-derived domains
inserting coding into a phage expression vector and isolating the
catalytic antibodies
XX
XX
Example 4; Fig 11; 117pp; English.
XX
XX
The invention relates to methods for producing catalytic antibodies
displayed on a phage. The method comprises: (a) generating a gene library
of antibody-derived domains; (b) inserting coding for the domains into a
phage expression vector; and (c) isolating the catalytic antibodies. The
phage expression vector incorporates a histidine peptide in tandem with a
myc peptide. The catalytic antibodies can be isolated by preparing an
antigen; optionally immunising an animal with the antigen; generating a
library of VH and VL domains from the immunised animal; cloning the VH
and VL domains into a phage expression vector to generate phage display
antibodies; selecting phage display antibodies which bind specifically
to the antigen; screening the selected phage display antibodies for

```

CC catalytic activity to substrate; and isolating the catalytic antibodies,
 CC where the phage expression vector incorporates a histidine peptide in
 CC tandem with a myc peptide. The processes are used to produce catalytic
 CC antibodies, which can be used for in vivo activation of a prodrug. The
 CC present sequence represents a genetic sequence of light chain PCR
 CC pattern C from mouse derived RT3 phage antibodies.

XX Sequence 276 BP; 67 A; 65 C; 64 G; 80 T; 0 other;

Query Match 23.0%; Score 100; DB 20; Length 276;
 Best Local Similarity 99.3%; Pred. No. 2e-40;
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 163 TGGCTTCAGCAGGAGCAGATGGAACCTATTAAACGGCTGATCTACGCCACATCCAGTTTA 222

Db 79 TGGCTTCAGCAGGAGCAGATGGAACCTATTAAACGGCTGATCTACGCCACATCCAGTTTA 138

QY 223 GGTTCGGTGTCCTCCCAAGAGTTTCAGTGGCAGTAGTCTGGGTCAGATTATCTCTCACC 282

Db 139 GATTCGGTGTCCTCCCAAGAGTTTCAGTGGCAGTAGTCTGGGTCAGATTATCTCTCACC 198

QY 283 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 313

Db 199 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 229

RESULT 10

AAAX00875

ID AAX00875 standard; DNA: 276 BP.

XX AAX00875;

XX 29-MAR-1999 (first entry)

XX Mouse derived RT3 phage antibody light chain pattern A genetic sequence.

XX Catalytic; antibody; phage display; immunising; phage expression vector;

XX prodrug; scFv; ss.

XX Mus sp.

XX Key Location/Qualifiers

FT CDS 1..276

FT /*tag= a

FT /note= "the start and stop codons are not indicated"

XX US5855885-A.

XX 05-JAN-1999.

XX 14-JUL-1994; 94US-0273146.

XX 22-JAN-1993; 93US-0007684.

XX 14-JUL-1994; 94US-0273146.

XX (CHIS/) CHISWELL D.

XX (DARS/) DARSLEY M J.

XX (FITZ/) FITZGERALD K.

XX (KENT/) KENTEN J H.

XX (MART/) MARTIN M T.

XX (MCCA/) MCCAFFERTY J.

XX (SMIT/) SMITH R.

XX (TITM/) TITMAS R C.

XX (WILL/) WILLIAMS R O.

XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;

PI Martin WT, McCafferty J, Smith R, Titmas RC, Williams RO;

XX WPI; 1999-105036/09.

DR P-PSDB; AAW95476.

XX Production of catalytic antibodies displayed on bacteriophages -

PT comprises generating a gene library of antibody-derived domains

PT inserting coding into a phage expression vector and isolating the
 catalytic antibodies

XX Example 4; Fig 9A-F; 117pp; English.

XX The invention relates to methods for producing catalytic antibodies
 displayed on a phage. The method comprises: (a) generating a gene library
 of antibody-derived domains; (b) inserting coding for the domains into a
 phage expression vector; and (c) isolating the catalytic antibodies. The
 phage expression vector incorporates a histidine peptide in tandem with a
 myc peptide. The catalytic antibodies can be isolated by preparing an
 antigen; optionally immunising an animal with the antigen; generating a
 library of VH and VL domains from the immunised animal; cloning the VH
 and VL domains into a phage expression vector to generate phage display
 antibodies; selecting phage display antibodies which bind specifically
 to the antigen; screening the selected phage display antibodies for
 catalytic activity to substrate; and isolating the catalytic antibodies,
 where the phage expression vector incorporates a histidine peptide in
 tandem with a myc peptide. The processes are used to produce catalytic
 antibodies, which can be used for in vivo activation of a prodrug. The
 present sequence represents a genetic sequence of light chain pattern A
 from mouse derived RT3 phage antibodies.

XX Sequence 276 BP; 68 A; 65 C; 63 G; 80 T; 0 other;

Query Match 23.0%; Score 100; DB 20; Length 276;

Best Local Similarity 99.3%; Pred. No. 2e-40;

Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 163 TGGCTTCAGCAGGAGCAGATGGAACCTATTAAACGGCTGATCTACGCCACATCCAGTTTA 222

Db 79 TGGCTTCAGCAGGAGCAGATGGAACCTATTAAACGGCTGATCTACGCCACATCCAGTTTA 138

QY 223 GGTTCGGTGTCCTCCCAAGAGTTTCAGTGGCAGTAGTCTGGGTCAGATTATCTCTCACC 282

Db 139 GATTCGGTGTCCTCCCAAGAGTTTCAGTGGCAGTAGTCTGGGTCAGATTATCTCTCACC 198

QY 283 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 313

Db 199 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 229

RESULT 11

AAAN30165

ID AAN30165 standard; DNA: 450 BP.

XX AAN30165;

XX 25-MAY-1992 (first entry)

XX Sequence encoding the leader, variable region and first 16 AAs of
 the constant region of the kappa-chain (light chain) of MOPC41.

XX Diagnosis; therapy; immunoglobulin; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 13..78

FT /*tag= a

FT /product= leader

FT CDS 79..402

FT /*tag= b

FT /product= variable region

FT CDS 403..450

FT /*tag= c

FT /product= constant region

XX EP88994-A.

XX 21-SEP-1983.

XX 10-MAR-1983; 83EP-0001655.

```

XX 15-MAR-1982; 820S-0358414.
PR 05-DEC-1983; 830S-0558551.
XX
XX (SCHE ) SCHERING CORP.
PA (DNAX-) DNAX RES INST.
XX
XX Moore KW, Zaffaroni A;
PI
XX WPI; 1983-772290/39.
DR P-PSDB; AAP30251.
XX
XX Transformed expression vectors or plasmid(s) - with double
PT stranded DNA sequence coding only for desired part of polypeptide
PT chain
XX
XX Example; Page 40-41; 68pp; English.
XX
XX The pref. vector or plasmid of the invention has a double-stranded
CC DNA seq. coding for a variable region of a light or heavy chain of
CC IgG, or for a variable region of a light or heavy chain of an
CC immunoglobulin specific for an enzyme or surface protein. The
CC sequence esp. codes for a variable region of a light chain having 95-
CC 115 AAs or for a variable region of a heavy chain having 110-125 AAs
CC esp. including the D region of the heavy chain.
XX
XX Sequence 450 BP; 108 A; 114 C; 104 G; 124 T; 0 other;
SQ
Query Match 23.0%; Score 100; DB 4; Length 450;
Best Local Similarity 99.3%; Pred. No. 1.9e-40;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 163 TGGCTTCAGCAGGAACACGATGGAACCTATTAAACGGCTGATCAGCCACATCCAGTTTA 222
DB 181 TGGCTTCAGCAGGAACACGATGGAACCTATTAAACGGCTGATCAGCCACATCCAGTTTA 240
QY 223 GGTCTGGTGTCGCCAAAGGTTTCAGTGGCAGTAGGTGGGTGAGATTATTCCTCACC 282
DB 241 GATTCTGGTGTCGCCAAAGGTTTCAGTGGCAGTAGGTGGGTGAGATTATTCCTCACC 300
QY 283 ATCAGCAGCCTTCAGTCTGAAGATTTTGTAG 313
DB 301 ATCAGCAGCCTTCAGTCTGAAGATTTTGTAG 331
RESULT 12
AAV20086
ID AAV20086 standard; DNA; 535 BP.
XX
XX AAV20086;
XX
XX 14-JUL-1998 (first entry)
XX
XX Consensus DNA sequence of the murine variable light chain region.
XX
XX Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KW Muscosal addressin cell adhesion molecule-1; MadCAM-1;
KW humanised antibody; murine antigen binding region; inhibition;
KW leukocyte infiltration of tissue; treatment; inflammatory disease;
KW inflammatory bowel disease; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FT CDS 16..435
FT FT /*tag= a
FT FT /note= "no stop codon given"
FT sig_peptide 16..75
FT /*tag= b
FT mat_peptide 76..435
FT /*tag= c
XX
XX WO9806248-A2.

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```

XX 19-FEB-1998.
XX
XX 06-AUG-1997; 97WO-US13884.
XX
XX 15-AUG-1996; 96US-0700737.
XX
XX (LEUK-) LEUKOSITE INC.
XX
XX Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
PI Saldanha J;
PI
XX WPI; 1998-159172/14.
DR P-PSDB; AAW53817.
XX
XX Humanised immunoglobulin reactive with alpha4-beta7 integrin -
PT used for treating inflammatory disease, pancreatitis, diabetes,
PT asthma, graft versus host disease and sarcoidosis
XX
XX Example 1; Fig 3; 145pp; English.
XX
XX The present sequence represents the consensus nucleotide sequence
CC comprising the variable region of murine Act-1 antibody determined from
CC several independent mouse light chain variable region clones. Act-1 is
CC active against human alpha4-beta7 integrin. Muscosal addressin cell
CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
CC MadCAM-1, which is present of high endothelial venules in muscosal
CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
CC using degenerate PCR primers AAV20083-84. The degeneracy of the PCR
CC primers produced several different sequences, of which the present
CC sequence is a consensus sequence. The present sequence was used to
CC construct chimeric, humanised Act-1 antibodies, which contain murine
CC antigen binding regions. The humanised immunoglobulin can be used to
CC inhibit the interaction of cells bearing alpha4-beta7 with cells bearing
CC a ligand for alpha4-beta7. It can be used for inhibiting leukocyte
CC infiltration of tissues, e.g. for treating inflammatory diseases such
CC as inflammatory bowel disease. The immunoglobulin can also be used for
CC detection, isolation and diagnosis.
XX
XX Sequence 535 BP; 126 A; 128 C; 132 G; 149 T; 0 other;
SQ
Query Match 21.4%; Score 93; DB 19; Length 535;
Best Local Similarity 100.0%; Pred. No. 6.7e-37;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 343 CCGTACACGTTTCGGAGGGGGGACCAAGCTGGAATAAAGCGGTGATGCTGCACCAACT 402
DB 373 CCGTACACGTTTCGGAGGGGGGACCAAGCTGGAATAAAGCGGTGATGCTGCACCAACT 432
QY 403 GTATCCATCTTCCACCATCCAGTAAGCTTTGGG 435
DB 433 GTATCCATCTTCCACCATCCAGTAAGCTTTGGG 465
RESULT 13
AAQ90431
ID AAQ90431 standard; DNA; 438 BP.
XX
XX AAQ90431;
XX
XX 02-FEB-1996 (first entry)
XX
XX DNA encoding anti-idiotypic antibody Idiol7 clone 17Kb1.
XX
XX Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW complementarity determining region, ds.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FT CDS 1..438
FT FT /*tag= a

```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2003, 19:44:55 ; Search time 158.756 Seconds
(without alignments)
6286.388 Million cell updates/sec

Title: US-08-836-455-1
Perfect score: 435
Sequence: 1 ATGGGGGCCCTGCTCAGAT.....CACCATCCAGTAAGCTTGGG 435

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1533700 seqs, 1147125425 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3067400

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	435	100.0	435	9 US-09-861-294-1	Sequence 1, Appli
2	435	100.0	435	12 US-10-367-506-1	Sequence 1, Appli
3	108	24.8	402	8 US-08-779-784-5	Sequence 5, Appli
4	102	23.4	387	9 US-09-007-093-1	Sequence 1, Appli
5	100	23.0	351	8 US-08-779-784-17	Sequence 17, Appli
6	85	19.5	698	13 US-10-006-773-18	Sequence 18, Appli
7	82	18.9	324	10 US-09-924-099-11	Sequence 11, Appli
8	82	18.9	407	10 US-09-924-099-27	Sequence 27, Appli
9	82	18.9	711	10 US-09-924-099-19	Sequence 19, Appli
10	82	18.9	729	10 US-09-924-099-20	Sequence 20, Appli
11	80	18.4	729	13 US-10-006-773-10	Sequence 10, Appli
12	79	18.2	351	8 US-08-779-784-16	Sequence 16, Appli
13	79	18.2	426	10 US-09-840-459-95	Sequence 95, Appli
14	79	18.2	426	10 US-09-840-459-101	Sequence 101, App
15	77	17.7	504	13 US-10-006-773-14	Sequence 14, Appli
16	73	16.8	390	12 US-10-268-883-10	Sequence 10, Appli

17	64	14.7	363	11	US-09-929-665-9	Sequence 9, Appli
18	64	14.7	363	11	US-09-929-665-10	Sequence 10, Appli
19	64	14.7	363	11	US-09-929-546-9	Sequence 9, Appli
20	64	14.7	363	11	US-09-929-546-10	Sequence 10, Appli
21	61	14.0	739	10	US-09-887-853-5	Sequence 5, Appli
22	57	13.1	390	13	US-10-146-305-5	Sequence 5, Appli
23	57	13.1	447	10	US-09-990-205-1	Sequence 1, Appli
24	57	13.1	447	14	US-10-153-401-1	Sequence 1, Appli
25	54	12.4	443	11	US-09-967-719C-3	Sequence 3, Appli
26	48	11.0	51	8	US-08-779-784-18	Sequence 18, Appli
27	48	11.0	391	11	US-09-726-258-34	Sequence 34, Appli
28	48	11.0	705	12	US-10-281-479A-22	Sequence 22, Appli
29	48	11.0	714	14	US-10-216-484-10	Sequence 10, Appli
30	48	11.0	831	10	US-09-903-327A-3	Sequence 3, Appli
31	48	11.0	3344	14	US-10-176-380-17	Sequence 17, Appli
32	48	11.0	5691	10	US-09-897-006-11	Sequence 11, Appli
33	48	11.0	5691	11	US-09-897-511A-11	Sequence 11, Appli
34	48	11.0	5711	10	US-09-897-006-8	Sequence 8, Appli
35	48	11.0	5711	11	US-09-897-511A-8	Sequence 8, Appli
36	48	11.0	6255	10	US-09-897-006-13	Sequence 13, Appli
37	48	11.0	6255	11	US-09-897-511A-13	Sequence 13, Appli
38	45	10.3	384	9	US-09-905-243-20	Sequence 20, Appli
39	45	10.3	737	10	US-09-919-344-7	Sequence 7, Appli
40	44	10.1	364	10	US-09-797-941A-3	Sequence 3, Appli
41	44	10.1	387	9	US-09-905-243-27	Sequence 27, Appli
42	44	10.1	472	9	US-09-797-481-5	Sequence 5, Appli
43	43	9.9	358	10	US-09-800-908-10	Sequence 10, Appli
44	42	9.7	351	11	US-09-469-485-3	Sequence 3, Appli
45	42	9.7	393	14	US-10-195-752-2	GENERAL INFORMA

ALIGNMENTS

RESULT 1

US-09-861-294-1
; Sequence 1, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE OF INVENTION: 304142000620
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(435)
; NAME/KEY: sig_peptide
; LOCATION: (1)...(60)
; NAME/KEY: mat_peptide
; LOCATION: (61)...(435)
US-09-861-294-1

Query Match 100.0%; Score 435; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 4.6e-232;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGGCCCCGCTCAGATTTCTTGGTCTTCTTGTTCCTTTCCAGGTACCATGT 60
DB 1 ATGGGGGGCCCCGCTCAGATTTCTTGGTCTTCTTGTTCCTTTCCAGGTACCATGT 60

QY 61 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCTCTCTGGGACAAAGAGTCAGT 120
DB 61 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCTCTCTGGGACAAAGAGTCAGT 120
QY 121 CTCACCTTGTGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGGCTTCAGCAGGAACCA 180
DB 121 CTCACCTTGTGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGGCTTCAGCAGGAACCA 180
QY 181 GATGGAACCTATTAAACGCCCTGATCTACGCCACATCCAGTTTGGTGTCTCCCAAA 240
DB 181 GATGGAACCTATTAAACGCCCTGATCTACGCCACATCCAGTTTGGTGTCTCCCAAA 240
QY 241 AGTTTCAGTGGCAGTAGTCTGGGTGAGATTATTTCTTCACCATCAGCAGCCTTGAAGTCT 300
DB 241 AGTTTCAGTGGCAGTAGTCTGGGTGAGATTATTTCTTCACCATCAGCAGCCTTGAAGTCT 300
QY 301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTTCTCGGTACACGTTCCGGAGGG 360
DB 301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTTCTCGGTACACGTTCCGGAGGG 360
QY 361 GGGACCAAGCTGGAAATAAAACGGCTGATGCTGCACCAACTGTATCCATCTTCCCAACCA 420
DB 361 GGGACCAAGCTGGAAATAAAACGGCTGATGCTGCACCAACTGTATCCATCTTCCCAACCA 420
QY 421 TCCAGTAAGCTTGGG 435
DB 421 TCCAGTAAGCTTGGG 435

RESULT 2

US-10-367-506-1
; Sequence 1, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMGF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(435)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(60)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (61)...(435)
US-10-367-506-1

Query Match 100.0%; Score 435; DB 12; Length 435;
Best Local Similarity 100.0%; Pred. No. 4.6e-232;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGCCCCGTCTCAGATCTTGGGTCTTGTGCTCTGTTCAGGTACAGATGT 60
DB 1 ATGGGGGCCCCGTCTCAGATCTTGGGTCTTGTGCTCTGTTCAGGTACAGATGT 60
QY 61 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCTCTCTGGGACAAAGAGTCAGT 120

DB 61 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCTCTCTGGGACAAAGAGTCAGT 120
QY 121 CTCACCTTGTGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGGCTTCAGCAGGAACCA 180
DB 121 CTCACCTTGTGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGGCTTCAGCAGGAACCA 180
QY 181 GATGGAACCTATTAAACGCCCTGATCTACGCCACATCCAGTTTGGTGTCTCCCAAA 240
DB 181 GATGGAACCTATTAAACGCCCTGATCTACGCCACATCCAGTTTGGTGTCTCCCAAA 240
QY 241 AGTTTCAGTGGCAGTAGTCTGGGTGAGATTATTTCTTCACCATCAGCAGCCTTGAAGTCT 300
DB 241 AGTTTCAGTGGCAGTAGTCTGGGTGAGATTATTTCTTCACCATCAGCAGCCTTGAAGTCT 300
QY 301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTTCTCGGTACACGTTCCGGAGGG 360
DB 301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTTCTCGGTACACGTTCCGGAGGG 360
QY 361 GGGACCAAGCTGGAAATAAAACGGCTGATGCTGCACCAACTGTATCCATCTTCCCAACCA 420
DB 361 GGGACCAAGCTGGAAATAAAACGGCTGATGCTGCACCAACTGTATCCATCTTCCCAACCA 420
QY 421 TCCAGTAAGCTTGGG 435
DB 421 TCCAGTAAGCTTGGG 435

RESULT 3

US-08-779-784-5
; Sequence 5, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 base pairs
; TYPE: nucleic acid

Db 229 GATTCTGGTGTCCCAAAAGGTTAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCAAC 288
Qy 283 ATCAGCAGCCTTGAGTCTGAAGATTCTTAG 313
Db 289 ATCAGCAGCCTTGAGTCTGAAGATTCTTAG 319

RESULT 6
US-10-006-773-18
; Sequence 18, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Ant
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 698
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(401)
; OTHER INFORMATION: 3ell Light chain V region, plus leader
US-10-006-773-18

Query Match 19.5%; Score 85; DB 13; Length 698;
Best Local Similarity 100.0%; Pred. No. 6.2e-37;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 342 TCCGTACACGTCGGAGGGGACCAAGCTGGAATAAAACGGCTGATGCTGCACCAAC 401
Db 359 TCCGTACACGTCGGAGGGGACCAAGCTGGAATAAAACGGCTGATGCTGCACCAAC 418

Qy 402 TGTATCCATCTTCCACCATCCAGT 426
Db 419 TGTATCCATCTTCCACCATCCAGT 443

RESULT 7
US-09-924-099-11
; Sequence 11, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 11
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-924-099-11

Query Match 18.9%; Score 82; DB 10; Length 324;
Best Local Similarity 99.2%; Pred. No. 2.9e-35;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 241 AGGTTCAAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 300
Db 181 AGGTTCAAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
Qy 301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCCTCGGTACAGTTCGGAGGG 360
Db 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCCTCGGTACAGTTCGGAGGG 300

Qy 361 GGGACCAAGCTGG 373
Db 301 GGGACCAAGCTGG 313

RESULT 8
US-09-924-099-27
; Sequence 27, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 27
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(407)
; NAME/KEY: sig peptide
; LOCATION: (1)...(60)
US-09-924-099-27

Query Match 18.9%; Score 82; DB 10; Length 407;
Best Local Similarity 99.2%; Pred. No. 2.9e-35;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 241 AGGTTCAAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 300
Db 241 AGGTTCAAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 300

Qy 301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCCTCGGTACAGTTCGGAGGG 360
Db 301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCCTCGGTACAGTTCGGAGGG 360

Qy 361 GGGACCAAGCTGG 373
Db 361 GGGACCAAGCTGG 373

RESULT 9
US-09-924-099-19
; Sequence 19, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:

QY	301	GAAGATTTTGTAGCCTATTACTGTCTACATATGCTAGTTCTCGGTACACGTTTCGGAGGG	369
Db	631	GAAGATTTTGTAGACATTTACTGTCTACAATATGTTCTCGGTACACGTTTCGGAGGG	690
QY	361	GGGACCAAGCTGG	373
Db	691	GGGACCAAGCTGG	703

RESULT 11

US-10-006-773-10

; Sequence 10, Application US/10006773

; Publication No. US20020132983A1

; GENERAL INFORMATION:

; APPLICANT: Junghans, Richard P.

; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against

; FILE REFERENCE: 003

; CURRENT APPLICATION NUMBER: US/10/006,773

; CURRENT FILING DATE: 2001-12-10

; PRIOR APPLICATION NUMBER: 60/250,089

; PRIOR FILING DATE: 2000-11-30

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 729

; TYPE: DNA

; ORGANISM: Mus sp.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (15)..(410)

; OTHER INFORMATION: 3D8 Light chain V region, plus leader

US-10-006-773-10

Query Match 18.4%; Score 80; DB 13; Length 729; -

Best Local Similarity 100.0%; Pred. No. 3.8e-34;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY	347	ACACGTTTCGGAGGGGGGACCAAGCTGGGAATATAAACGGGCTGATGCTGCACCAACTGTAT	406
Db	373	ACACGTTTCGGAGGGGGGACCAAGCTGGGAATATAAACGGGCTGATGCTGCACCAACTGTAT	432
QY	407	CCATCTTCCACCATCCAGT	426
Db	433	CCATCTTCCACCATCCAGT	452

RESULT 12

US-08-779-784-16

; Sequence 16, Application US/08779784

; Publication No. US20020164325A1

; GENERAL INFORMATION:

; APPLICANT: Rodriguez, Moses

; APPLICANT: Miller, David J.

; APPLICANT: Asakura, Kunihiko

; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM

; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th

; STREET: Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/779,784

;; FILING DATE: 07-JAN-1997
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/692,084
;; FILING DATE: 08-AUG-1996
;; PRIOR APPLICATION DATA: US 08/236,520
;; APPLICATION NUMBER: US 08/236,520
;; FILING DATE: 29-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-487-5800
;; TELEFAX: 201-343-1684
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 351 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
US-08-779-784-16

Query Match 18.2%; Score 79; DB 8; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.3e-33;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 CCCAAGGTCAGTCGACGAGTCTGGGTCAGATTATCTCACCATCAGCAGCCTT 294
Db 241 CCCAAGGTCAGTCGACGAGTCTGGGTCAGATTATCTCACCATCAGCAGCCTT 300

QY 295 GAGTCTGAAGATTTGTAG 313
Db 301 GAGTCTGAAGATTTGTAG 319

RESULT 13
US-09-840-459-95
; Sequence 95, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Slobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 95
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-840-459-95

Query Match 18.2%; Score 79; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TCCGTACAGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATCTGCACCAAC 401
Db 348 TCCGTACAGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATCTGCACCAAC 407

QY 402 TGTATCCATCTTCCACCA 420
Db 408 TGTATCCATCTTCCACCA 426

RESULT 14
US-09-840-459-101/C
; Sequence 101, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Slobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-840-459-101

Query Match 18.2%; Score 79; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TCCGTACAGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATCTGCACCAAC 401
Db 79 TCCGTACAGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATCTGCACCAAC 20

QY 402 TGTATCCATCTTCCACCA 420
Db 19 TGTATCCATCTTCCACCA 1

RESULT 15
US-10-006-773-14
; Sequence 14, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor A
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Mus sp.

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(402)
; OTHER INFORMATION: 4D4 Light chain V region, plus leader
US-10-006-773-14

Query Match      17.7%; Score 77; DB 13; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 CGTTCGGAGGGGGACCAAGCTGGAATAAACGGGCTGATGCTGCACCAACTGTATCCA 409
Db 368 CGTTCGGAGGGGGACCAAGCTGGAATAAACGGGCTGATGCTGCACCAACTGTATCCA 427
QY 410 TCTTCCCAACCATCCAGT 426
Db 428 TCTTCCCAACCATCCAGT 444
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Search completed: August 30, 2003, 22:02:42
Job time : 160.756 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2003, 18:52:40 ; Search time 1513.76 Seconds
(without alignments)
6984.224 Million cell updates/sec

Title: US-08-836-455-1

Perfect score: 435

Sequence: 1 ATGGGGGCCCTGCTCAGAT.....CACCATCCAGTAAGCTTGGG 435

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST.*

1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pin.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	87	20.0	594	10	BE309592 601094848
2	85	19.8	805	12	BI454240 603170666
3	85	19.5	585	12	BM194777 L0700H12-
4	85	19.5	725	12	BG963055 602828068

ALIGNMENTS

RESULT 1
BE309592
LOCUS
DEFINITION
mRNA sequence.
ACCESSION
BE309592
VERSION
BE309592.1
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
1 (bases 1 to 594)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM8530 row: o column: 12
High quality sequence stop: 591.

85	19.5	891	10	BF579422	BF579422	602093833
85	19.5	906	10	BF785914	BF785914	602112548
85	19.5	926	13	BQ959057	BQ959057	AGENCOURT
85	19.5	935	11	BC031349	BC031349	MUS MUSCU
84	19.3	606	13	BQ922747	BQ922747	AGENCOURT
84	19.3	854	13	BQ947692	BQ947692	AGENCOURT
84	19.3	871	13	BQ956722	BQ956722	AGENCOURT
84	19.3	886	13	BQ940987	BQ940987	AGENCOURT
84	19.3	908	13	BQ524124	BQ524124	AGENCOURT
84	19.3	941	13	BQ523453	BQ523453	AGENCOURT
84	19.3	975	12	BG961850	BG961850	602826515
83	19.1	750	12	BG965050	BG965050	602829112
81	18.6	374	13	BY083003	BY083003	BY083003
81	18.6	630	10	BF138788	BF138788	601780387
81	18.6	707	12	BI250555	BI250555	602931614
79	18.2	712	12	BI100311	BI100311	602885776
79	18.2	778	12	BG964076	BG964076	602828830
79	18.2	798	12	BG968518	BG968518	602835104
78	17.9	959	13	BQ939046	BQ939046	AGENCOURT
75	17.2	944	10	BF687485	BF687485	602102475
75	17.2	967	10	BF687410	BF687410	602102583
73	16.8	793	12	BG965736	BG965736	602830592
67	15.4	532	12	BI104783	BI104783	602891329
67	15.4	624	10	BE306691	BE306691	601104076
67	15.4	685	10	BE369854	BE369854	601221265
67	15.4	695	10	BE284224	BE284224	601099161
67	15.4	755	12	BI150509	BI150509	602915167
67	15.4	762	10	BF144806	BF144806	601791486
67	15.4	772	10	BE285427	BE285427	601096728
67	15.4	827	12	BI152061	BI152061	602916512
67	15.4	865	12	BI659552	BI659552	603303102
67	15.4	874	10	BG518527	BG518527	602578261
67	15.4	876	12	BI107286	BI107286	602894285
67	15.4	882	10	BF159226	BF159226	601766681
67	15.4	918	10	BF135931	BF135931	601781261
67	15.4	936	10	BF164906	BF164906	601778137
67	15.4	997	12	BI107100	BI107100	602894523
66	15.2	748	12	BG963884	BG963884	602828572
64	14.7	354	13	BY085718	BY085718	BY085718
57	13.1	698	12	BI109045	BI109045	602896878
57	13.1	849	10	BF583521	BF583521	602101553

FEATURES
source

Location/Qualifiers
1. .594
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3489635"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 158 a 149 c 143 g 144 t
ORIGIN

Query Match 20.0%; Score 87; DB 10; Length 594;
Best Local Similarity 100.0%; Pred. No. 6.6e-35;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 340 TCTCCGTACACGTCGGAGGGGGGACCAACGCTGGAATAAAACGGGCTGATGCTGCACCA 399
|||||
Db 326 TCTCCGTACACGTCGGAGGGGGGACCAACGCTGGAATAAAACGGGCTGATGCTGCACCA 385
|||||
QY 400 ACTGTATCCATCTTCCCACCATCCAGT 426
|||||
Db 386 ACTGTATCCATCTTCCCACCATCCAGT 412
|||||

RESULT 2

BI454240 603170666F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5250017 5',
LOCUS mRNA sequence.
DEFINITION BI454240 805 bp mRNA linear EST 21-AUG-2001

ACCESSION BI454240.1 GI:152444896
VERSION
KEYWORDS
SOURCE

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 805)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L14M11631 row: d column: 18

High quality sequence stop: 790.

FEATURES
source

Location/Qualifiers
1. .805
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5250017"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
BASE COUNT 230 a 209 c 186 g 180 t
ORIGIN

Query Match 19.8%; Score 86; DB 12; Length 805;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 CTCCTACAGTTCGGAGGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCA 400
|||||
Db 356 CTCCTACAGTTCGGAGGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCA 415
|||||
QY 401 CTGTATCCATCTTCCCACCATCCAGT 426
|||||
Db 416 CTGTATCCATCTTCCCACCATCCAGT 441
|||||

RESULT 3

BM194777/c
LOCUS

DEFINITION BM194777 585 bp mRNA linear EST 30-JAN-2002

musculus cDNA clone L0700H12 3', mRNA sequence.

ACCESSION BM194777 GI:17745971

VERSION

KEYWORDS

SOURCE EST.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 585)

Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Klotz,E.,
Kelsoe,G., Hodges,R. and Ko,M.S.H.

Systematic Analyses of NIA Mouse Germinal Center B Cell cDNA

Library

Unpublished

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsun.grc.nia.nih.gov

Plate: L0700 row: H column: 12

Seq primer: -21M13 Forward

High quality sequence stop: 585

POLYA=Yes.

FEATURES

source

Location/Qualifiers
1. .585
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="niaEST:L0700H12-3"
/db_xref="taxon:10090"
/clone="L0700H12"
/tissue_type="Germinal Center B Cell"
/lab_host="DH10B"
/clone_lib="NIA Mouse Germinal Center B Cell cDNA Library"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA
). FACS-sorted Germinal Center B cells were provided by
Drs. Richard Hodges, Emily Klotz (National Institute on
Aging and National Cancer Institute, USA) and Garnett
Kelsoe (Duke University, USA). Double-stranded cDNAs were
synthesized from 0.46 ug of total RNA with an Oligo(dT)
primer [Invitrogen]:
5'-pGACTAGTCTAGATCGGAGCGGCCCTTTT-3'],

treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker LL-Sal3 (Ref. Development 127: 1737-1749 (2000
) [PMID: 1072549]), purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, cDNAs
were amplified by long-range high fidelity PCR using Ex
Taq polymerase (Takara) and purified by phenol/chloroform,

followed by Centricon 100 purification. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is 1.2 kb. The library was constructed by Yulan Piao (NIA)."

BASE COUNT 137 a 121 c 167 g 160 t
ORIGIN

Query Match 19.5%; Score 85; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.6e-34;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAAC 401
|||||
Db 572 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAAC 513
|||||

QY 402 TGTATCCATCTTCCACCACATCCAGT 426
|||||
Db 512 TGTATCCATCTTCCACCACATCCAGT 488
|||||

RESULT 4
LOCUS
DEFINITION 602828068F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982825 5',
mRNA sequence.
ACCESSION BG963055
VERSION BG963055.1 GI:14350692
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 725)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10986 row: g column: 18
High quality sequence stop: 719.

FEATURES
source
Location/Qualifiers
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4982825"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 195 a 182 c 174 g 174 t
ORIGIN

Query Match 19.5%; Score 85; DB 12; Length 725;
Best Local Similarity 100.0%; Pred. No. 8.1e-34;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAAC 401
|||||
Db 372 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAAC 431
|||||

QY 402 TGTATCCATCTTCCACCACATCCAGT 426
|||||
Db 432 TGTATCCATCTTCCACCACATCCAGT 456
|||||

RESULT 5
LOCUS
DEFINITION 602093833F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208144 5',
mRNA sequence.
ACCESSION BF579422
VERSION BF579422.1 GI:11653134
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 891)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9772 row: a column: 09
High quality sequence stop: 711.

FEATURES
source
Location/Qualifiers
1..891
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/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4208144"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 246 a 226 c 204 g 215 t
ORIGIN

Query Match 19.5%; Score 85; DB 10; Length 891;
Best Local Similarity 100.0%; Pred. No. 8.6e-34;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAAC 401
|||||
Db 353 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAAC 412
|||||

QY 402 TGTATCCATCTTCCACCACATCCAGT 426
|||||
Db 413 TGTATCCATCTTCCACCACATCCAGT 437
|||||

RESULT 6
LOCUS
DEFINITION 602112548F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240762
5', mRNA sequence.
ACCESSION BF785914
VERSION BF785914.1 GI:12090950
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE 1 (bases 1 to 906)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: crapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9855 row: p column: 11
High quality sequence stop: 718.
Location/Qualifiers
1..906
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4240762"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Kid14"
/notes="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT 243 a 232 c 237 g 194 t
ORIGIN
Query Match 19.5%; Score 85; DB 10; Length 906;
Best Local Similarity 100.0%; Pred. No. 8.6e-34;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAAC 401
Db 371 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAAC 430

QY 402 TGTATCCATCTTCCACCATCCAGT 426
Db 431 TGTATCCATCTTCCACCATCCAGT 455

RESULT 7
LOCUS BQ959057 926 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_10049748 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6479377 5', mRNA sequence.
ACCESSION BQ959057
VERSION BQ959057.1 GI:22374535
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: crapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14024 row: h column: 02
High quality sequence stop: 692.
Location/Qualifiers
1..926
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4240762"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Kid14"
/notes="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT 243 a 232 c 237 g 194 t
ORIGIN
Query Match 19.5%; Score 85; DB 10; Length 906;
Best Local Similarity 100.0%; Pred. No. 8.6e-34;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAAC 401
Db 371 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAAC 430

QY 402 TGTATCCATCTTCCACCATCCAGT 426
Db 431 TGTATCCATCTTCCACCATCCAGT 455

RESULT 8
LOCUS BC031349 935 bp mRNA linear HTC 03-JUN-2002
DEFINITION MUS musculus, clone IMAGE:1514385, mRNA.
ACCESSION BC031349
VERSION BC031349.1 GI:21315064
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: crapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: Soares Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pavan Pandoh, Anna-Lisa Prabhu, Parvaneh Saedi, Jacqueline
Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 67 Row: j Column: 4
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein
This clone has the following problem: no cloning site /
microdeletion.
Location/Qualifiers
1..935

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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1514385"
/tissue_type="Mammary gland, lactating mouse"
/clone_lib="Soares_mammary_gland_NMLMG"
/lab_host="DH10B"
/note="vector: pT7T3D-Pac"
BASE COUNT      251 a   247 c   208 g   229 t
ORIGIN

Query Match      19.5%; Score 85; DB 11; Length 935;
Best Local Similarity 100.0%; Pred. No. 8.7e-34;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TCGGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAAC 401
      |||||||
Db 344 TCGGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAAC 403
      |||||||

QY 402 TGTATCCATCTCCACCATCCAGT 426
      |||||||
Db 404 TGTATCCATCTCCACCATCCAGT 428

RESULT 9
BQ922747
LOCUS
DEFINITION
AGENCOURT_8921909 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6395978 5', mRNA sequence.
ACCESSION
BQ922747
VERSION
BQ922747.1 GI:223337778
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 606)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLMI3891 row: 1 column: 03
High quality sequence stop: 605.
FEATURES
Location/Qualifiers
1..606
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="FVB/N"
/clone="IMAGE:6395978"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      181 a   169 c   121 g   135 t
ORIGIN

Query Match      19.3%; Score 84; DB 13; Length 606;
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAACT 402
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Db 15 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAACT 74
QY 403 GTATCCATCTCCACCATCCAGT 426
      |||||||
Db 75 GTATCCATCTCCACCATCCAGT 98
      |||||||

RESULT 10
BQ947692
LOCUS
DEFINITION
AGENCOURT_8909039 NCI_CGAP_Mam2 Mus musculus cDNA clone
IMAGE:6441024 5', mRNA sequence.
ACCESSION
BQ947692
VERSION
BQ947692.1 GI:223631170
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 854)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLMI3963 row: j column: 01
High quality sequence stop: 671.
FEATURES
Location/Qualifiers
1..854
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="FVB/N-3"
/clone="IMAGE:6441024"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT      234 a   237 c   190 g   193 t
ORIGIN

Query Match      19.3%; Score 84; DB 13; Length 854;
Best Local Similarity 100.0%; Pred. No. 2.9e-33;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAACT 402
      |||||||
Db 361 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAACT 420
      |||||||

QY 403 GTATCCATCTCCACCATCCAGT 426
      |||||||
Db 421 GTATCCATCTCCACCATCCAGT 444
      |||||||

RESULT 11
BQ956722
LOCUS
DEFINITION
AGENCOURT_8880991 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6396481 5', mRNA sequence.
ACCESSION
BQ956722
VERSION
BQ956722.1 GI:22372200
KEYWORDS
EST.

```

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 871)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13892 row: n column: 02
 High quality sequence stop: 630.
 Location/Qualifiers
 1..871
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:6396481"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Co24"
 /notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 218 a 268 c 182 g 193 t 10 others
 ORIGIN
 Query Match 19.3%; Score 84; DB 13; Length 871;
 Best Local Similarity 100.0%; Pred. No. 2.9e-33;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 343 CCGTACACGTTCCGAGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAACT 402
 Db 190 CCGTACACGTTCCGAGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAACT 249
 QY 403 GTATCCATCTCCACCATCCAGT 426
 Db 250 GTATCCATCTCCACCATCCAGT 273
 RESULT 12
 LOCUS BQ940987 886 bp mRNA linear EST 21-AUG-2002
 DEFINITION AGENCOURT_8881891 NCI_CGAP_Co24 Mus musculus cDNA clone
 IMAGE:6476176 5', mRNA sequence.
 ACCESSION BQ940987
 VERSION BQ940987.1 GI:223556465
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 886)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM14016 row: b column: 17
 High quality sequence stop: 626.
 Location/Qualifiers
 1..886
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:6476176"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Co24"
 /notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 242 a 243 c 183 g 216 t 2 others
 ORIGIN
 Query Match 19.3%; Score 84; DB 13; Length 886;
 Best Local Similarity 100.0%; Pred. No. 2.9e-33;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 343 CCGTACACGTTCCGAGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAACT 402
 Db 316 CCGTACACGTTCCGAGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAACT 375
 QY 403 GTATCCATCTCCACCATCCAGT 426
 Db 376 GTATCCATCTCCACCATCCAGT 399
 RESULT 13
 LOCUS BU524124 908 bp mRNA linear EST 13-SEP-2002
 DEFINITION AGENCOURT_10126425 NCI_CGAP_Co24 Mus musculus cDNA clone
 IMAGE:6530882 5', mRNA sequence.
 ACCESSION BU524124
 VERSION BU524124.1 GI:22834563
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 908)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM14133 row: f column: 02
 High quality sequence stop: 604.
 Location/Qualifiers
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 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:6530882"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Co24"
 /notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 238 a 270 c 194 g 206 t
 ORIGIN

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Query Match      19.3%; Score 84; DB 13; Length 908;
Best Local Similarity 100.0%; Pred. No. 2.9e-33;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGTCGACCAACT 402
Db 173 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGTCGACCAACT 232
QY 403 GTATCCATCTCCACCACCTCCAGT 426
Db 233 GTATCCATCTCCACCACCTCCAGT 256

RESULT 14
BU523453      941 bp      mRNA      linear      EST 13-SEP-2002
LOCUS AGENCOURT_10169180 NCI_CGAP_Co24 Mus musculus cDNA clone
DEFINITION IMAGE:6530124 5', mRNA sequence.
ACCESSION BU523453
VERSION BU523453.1 GI:22833892
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC).
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM14131 row: f column: 12
High quality sequence stop: 646.
Location/Qualifiers
1. .941
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6530124"
/lab_host="NCI_CGAP_Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      249 a      261 c      214 g      217 t
ORIGIN
Query Match      19.3%; Score 84; DB 13; Length 941;
Best Local Similarity 100.0%; Pred. No. 3e-33;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGTCGACCAACT 402
Db 380 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGTCGACCAACT 439
QY 403 GTATCCATCTCCACCACCTCCAGT 426
Db 440 GTATCCATCTCCACCACCTCCAGT 463

RESULT 15
BG961850
LOCUS      975 bp      mRNA      linear      EST 12-JUN-2001

```

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DEFINITION 602826515F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4981443 5',
mRNA sequence.
ACCESSION BG961850
VERSION BG961850.1 GI:14349487
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10982 row: n column: 04
High quality sequence stop: 743.
Location/Qualifiers
1. .975
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4981443"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

```

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FEATURES
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BASE COUNT      288 a      264 c      210 g      213 t
ORIGIN
Query Match      19.3%; Score 84; DB 12; Length 975;
Best Local Similarity 100.0%; Pred. No. 3e-33;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGTCGACCAACT 402
Db 363 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGTCGACCAACT 422
QY 403 GTATCCATCTCCACCACCTCCAGT 426
Db 423 GTATCCATCTCCACCACCTCCAGT 446

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Search completed: August 30, 2003, 21:57:07
Job time : 1518.76 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2003, 13:43:39 ; Search time 1971.09 Seconds
(without alignments)
9028.331 Million cell updates/sec

Title: US-08-836-455-1

Perfect score: 435

Sequence: 1 ATGGGGGCCCTGCTCAGAT.....CACCATCCAGTAAGCTTGGG 435

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:**

- 1: gb_ba:**
- 2: gb_htg:**
- 3: gb_in:**
- 4: gb_cm:**
- 5: gb_ov:**
- 6: gb_pat:**
- 7: gb_ph:**
- 8: gb_pl:**
- 9: gb_pr:**
- 10: gb_ro:**
- 11: gb_sts:**
- 12: gb_sy:**
- 13: gb_un:**
- 14: gb_vl:**
- 15: em_ba:**
- 16: em_fun:**
- 17: em_hum:**
- 18: em_in:**
- 19: em_mu:**
- 20: em_om:**
- 21: em_or:**
- 22: em_ov:**
- 23: em_pat:**
- 24: em_ph:**
- 25: em_pl:**
- 26: em_ro:**
- 27: em_sts:**
- 28: em_un:**
- 29: em_vl:**
- 30: em_htg_hum:**
- 31: em_htg_inv:**
- 32: em_htg_other:**
- 33: em_htg_mus:**
- 34: em_htg_pln:**
- 35: em_htg_rod:**
- 36: em_htg_mam:**
- 37: em_htg_vrt:**
- 38: em_sy:**
- 39: em_htgo_hum:**
- 40: em_htgo_mus:**
- 41: em_htgo_other:**

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	435	100.0	435	6	AR164505	AR164505 Sequence
2	435	100.0	435	6	BD085737	BD085737 Methods o
3	384.6	88.4	407	6	E54981	E54981 Peptide. 1/
4	379.4	87.2	381	10	AF124721	AF124721 Mus muscu
5	361.6	83.1	384	10	AB017434	AB017434 Mus muscu
6	361.6	83.1	390	10	MUSIKCC	L41880 Mus musculu
7	352.2	81.0	381	10	AF045508	AF045508 Mus muscu
8	349	80.2	381	10	AF045495	AF045495 Mus muscu
9	345.8	79.5	381	10	AF045510	AF045510 Mus muscu
10	332	76.3	380	10	MMIGGVJ1	X02177 M.musculus
11	327.2	75.2	381	10	MMIGGVJ2	X02178 M.musculus
12	325.4	74.8	383	10	MUSIGKMA	M12191 Mouse Ig ac
13	323.8	74.4	405	10	AB016620	AB016620 Mus muscu
14	323.4	74.3	387	6	AR169918	AR169918 Sequence
15	317.2	72.9	354	10	AB089681	AB089681 Mus muscu
16	316	72.6	684	10	MUSIGKAC1	J00565 Mus musculu
17	314.4	72.3	685	10	MMIGK7	V00808 Part of the
18	311.6	71.6	348	10	MMVJIG	X54755 Mouse rear
19	309.8	71.2	321	10	AF163749	AF163749 Mus muscu
20	309.4	71.1	739	6	AR007981	AR007981 Sequence
21	309.4	71.1	739	6	AR058996	AR058996 Sequence
22	309.4	71.1	739	6	I23446	I23446 Sequence 5
23	308.6	70.9	324	6	AX722008	AX722008 Sequence
24	308.4	70.9	729	6	E54976	E54976 Peptide. 1/
25	307.6	70.7	324	10	MUSX	L48667 Mus musculu
26	307.4	70.7	711	6	E54975	E54975 Peptide. 1/
27	306.4	70.4	324	6	E54967	E54967 Peptide. 1/
28	305.4	70.2	328	10	MMU55591	U55591 Mus musculu
29	301.4	69.3	756	6	AX256284	AX256284 Sequence
30	301.4	69.3	771	6	AX256296	AX256296 Sequence
31	301.4	69.3	1497	6	AX256302	AX256302 Sequence
32	300.6	69.1	324	6	I03643	I03643 Sequence 4
33	300.6	69.1	324	6	I07835	I07835 Sequence 4
34	299	68.7	323	10	AY229938	AY229938 Mus muscu
35	298.6	68.6	321	10	MUSIGKAA3	M59920 Mouse IG ge
36	298.4	68.6	348	10	AY245603	AY245603 Mus muscu
37	297.2	68.3	1019	10	BC027418	BC027418 Mus muscu
38	296.2	68.1	413	10	MUSIGKCLN	M20832 Mouse Igmk
39	295.6	68.0	972	10	AF466770	AF466770 Mus muscu
40	292.4	67.2	959	10	BC015292	BC015292 Mus muscu
41	292.2	67.2	321	6	AR081902	AR081902 Sequence
42	292.2	67.2	321	6	AR081905	AR081905 Sequence
43	291.6	67.0	326	10	MMVJIG3	X54756 Mouse rear
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ALIGNMENTS

RESULT 1
AR164505
LOCUS AR164505 435 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence.1 from patent US 6274143.
ACCESSION AR164505
VERSION AR164505.1 GI:16237555
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 435)
AUTHOR Chatterjee, M. and Foon, K.A.
TITLE Methods of delaying development of HMFG-associated tumors using anti-idiotype antibody 11D10
JOURNAL Patent: US 6274143-A 1 14-AUG-2001;


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FH Key Location/Qualifiers
FT CDS (1)..(407)
FT sig peptide (1)..(60).
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Best Local Similarity 96.6%; Pred. No. 3.1e-105;
Matches 393; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGGGGGCCCTGCTCAGATCTTGGTCTTCTTGTCTTCTTCCAGGTACCATGCT 60
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QY 181 GATGAACTATTAAACGGCTGATACGCACATCCAGTTTGGTCTGCTGCCCAA 240
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QY 241 AGGTTACAGGCGAGTAGTCTGGGTCAGATTTATCTCACCATCAGCAGCCTTGAGTCT 300
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Db 361 GGGACCAAGCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATC 407
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LOCUS Mus musculus immunoglobulin light chain mRNA, partial cds.
ACCESSION AF124721
VERSION AF124721.1 GI:14164546
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Tripathi,P.K., Qin,H., Bhattacharya-Chatterjee,M., Ceriani,L.R.,
Foon,K.A. and Chatterjee,S.K.
TITLE Construction and characterization of a chimeric fusion protein
consisting of an anti-idiotypic antibody mimicking a breast
cancer-associated antigen and the cytokine GM-CSF
JOURNAL Hybridoma 18 (2), 193-202 (1999)
MEDLINE 99306687
PUBMED 10380019
REFERENCE
AUTHORS Chatterjee,S.K. and Tripathi,P.K.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-1999) Internal Medicine, University of Kentucky,
800 Rose Street, Lexington, KY 40536, USA
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BASE COUNT 90 a 93 c 89 g 109 t
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Best Local Similarity 99.7%; Pred. No. 1.2e-103;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGGGCCCTGCTCAGATCTTGGTCTTCTTGTCTTCTTCCAGGTACCATGCT 60
Db 1 ATGAGGGCCCTGCTCAGATCTTGGTCTTCTTGTCTTCTTCCAGGTACCATGCT 60
QY 61 GACATCCAGATGACCCAGTCTCCATCTTATCTGCTCTCTCTGGGACAAAGAGTCAGT 120
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Db 301 GAAGATTTGTAGCTATTACTGCTACAAATAGTCTCCGTCACAGCTTCGGAGG 360
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Db 361 GGGACCAAGCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATC 381
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LOCUS Mus musculus mRNA for anti-IL-18 IgG Light chain, clone 125-2H,
partial cds.
ACCESSION AB017434
VERSION AB017434.1 GI:6683473
KEYWORDS variable region precursor of anti-IL-18 IgG Light chain; anti-IL-18
IgG Light chain.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Nishida,Y.
TITLE Variable region of anti Human IL-18 IgG Light(kappa) chain
JOURNAL Published Only in DataBase (2000)
REFERENCE
AUTHORS Nishida,Y.
TITLE Direct Submission
JOURNAL Submitted (02-SEP-1998) Yoshihiro Nishida, Hayashibara Biochemical
Laboratories, Inc., Fujisaki Institute; 675-1, Fujisaki, Okayama,
Okayama 702-8006, Japan (E-mail:fujihpo.harenet.or.jp,
Tel:+81-86-276-3141, Fax:+81-86-276-6885)
FEATURES
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 381)
O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
Anti-DNA antibodies of normal mice immunized with poly(dC) are
structurally similar to natural autoantibodies
Unpublished
2 (bases 1 to 381)
O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
Direct Submission
Submitted (02-FEB-1998) Biochemistry, Tufts University School of
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
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RESULT 8
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LOCUS      381 bp      mRNA      linear      ROD 28-FEB-1998
DEFINITION Mus musculus dC4 anti-poly(dC) monoclonal antibody kappa light
chain variable region, (Igk) mRNA, partial cds.
ACCESSION AF045495
VERSION    AF045495.1
KEYWORDS   GI:2906073
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
Anti-DNA antibodies of normal mice immunized with poly(dC) are
structurally similar to natural autoantibodies
Unpublished
2 (bases 1 to 381)
O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
Direct Submission
Submitted (02-FEB-1998) Biochemistry, Tufts University School of
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
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C region

BASE COUNT

ORIGIN

94 a 88 c 88 q 113 t

**BASE COUNT
ORIGIN**

Query Match	74.8%;	Score 325.4;	DB 10;	Length 383;
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Qy	71	TGACCCAGTCTCCATCTCCCTTATCTGCCTCTCTGGGACAAAGTCTCAGTCTCACTTGTC	130	
Db	61	TGACCCAGTCTCCATCTCCCTTATCTGCCTCTCTGGGACAAAGTCTCAGTCTCACTTGTC	120	
Qy	131	GGGCAAGTCAGGACATTCGTTATTAACCTTACATTCGCTTCAGCAGGAACAGATGAACTA	190	
Db	121	GGGCAAGTCAGGACATTCGTTATTAACCTTACATTCGCTTCAGCAGGAACAGATGAACTA	180	
Qy	191	TTAACGCCCTGATCTACGCCACATCCAGTTAGTCTTGTGTTCCCAAAAGGTTTCAGTG	250	
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Db	301	CAGACTATTACTGTCTACAATATGCTAGTCTTCCTCCACGTTTCGGAGGGGGGACCAAGC	360	
Qy	371	TGGAATAAAGGCGTGATGCT 393		
Db	361	TGGAATAAAGGCGTGATGCT 383		
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DEFINITION	Mus musculus mRNA for Immnogloblin light chain variable region, partial cds.			
ACCESSION	AB016620.1			
VERSION	1			
KEYWORDS	Immnogloblin light chain variable region.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1			
TITLE	Arakawa, F., Yamamoto, T., Kanda, H., Watanabe, T. and Kuroki, M. cDNA sequence analysis of monoclonal antibody FU-MK-1 specific for a transmembrane carcinoma-associated antigen, and construction of a mouse/human chimeric antibody			
JOURNAL	Hybridoma 18 (2), 131-138 (1999)			
MEDLINE	99306680			
PUBMED	10380012			
REFERENCE	2 (bases 1 to 405)			
AUTHORS	Arakawa, F.			
TITLE	Direct Submission			
JOURNAL	Submitted (30-JUL-1998) Fumiko Arakawa, School of Medicine, Fukuoka University, First Department of Biochemistry; 7-45-1 Nanakuma, Jonan-ku, Fukuoka, Fukuoka 814-80, Japan			
	(E-mail: farakawa@msat.fukuoka-u.ac.jp, Tel: 092-801-1011(ex. 3246), Fax: 092-801-3600)			
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Best Local Similarity	90.3%;	Pred. No. 8.1e-87;		
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Qy	121	CTCACTTGTGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGGCTTCAGCAGAAACCA	180	
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Qy	181	GATGAACTATTAAACGCTGATCTACGCACATCCAGATTTAGTCTTGGTGTCCCAAA	240	
Db	191	GATGAACTATTAAACGCTGATCTACGCACATCCAGATTTAGTCTTGGTGTCCCAAA	250	
Qy	241	AGGTTTCAGTGGCAGTCTGGGTCAGATTTATCTCTCACCATCAGCAGCTTCAGTCT	300	
Db	251	AGGTTTCAGTGGCAGTCTGGGTCAGATTTATCTCTCACCATCAGCAGCTTCAGTCT	310	
Qy	301	GAAGATTTTGTAGCTTATCTGCTACAATATCTAGTCTTCGTCACACGCTTCGGAGGG	360	
Db	311	GACGATTTTGCAGACTATTACTGCTACAGTATCTAGTATCGTGGACGCTTCGGTGA	370	
Qy	361	GGGACCAAGCTGGAATAAACAACG 383		
Db	371	GGCACCAGCTGGAATAAACAACG 393		
RESULT 14				
ARI69918				
LOCUS	ARI69918	387 bp	DNA	linear
DEFINITION	Sequence 1 from patent US 6291208.			
ACCESSION	ARI69918			
VERSION	ARI69918.1			
KEYWORDS	GI:17907877			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 387)			
AUTHORS	Anand, N.N., Barber, B.H., Cates, G.C., Caterini, J.E. and Klein, M.H.			
TITLE	Chimeric antibodies for delivery of antigens to selected cells of the immune system			
JOURNAL	Patent: US 6291208-A 1 18-SEP-2001;			
FEATURES	Location/Qualifiers			
source	1. .387			
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BASE COUNT	90 a 95 c 90 g 112 t			
ORIGIN				
Query Match	74.3%;	Score 323.4;	DB 6;	Length 387;
Best Local Similarity	90.6%;	Pred. No. 1.1e-86;		
Matches 345;	Conservative 0;	Mismatches 36;	Indels 0;	Gaps 0;

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KLEIKRAADAPTIVSIF"

BASE COUNT 87 a 86 c 83 g 98 t
ORIGIN

Query Match 72.9%; Score 317.2; DB 10; Length 354;
Best Local Similarity 94.8%; Pred. No. 8.3e-85;
Matches 328; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 69 GATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCAGTTG 128
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Db 69 TCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCCAGATGGAAC 128
QY 189 TATTAAACGCCCTGATCTAGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAAGGTTTCAG 248
Db 129 TATTAAACGCCCTGATCTAGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAAGGTTTCAG 188
QY 249 TGGCAGTAGGCTCTGGGTCAGATTATTTCTTCACCATCAGAGCCTTGAGTCTGAAGATT 308
Db 189 TGGCAGTAGGCTCTGGGTCAGATTATTTCTTCACCATCAGAGCCTTGAGTCTGAAGATT 248
QY 309 TGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGGAGGGGGACCAA 368
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QY 369 GCTGGAATAAAGCGGCTGATCTGCACCAACTGTATCCATCTTC 414
Db 309 GCTGGAATAAAGCGGCTGATCTGCACCAACTGTATCCATCTTC 354

Search completed: August 30, 2003, 18:45:52
Job time : 1975.09 secs

QY 1 ATGGGGGCCCTGCTCAGATCTCTGGGTTCTTGTCTCTTGTTCAGGTACCATGATGT 60
Db 7 ATGAGGGTTCTGCTCAGCTTTTGGCTTCTTGTCTCTGTTCCAGGTACCATGATGT 66
QY 61 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 120
Db 67 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 126
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Db 247 AGGTTCAAGTGGCAGTAGGCTCTGGGTCAGATTATTTCTTCACCATCAGCAGCCTTGAGTCT 306
QY 301 GAAGATTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG 360
Db 307 GAAGATTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG 366
QY 361 GGGACCAAGCTGGAAATAAAA 381
Db 367 GGGACCAAGCTGGAGCTGAAA 387

RESULT 15

AB089681
LOCUS Mus musculus mga5th102 mRNA for anti-glycyrrhetic acid antibody
DEFINITION GA102 light chain, partial cds.
ACCESSION AB089681
VERSION AB089681.1 GI:28316363

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 Tomioka, Y., Kato, Y., Tsuruta, L.R., Kudo, Y., Hishinuma, T., Itoh, K., Hirama, M., Goto, J. and Mizugaki, M.
TITLE Characterization of anti-glycyrrhetic acid monoclonal antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 354)
Tomioka, Y., Kato, Y., Tsuruta, L.R., Kudo, Y., Hishinuma, T., Hirama, M., Mizugaki, M. and Goto, J.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-2002) Yoshihisa Tomioka, Tohoku University Hospital, Department of Pharmaceutical Sciences, 1-1, Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8574, Japan
(E-mail: ytomio@kaes.rim.or.jp, Tel: 81-22-717-7543, Fax: 81-22-717-7545)

FEATURES

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/db_xref="taxon:10090"
/tissue_type="spleen"
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/db_xref="GI:28316364"

gene

CDS

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Result No.	Score	Query Match %	Length	DB	ID	Description
1	435	100.0	435	18	AAT85149	Murine monoclonal
2	435	100.0	435	20	AAV83772	Antibody 11D10 li
3	435	100.0	435	25	AAI51273	Mouse 11D10 anti
4	394.8	90.8	450	4	AA30165	Sequence encoding
5	384.6	88.4	407	21	AZ49548	Mouse light chain
6	323.4	74.3	387	18	AZ47851	Murine anti-human
7	323.4	74.3	387	24	AAQ32138	Murine 44H104 mab
8	309.4	71.1	739	14	AAQ46084	Sequence encoding

XX (KENT) UNIV KENTUCKY.
XX Chatterjee M, Chatterjee SK, Foon KA;
XX WPI; 1997-341690/31.
XX P-PSDB; AAW27119.
XX Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
XX against human milk fat globule disease associated tumours,
XX especially breast cancer
XX Claim 11; Page 94; 130pp; English.
XX This CDNA sequence encodes the light chain variable region VL
XX (AAW85149) of monoclonal anti-idiotypic antibody 11D10 produced by
XX hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
XX naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotypic
XX response. It elicits an immune response against a specific epitope
XX of a high mol.wt. mucin of human milk fat globule (HMFG). It
XX induces an immunological response to HMFG in mice, rabbits, monkeys
XX and patients with advanced HMFG-associated tumours. Pharmaceutical
XX compositions and vaccines comprising 11D10, 11D10 polypeptides
XX and/or 11D10 polynucleotides are claimed. Also claimed are
XX diagnostic kits and methods of using 11D10, 11D10 polypeptides
XX and/or 11D10 polynucleotides, including methods of treating HMFG-
XX associated tumours.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;

Query Match 100.0%; Score 435; DB 18; Length 435;
Best Local Similarity 100.0%; Pred. No. 6.8e-128;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGGCCCTGCTCAGATTCCTGGGTTCTTGTCTCTGTTCAGGTACAGATGT 60
DB 1 ATGGGGCCCTGCTCAGATTCCTGGGTTCTTGTCTCTGTTCAGGTACAGATGT 60
QY 61 GACATCCAGATGACCCAGTCTCCATCCTCTATCTGCTCTCTGCGACAAAGAGTCAGT 120
DB 61 GACATCCAGATGACCCAGTCTCCATCCTCTATCTGCTCTCTGCGACAAAGAGTCAGT 120
QY 121 CTCACCTGTGCGGCAAGTCAGGACATGTTAACTTACCTTACCTTACCTTACCTTACCTT 180
DB 121 CTCACCTGTGCGGCAAGTCAGGACATGTTAACTTACCTTACCTTACCTTACCTTACCTT 180
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DB 121 CTCACCTGTGCGGCAAGTCAGGACATGTTAACTTACCTTACCTTACCTTACCTTACCTT 180
QY 181 GATGGAACTATTAAACGCTGATCTACGCCACATCCAGTTTGTGTTGTCGCCAACA 240
DB 181 GATGGAACTATTAAACGCTGATCTACGCCACATCCAGTTTGTGTTGTCGCCAACA 240
QY 241 AGTTTCAGTGGCAGTGTGCTGGGTCAGATTAATCTCTCACCACATCAGCGCTTGTGCT 300
DB 241 AGTTTCAGTGGCAGTGTGCTGGGTCAGATTAATCTCTCACCACATCAGCGCTTGTGCT 300
QY 301 GAACATTTGTAGCCTATTACTGTCTACATATGCTAGTTCCTCGTACAGTTCGGAGGG 360
DB 301 GAACATTTGTAGCCTATTACTGTCTACATATGCTAGTTCCTCGTACAGTTCGGAGGG 360
QY 361 GGGACCAAGCTGGAATAAAGCGGCTGATCTGCACCAACTGATCTTCCCTTCCACCA 420
DB 361 GGGACCAAGCTGGAATAAAGCGGCTGATCTGCACCAACTGATCTTCCCTTCCACCA 420
QY 421 TCCAGTAAGCTTGGG 435
DB 421 TCCAGTAAGCTTGGG 435

RESULT 2
AAV83772
ID AAV83772 standard; cDNA; 435 BP.
XX
AC AAV83772;

XX 16-MAR-1999 (first entry)
XX Antibody 11D10 light chain variable region coding sequence.
XX Murine; mouse; antibody; light chain; variable region; anti-idiotypic; ss;
XX human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
XX Mus sp.
XX Key Location/Qualifiers
XX CDS 1..435
XX /tag= a
XX /product= "antibody 11D10 light chain variable region"
XX /transl_except= (pos:163..165, aa:Thr)
XX /note= "no stop codon is given at the 3' end of the
XX sequence"
XX sig_peptide 1..60
XX /tag= b
XX mat_peptide 61..435
XX /tag= c
XX WO9856419-A1.
XX 17-DEC-1998.
XX 12-JUN-1998; 98WO-US12250.
XX 11-JUN-1998; 98US-0096244.
XX 13-JUN-1997; 97US-0049540.
XX (KENT) UNIV KENTUCKY RES FOUND.
XX Chatterjee M, Foon KA;
XX WPI; 1999-060029/05.
XX P-PSDB; AAW87593.
XX Delaying development of, or treating, HMFG-associated tumours -
XX using anti-idiotypic antibody 11D10 raised against antibodies to
XX human milk fat globule protein
XX Disclosure; Fig 1; 54pp; English.
XX This sequence represents the coding sequence for the murine antibody
XX 11D10 light chain variable region. This anti-idiotypic antibody is used
XX to delay the development of, or treat, a human milk fat globule (HMFG)
XX associated tumour in an individual having low tumour burden.
XX The antibody 11D10 is used to prevent the recurrence of HMFG-associated
XX tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma,
XX especially for treating breast tumours.
XX Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;

Query Match 100.0%; Score 435; DB 20; Length 435;
Best Local Similarity 100.0%; Pred. No. 6.8e-128;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGGCCCTGCTCAGATTCCTGGGTTCTTGTCTCTGTTCAGGTACAGATGT 60
DB 1 ATGGGGCCCTGCTCAGATTCCTGGGTTCTTGTCTCTGTTCAGGTACAGATGT 60
QY 61 GACATCCAGATGACCCAGTCTCCATCCTCTATCTGCTCTCTGCGACAAAGAGTCAGT 120
DB 61 GACATCCAGATGACCCAGTCTCCATCCTCTATCTGCTCTCTGCGACAAAGAGTCAGT 120
QY 121 CTCACCTGTGCGGCAAGTCAGGACATGTTAACTTACCTTACCTTACCTTACCTTACCTT 180
DB 121 CTCACCTGTGCGGCAAGTCAGGACATGTTAACTTACCTTACCTTACCTTACCTTACCTT 180
QY 181 GATGGAACTATTAAACGCTGATCTACGCCACATCCAGTTTGTGTTGTCGCCAACA 240
DB 181 GATGGAACTATTAAACGCTGATCTACGCCACATCCAGTTTGTGTTGTCGCCAACA 240

QY 241 AGTTTCAGTGGCAGTAGTCTGGTCTAGATTTATCTCTCACCATCAGCAGCCTTGAGTCT 300
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 Db 241 AGTTTCAGTGGCAGTAGTCTGGTCTAGATTTATCTCTCACCATCAGCAGCCTTGAGTCT 300
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 QY 301 GAAGATTTGTAGCCTTATCTCTCTACAAATATGCTAGTCTCCGTACAGCTTCGGAGGG 360
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 Db 301 GAAGATTTGTAGCCTTATCTCTCTACAAATATGCTAGTCTCCGTACAGCTTCGGAGGG 360
 |||||
 QY 361 GGGACCAAGCTGGAATAAAACGGGTGATGCTGCACCAACTGTATCCATCTTCCACCA 420
 |||||
 Db 361 GGGACCAAGCTGGAATAAAACGGGTGATGCTGCACCAACTGTATCCATCTTCCACCA 420
 |||||
 QY 421 TCCAGTAAGCTTGGG 435
 |||||
 Db 421 TCCAGTAAGCTTGGG 435
 |||||

RESULT 3

AAL51273
 ID AAL51273 standard; cDNA; 435 BP.

XX AAL51273;

XX AC (first entry)

XX 20-MAR-2003 (first entry)

XX Mouse 11D10 antibody light chain variable region coding sequence.
 DE Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; HMFG;
 KW carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour;
 KW CEA-associated tumour; anti-idiotypic antibody.

XX Mus musculus.

OS Key Location/Qualifiers

FH 1..435

FT /*tag= a

FT /partial

FT /product= "Mouse 11D10 anti-idiotypic antibody light chain

FT variable region"

FT /note= "No stop codon is given"

FT sig_peptide 1..60

FT /*tag= b

FT mat_peptide 61..435

FT /*tag= c

XX WO200292012-A2.

XX PN 21-NOV-2002.

XX 17-MAY-2002; 2002WO-US15840.

XX PR 17-MAY-2001; 2001US-0861294.

XX (KENT) UNIV KENTUCKY RES FOUND.

XX Chatterjee M, Foon KA;

XX WPI; 2003-129216/12.

XX P-PSDB; AAO16292.

XX Use of anti-idiotypic antibodies for human milk fat globules (HMFG) - or

XX carcinoembryonic antigen (CEA)-associated tumor for delaying the

XX development of, or treating a HMFG- or CEA-associated tumor (e.g.

XX breast tumor) in humans

XX Disclosure; Fig 1; 98pp; English.

XX The invention comprises a method for delaying the development of, or

XX treating a tumour that is associated with human milk fat globules (HMFG)

XX or carcinoembryonic antigen (CEA). The method of the invention involves

XX administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an

XX anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for

CC delaying the development, of or treating HMFG/CEA-associated tumours. The
 CC present cDNA sequence encodes the light chain variable region of the
 CC mouse 11D10 anti-idiotypic antibody.

XX Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;

XX Query Match 100.0%; Score 435; DB 25; Length 435;

XX Best Local Similarity 100.0%; Pred. No. 6.8e-128;

XX Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGCCCCCTGCTCAGATTTCTGGGTTCTTGGTCTTGTGCTTGTTCAGGTACACAGTGT 60

Db 1 ATGGGGCCCCCTGCTCAGATTTCTGGGTTCTTGGTCTTGTGCTTGTTCAGGTACACAGTGT 60

QY 61 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCCTCTCTGGGACAAAGAGTCAGT 120

Db 61 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCCTCTCTGGGACAAAGAGTCAGT 120

QY 121 CTCACCTTGTGGGCAAGTCTAGGACATTTGGTATTAACTTACATTTAGGCTTGTGCTTGTTCAGGACCA 180

Db 121 CTCACCTTGTGGGCAAGTCTAGGACATTTGGTATTAACTTACATTTAGGCTTGTGCTTGTTCAGGACCA 180

QY 181 GATGGAACTATTAAACGCTGATCTAGCCACATCCAGTTTGGTCTTGTGCTTGTTCAGGACCA 240

Db 181 GATGGAACTATTAAACGCTGATCTAGCCACATCCAGTTTGGTCTTGTGCTTGTTCAGGACCA 240

QY 241 AGTTCAGTGGCAGTAGTCTGGTCTGAGATTTATCTCTCACCATCAGCAGCCTTGAGTCT 300

Db 241 AGTTCAGTGGCAGTAGTCTGGTCTGAGATTTATCTCTCACCATCAGCAGCCTTGAGTCT 300

QY 301 GAAGATTTGTAGCCTTATCTCTCTACAAATATGCTAGTCTCCGTACAGCTTCGGAGGG 360

Db 301 GAAGATTTGTAGCCTTATCTCTCTACAAATATGCTAGTCTCCGTACAGCTTCGGAGGG 360

QY 361 GGGACCAAGCTGGAATAAAACGGGTGATGCTGCACCAACTGTATCCATCTTCCACCA 420

Db 361 GGGACCAAGCTGGAATAAAACGGGTGATGCTGCACCAACTGTATCCATCTTCCACCA 420

QY 421 TCCAGTAAGCTTGGG 435

Db 421 TCCAGTAAGCTTGGG 435

RESULT 4

AAN30165

ID AAN30165 standard; DNA; 450 BP.

XX AAN30165;

XX 25-MAY-1992 (first entry)

XX Sequence encoding the leader, variable region and first 16 AAs of

XX the constant region of the kappa-chain (light chain) of MOPC41.

XX Diagnosis; therapy; immunoglobulin; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 13..78

XX /*tag= a

XX /product= leader

XX CDS 79..402

XX /*tag= b

XX /product= variable region

XX FT 403..450

XX /*tag= c

XX /product= constant region

XX EP88994-A.

XX 21-SEP-1983.

XX PD

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QY	301	GAAGATTTGTAGCCTATTACTGTCTCAATATGCTAGTTCTCGGTACAGTTCGGAGGG	360
Db	301	GAAGATTTGTAGCCTATTACTGTCTCAATATGCTAGTTCTCGGTACAGTTCGGAGGG	360
QY	361	GGGACCAAGCTGGAAATAAAGGGCTGTAGTCTGCACCAACTGTATC	407
Db	361	GGGACCAAGCTGGCAATAAAGGGCTGTAGTCTGCACCAACTGTATC	407

RESULT. 6

RESOLUT	
AAAT77851	
ID	AAAT77851 standard; cDNA; 387 BP.
XX	
XX	AAAT77851;
XX	
DT	03-NOV-1997 (first entry)
XX	
DE	Murine anti-human class II monoclonal antibody 44H104 VL chain cDNA
XX	
KW	Antibody; light chain; variable region; hybridoma cell line 44H104;
KW	immune response; enhance; stimulate; vaccine; immunodiagnosis;
KW	antigen delivery; ss.
XX	
OS	Mus musculus.
XX	
Key	Location/Qualifiers
CDS	1..387
FT	/*tag= a
FT	/note= "Encodes 44H104 light chain variable region,
FT	including secretion signal; termination
FT	codon not given"
FT	

WO9640941-A1.

19-DEC-1996.

07-JUN-1996: 96WO-CA00400.

07-JUN-1995; 95US-0483576;

(CONN-) CONNAUGHT LAB LTD.

Anand NN, Barber BH, Caterini JE, Cates GC, Klejn MH:

WPI: 1997-077271/07.

P-PSDB; AAW22537

Recombinant conjugate antibody mol., modified for delivering an antigen - elicits enhanced immune response without the use of adjuvant to generate antibodies which are useful in vaccines or immuno-diagnosis

Example 1: Fig 1A: 64pp: English.

Novel recombinant conjugate antibody molecules comprise a monoclonal antibody specific for a surface structure of antigen presenting cells (APC), genetically modified to contain at least one antigen exclusively at one or more presselected sites. The conjugate is capable of delivering the antigen to APC and eliciting an immune response to the antigen. The new conjugates are useful as vaccines and are able to elicit an enhanced immune response without the use of an adjuvant. In a specific example, a conjugate was constructed using the murine anti-human class II monoclonal antibody secreted by hybridoma 44H104. The peptide CLTB36 was chosen as antigen; it consists of a tandemly linked T and B cell epitope derived from HIV MN strain. The present sequence encodes the light chain variable region which was PCR amplified from 44H104 and used in the preparation of a conjugate with antigen CLTB36.


```

XX AC AAT36880;
XX
XX 25-MAR-2003 (updated)
XX 29-OCT-1996 (first entry)
XX
XX 520C9 anti-c-erbB-2 two single chain Fv construct.
XX
XX 520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sfv;
XX construct; polypeptide linker; C-terminal amino acid sequence;
XX in vivo imaging; drug targeting experiment; homodimer;
XX increased; binding avidity; tissue retention time; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..732
XX /*tag= a
XX /note= "START codon absent"
XX
XX US5534254-A.
XX
XX 09-JUL-1996.
XX
XX 07-OCT-1993; 93US-0133804.
XX
XX 07-OCT-1993; 93US-0133804.
XX 06-FEB-1992; 92US-0831967.
XX
XX (CHIR ) CHIRON CORP.
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX Houston LL, Huston JS, Oppermann H, Ring DB;
XX
XX WPI: 1996-333194/33.
XX P-PSDB; AAW02280.
XX
XX Compens. contg. antigen-targeting antibody fragment constructs -
XX comprising dimer of single-chain Fv fragments
XX
XX Example 1; Columns 33-36; 30pp; English.
XX
XX Variable heavy (VH) and variable light (VL) genes were cloned from
XX a 520C9 hybridoma cDNA library, using probes directed toward the
XX antibody constant and joining regions. A two single chain Fv (sfv)
XX gene was constructed by connecting the VH and VL genes with a
XX Ser rich polypeptide linker. The resulting 520C9 two sfv gene, the
XX present sequence, was inserted into an expression vector,
XX transformed into E. coli, and protein expression induced by the
XX addn. of IPTG to the culture medium.
XX A compsn. comprising a carrier and the 2 sfv protein prod. can be
XX used for in vivo imaging, and drug targeting experiments. The
XX 2 sfv protein prod. is a homodimer, in which both fragments target
XX the same antigen, therefore giving greater binding avidity and
XX longer tissue retention times, compared to individual sfv protein
XX prod. fragments.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 739 BP; 188 A; 177 C; 181 G; 193 T; 0 other;
XX
Query Match 71.13; Score 309.4; DB 17; Length 739;
Best Local Similarity 95.28; Pred. No. 6.3e-88;
Matches 319; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 56 GATGTGATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGCGACAAAGAG 115
DB 395 GATCCGATATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGCGACAAAGAG 454
QY 116 TACGTCTCTACTGTGCGGCGAAGTCAGGACATTTGATTAACATTTGCTTCAGCAGG 175
DB 455 TCAGTCTCTACTGTGCGGCGAAGTCAGGACATTTGATTAACATTTGCTTCAGCAGG 514
QY 176 AACGAGATGGAACATTTAAAGCGCTGATCTACGCCACATCCAGTTTGGTCTGGTCTCC 235

```

```

Db 515 AACGAGATGGAACATTTAAAGCGCTGATCTACGCCACATCCAGTTTGGTCTCC 574
QY 236 CCAAAAGGTTTCAGTGGCAGTAGTCTGGGTTCAGATTATTCTCTCACCATCAGCAGCTTG 295
Db 575 CCAAAAGGTTTCAGTGGCAGTCGGTCTGGGTTCAGATTATTCTCTCACCATCAGTAGCCTTG 634
QY 296 AGTCTGAAGATTTTGTAGCCCTATTACTGTCTACAAATATGCTAGTCTCCGTCACACGTTTCG 355
Db 635 AGTCTGAAGATTTTGTAGTCTATTACTGTCTACAAATATGCTAGTCTCCGTCACACGTTTCG 694
QY 356 GAGGGGGGACCAAGCTGGAATAAAACGGGCTGAT 390
Db 695 GAGGGGGGACCAAGCTGGAATAAAACGGGCTGAT 729

RESULT 10
AAV21798
ID AAV21798 standard; cDNA; 739 BP.
XX
XX AAV21798;
XX
XX 16-JUL-1998 (first entry)
XX
XX 520C9 anti-c-erbB-2 sfv' dimeric construct gene sequence.
XX
XX Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer;
XX c-erbB-2; tumour; diagnosis; ss.
XX
XX Synthetic.
XX OS Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..732
XX /*tag= a
XX /product= "520C9 sfv' polypeptide"
XX
XX US5753204-A.
XX
XX 19-MAY-1998.
XX
XX 05-JUN-1995; 95US-0461838.
XX
XX 07-OCT-1993; 93US-0133804.
XX 06-FEB-1992; 92US-0831967.
XX 05-JUN-1995; 95US-0461838.
XX
XX (CHIR ) CHIRON CORP.
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX Houston LL, Huston JS, Oppermann H, Ring DB;
XX
XX WPI: 1998-311318/27.
XX P-PSDB; AAW53170.
XX
XX Imaging of antigens in vivo - using dimers of single-chain antibody
XX Fv fragments
XX
XX Example 1; Columns 33-36; 30pp; English.
XX
XX This is the nucleotide sequence of a 520C9 sfv' (single chain Fv)
XX construct. This was constructed by connecting the VH and VL genes with
XX a DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal
XX antibody useful in targeting c-erbB-2 antigen. This dimeric construct
XX can be used in the methods of invention of imaging a preselected antigen
XX expressed in a mammal. The methods are used in magnetic resonance imaging
XX of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic
XX constructs have enhanced properties as in vivo targeting agents in
XX comparison with intact monoclonal antibodies or their Fab fragments. The
XX dimeric constructs permit the in vivo targeting of an epitope on an
XX antigen with greater apparent avidity, including greater tumour
XX specificity, tumour localisation and tumour retention properties than
XX that of the Fab fragment having the same CDRs as the construct.

```

```
XX SQ Sequence 739 BP; 188 A; 177 C; 181 G; 193 T; 0 other;
Query Match 71.1%; Score 309.4; DB 19; Length 739;
Best Local Similarity 95.2%; Pred. No. 6.3e-88;
Matches 319; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 56 GATGTGACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGAG 115
Db 395 GATCCGATATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGAG 454
QY 116 TCAGTCTCACTTGTGGGCAAGTCAGACATTTGGTATTAACTTACATTGGCTTCAGCAGG 175
Db 455 TCAGTCTCACTTGTGGGCAAGTCAGACATTTGGTATTAACTTACATTGGCTTCAGCAGG 514
QY 176 AACCATGATGAACCTATTAAACGCTGATCTACGCCACATCCAGTTTAGTTCTGGTCTCC 235
Db 515 AACCATGATGAACCTATTAAACGCTGATCTACGCCACATCCAGTTTAGTTCTGGTCTCC 574
QY 236 CCAAAAGGTTCAAGTGGCAGTAGTCTCGGGTCAGATTATTCTTCCATCATCAGCAGCCTTG 295
Db 575 CCAAAAGGTTCAAGTGGCAGTAGTCTCGGGTCAGATTATTCTTCCATCATCAGTACGCTTG 634
QY 296 AGTCTGAAGATTTGTAGCTTATTAACGCTGATCTACGCCACATCCAGTTTAGTTCTGGTCTCC 355
Db 635 AGTCTGAAGATTTGTAGCTTATTAACGCTGATCTACGCCACATCCAGTTTAGTTCTGGTCTCC 694
QY 356 GAGGGGGGACCAAGCTGGAATAAAACGGGCTGAT 390
Db 695 GAGGGGGGACCAAGCTGGAATAAAACGGGCTGAT 729
RESULT 11
AAV63399
ID AAV63399 standard; cDNA; 739 BP.
AC AAV63399;
XX
XX 28-JAN-1999 (first entry)
XX 520C9 sfv DNA sequence.
XX
XX 520C9 sfv; antigen; tumour cell; antibody 520C9;
KW targeted delivery; antigen-expressing cell; ss.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 1..732
XX /tag= a
XX /product= 520C9 sfv
XX
XX US5837846-A.
XX
XX 17-NOV-1998.
XX
XX 05-JUN-1995; 95US-0461386.
XX
XX 07-OCT-1993; 93US-0133804.
XX 06-FEB-1992; 92US-0831967.
XX 05-JUN-1995; 95US-0461386.
XX
XX (CHIR ) CHIRON CORP.
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX Houston LL, Huston JS, Oppermann H, Ring DB;
XX
XX WPI; 1999-023541/02.
XX P-PSDB; AAW80424.
XX
XX Nucleic acid encoding single-chain Fv fragment specific for antigens
XX - and having C-terminal tail for crosslinking to form dimer with
XX improved pharmacokinetic properties, used to deliver drugs and
PT
```

```
PT imaging agents, especially to tumours
XX
XX Example 1; Columns 33-36; 29pp; English.
XX
XX The present sequence encodes an antibody 520C9 sfv. Variable heavy
CC and light sequences of antibody 7520C9 are connected, together with a
CC serine linker, to produce the present single chain Fv gene. The present
CC sequence exemplifies the invention. Dimers of the single chain Fv are
CC used for targeted delivery of drugs or imaging agents (e.g. cytotoxins,
CC prodrugs or 99m-technetium) to antigen-expressing cells, particularly
CC for treatment or diagnosis of tumours (especially of ovary or breast).
XX
XX Sequence 739 BP; 188 A; 177 C; 181 G; 193 T; 0 other;
SQ
Query Match 71.1%; Score 309.4; DB 20; Length 739;
Best Local Similarity 95.2%; Pred. No. 6.3e-88;
Matches 319; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 56 GATGTGACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGAG 115
Db 395 GATCCGATATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGAG 454
QY 116 TCAGTCTCACTTGTGGGCAAGTCAGACATTTGGTATTAACTTACATTGGCTTCAGCAGG 175
Db 455 TCAGTCTCACTTGTGGGCAAGTCAGACATTTGGTATTAACTTACATTGGCTTCAGCAGG 514
QY 176 AACCATGATGAACCTATTAAACGCTGATCTACGCCACATCCAGTTTAGTTCTGGTCTCC 235
Db 515 AACCATGATGAACCTATTAAACGCTGATCTACGCCACATCCAGTTTAGTTCTGGTCTCC 574
QY 236 CCAAAAGGTTCAAGTGGCAGTAGTCTCGGGTCAGATTATTCTTCCATCATCAGCAGCCTTG 295
Db 575 CCAAAAGGTTCAAGTGGCAGTAGTCTCGGGTCAGATTATTCTTCCATCATCAGTACGCTTG 634
QY 296 AGTCTGAAGATTTGTAGCTTATTAACGCTGATCTACGCCACATCCAGTTTAGTTCTGGTCTCC 355
Db 635 AGTCTGAAGATTTGTAGCTTATTAACGCTGATCTACGCCACATCCAGTTTAGTTCTGGTCTCC 694
QY 356 GAGGGGGGACCAAGCTGGAATAAAACGGGCTGAT 390
Db 695 GAGGGGGGACCAAGCTGGAATAAAACGGGCTGAT 729
RESULT 12
AAZ49543
ID AAZ49543 standard; cDNA; 729 BP.
XX
XX AAZ49543;
XX
XX 04-APR-2000 (first entry)
XX
XX pEscFv#125-2H.HT recombinant cDNA.
XX
XX pEscFv#125-2H.HT recombinant cDNA; EscFv#125-2H.HT; interleukin-18;
KW immunopathies; inflammatory disorder; autoimmune disease; mouse;
KW anti-allergic; anti-inflammatory; immunosuppressive; hematopoietic;
KW leukocytopenic; antialgic; antipyretic; ss.
XX
XX Mus musculus.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX mat_peptide 1..711
XX /tag= a
XX /note= "single chain variable region fragment
XX neutralising IL-18"
XX
XX mat_peptide 1..339
XX /tag= b
XX /note= "Encodes heavy chain variable region"
XX
XX mat_peptide 391..711
XX /tag= c
XX /note= "Encodes light chain variable region"
XX
```



```

Db      559 GGTGTCCTCCCAAGAGGTTTCAGTGGCAGTAGGTCTGGTCCAGATTATCTCCACCATCAGC 618
Qy      289 AGCTTCAGTCTGAAGATTTTGTAGCCATTACTGTCTACAATATGCTAGTCTCCGTAC 348
Db      619 AGCTTCAGTCTGAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTCTCCGTAC 678
Qy      349 ACGTTCGGAGGGGGACCAAGCTGGAATAAAA 381
Db      679 ACGTTCGGAGGGGGACCAAGCTGGCAATAAAA 711

RESULT 14
AAZ49534
ID      AAZ49534 standard; cDNA; 324 BP.
XX
AC      AAZ49534;
XX
DT      04-APR-2000 (first entry)
XX
DE      Mouse anti-IL-18 antibody VL encoding cDNA from hybridoma #125-2H.
XX
KW      Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
KW      hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18;
KW      antiinflammatory; immunosuppressive; leucocytopenic; antiallgic;
KW      antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
KW      immunopathy; inflammatory disorder; immunoreaction; ss.
XX
OS      Mus musculus.
XX
FH      Key Location/Qualifiers
FT      mat_peptide 1..324
FT      /*tag= a
FT      /label= Anti-IL-18_antibody_light_chain_variable_region
XX
PN      EP974600-A2.
XX
PD      26-JAN-2000.
XX
PF      24-JUN-1999; 99EP-0304977.
XX
PR      24-JUN-1998; 98JP-0177580.
PR      12-OCT-1998; 98JP-0289044.
PR      22-DEC-1998; 98JP-0365023.
XX
PA      (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI      Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX
WPI; 2000-118341/11.
DR      P-PSDB; AAY44587.
XX
PT      New artificially produced peptide for neutralizing biological activity
PT      of interleukin-18, useful for treating and preventing immunopathies,
PT      inflammatory disorders and autoimmune diseases -
XX
PS      Claim 11; Page 21; 36pp; English.
XX
CC      The present cDNA sequence derived from hybridoma #125-2H, encodes mouse
CC      anti-interleukin-18 antibody light chain variable region (VL). It can be
CC      used in the production of recombinant monoclonal antibody #125-2HmAb,
CC      which is capable of neutralising biological activities of interleukin-18.
CC      The antibody has antinflammatory, immunosuppressive, leucocytopenic,
CC      antiallgic, antipyretic, antiallergic and hepatotropic activity and can be
CC      used for prevention and treatment of autoimmune diseases, immunopathies
CC      and inflammatory disorders caused by excessive immunoreaction.
XX
SQ      Sequence 324 BP; 83 A; 78 C; 76 G; 87 T; 0 other;
Query Match 70.4%; Score 306.4; DB 21; Length 324;
Best Local Similarity 96.6%; Pred. No. 4.1e-87;
Matches 313; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy      61 GACATCCAGATGACCCAGTCTCCATCTCTATCTCTCTGTCGACAAAGAGTCAGT 120
Db      1 GACATCCAGATGACCCAGTCTCCATCTCTATCTCTCTGTCGACAAAGAGTCAGT 60
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Db      61 CTCACCTTGTGCGGCAAGTCAGGACATTTGGTATTAACTTACATTGGCTTCAGCAGAACCA 120
Qy      181 GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGTCTTGTTGCCCCAAA 240
Db      121 GATGGAACTTTTAAACGCCTGATCTACGCCACATCCAGTTTAGTCTTGTTGCCCCAG 180
Qy      241 AGTTTCAGTGGCAGTAGTCTGGTCCAGATTATTTCTCCACCATCAGCAGCCTTGAGTCT 300
Db      181 AGTTTCAGTGGCAGTAGTCTGGTCCAGATTATTTCTCCACCATCAGCAGCCTTGAGTCT 240
Qy      301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTCTCGGTACAGTTCCGGAGGG 360
Db      241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTCTCGGTACAGTTCCGGAGGG 300
Qy      361 GGGACCAAGCTGGAATAAAAACGG 384
Db      301 GGGACCAAGCTGGCAATAAAAACGG 324

RESULT 15
AAQ46086
ID      AAQ46086 standard; cDNA; 1605 BP.
XX
AC      AAQ46086;
XX
DT      25-MAR-2003 (updated)
DT      07-FEB-1994 (first entry)
XX
DE      Sequence encoding G-FIT.
XX
KW      Tumour antigen; c-erbB-2; G-FIT; ss.
XX
OS      Synthetic.
XX
FH      Key Location/Qualifiers
FT      CDS 1..1605
FT      /*tag= a
XX
PN      WO9316185-A2.
XX
PD      19-AUG-1993.
XX
PF      05-FEB-1993; 93WO-US01055.
XX
PR      06-FEB-1992; 92US-0831967.
XX
PA      (CETU ) CETUS ONCOLOGY CORP.
PA      (CREA-) CREATIVE BIOMOLECULES INC.
XX
PI      Houston LL, Huston JS, Oppermann H, Ring DB;
XX
WPI; 1993-272889/34.
DR      P-PSDB; AAR39571.
XX
PT      New single chain Fv polypeptide binding to C-erbB-2 tumour
PT      antigen - for imaging or treating breast or ovarian cancer etc.
XX
PS      Example; pages 65-68; 87pp; English.
XX
CC      c-erbB-2 refers to a protein antigen expressed on the surface of
CC      tumour cells, such as breast and ovarian tumour cells, which is an
CC      approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
CC      pt. of about 5.3 (see AAQ46083, AAR39568).
CC      (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ      Sequence 1605 BP; 434 A; 354 C; 373 G; 444 T; 0 other;

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Query Match 69.4%; Score 302; DB 14; Length 1605;
Best Local Similarity 92.7%; Pred. No. 1.9e-85;
Matches 317; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy	49	GGTACCAGATGTGACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGA	108
Db	1261	GGCGGGGATCGGATATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGA	1320
Qy	109	CAAAGAGTCAGTCTCACTTCTCGGCAAGTCAGGACATTTGATTAACATTACATTGGCTT	168
Db	1321	GAAGAGTCAGTCTCACTTCTCGGCAAGTCAGGACATTTGATTAACATTACATTGGCTT	1380
Qy	169	CAGCAGAACCCAGATGGAATATTAAACGCTGATCTACGCCACATCCAGTTTAGGTCT	228
Db	1381	TCACAGAACCCAGATGGAATATTAAACGCTGATCTACGCCACATCCAGTTTAGGTCT	1440
Qy	229	GGTGTCCTCCAAAGGTTCACTGGCAGTAGTCTGGGTCAGATTATTCTCACCACAGC	288
Db	1441	GGTGTCCTCCAAAGGTTCACTGGCAGTAGTCTGGGTCAGATTATTCTCACCACAGT	1500
Qy	289	AGCTTGAGTCTGAAGATTTTGTAGCTTATTACTGTCTACAATATGCTAGTTCTCCGTAC	348
Db	1501	AGCTTGAGTCTGAAGATTTTGTAGCTTATTACTGTCTACAATATGCTAGTTCTCCGTAC	1560
Qy	349	ACGTTGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGAT	390
Db	1561	ACGTTGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGAT	1602

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Job time : 192.798 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2003, 17:29:10 ; Search time 159,241 Seconds
(without alignments)
6267.222 Million cell updates/sec

Title: US-08-836-455-1
Perfect score: 435
Sequence: 1 ATGGGGGCCCTGCTCAGAT.....CACCATCAGTAAGCTTGGG 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1533700 seqs, 1147125425 residues

Total number of hits satisfying chosen parameters: 3067400

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	435	9	US-09-861-294-1
2	435	100.0	435	12	US-10-367-506-1
3	384.6	88.4	407	10	US-09-924-099-27
4	372	85.5	402	8	US-08-779-784-5
5	329.6	75.8	390	12	US-10-268-883-10
6	323.4	74.3	387	9	US-09-007-093-1
7	323.2	74.3	351	8	US-08-779-784-17
8	322.6	74.2	351	8	US-08-779-784-16
9	309.4	71.1	739	10	US-09-887-853-5
10	308.4	70.9	729	10	US-09-924-099-20
11	307.4	70.7	711	10	US-09-924-099-19
12	306.4	70.4	324	9	US-09-924-099-11
13	267.6	61.5	447	9	US-09-797-481-1
14	267.6	61.5	447	9	US-09-844-736-3
15	267.6	61.5	447	14	US-10-162-396-3
16	266	61.1	447	9	US-09-861-294-19

17	266	61.1	447	12	US-10-367-506-19	Sequence 19, Appl
18	265.2	61.0	490	11	US-09-918-995-37859	Sequence 37859, A
19	263.6	60.6	714	14	US-10-153-382-18	Sequence 18, Appl
20	261.6	60.1	520	10	US-09-878-178-1210	Sequence 1210, Ap
21	261.6	60.1	520	13	US-10-046-935-1210	Sequence 1210, Ap
22	261.6	60.1	520	14	US-10-146-935-1210	Sequence 1210, Ap
23	258.8	59.5	514	14	US-10-066-543-2025	Sequence 2025, Ap
24	258.8	59.5	537	14	US-10-066-543-186	Sequence 186, App
25	258.8	59.5	974	10	US-09-859-053-29	Sequence 29, Appl
26	258.6	59.4	393	8	US-08-779-784-20	Sequence 20, Appl
27	257.2	59.1	729	14	US-10-216-484-125	Sequence 125, App
28	252.2	58.0	737	10	US-09-919-344-7	Sequence 7, Appl
29	250.6	57.6	321	14	US-10-056-794-16	Sequence 16, Appl
30	249.6	57.4	634	14	US-10-158-646-55	Sequence 55, Appl
31	248	57.0	408	9	US-09-764-304-9	Sequence 9, Appl
32	248	57.0	408	14	US-10-265-713-9	Sequence 9, Appl
33	247.6	56.9	705	9	US-09-740-002-16	Sequence 16, Appl
34	246.4	56.6	408	14	US-10-195-752-19	GENERAL INFORMA
35	246	56.6	536	14	US-10-198-846-8024	Sequence 8024, Ap
36	246	56.6	698	10	US-09-844-684-11	Sequence 11, Appl
37	246	56.6	698	14	US-10-040-244-11	Sequence 11, Appl
38	246	56.6	728	10	US-09-844-684-15	Sequence 15, Appl
39	246	56.6	728	14	US-10-040-244-15	Sequence 15, Appl
40	246	56.6	819	14	US-10-158-646-65	Sequence 65, Appl
41	244.4	56.2	716	10	US-09-844-684-13	Sequence 13, Appl
42	244.4	56.2	716	14	US-10-040-244-13	Sequence 13, Appl
43	244	56.1	990	9	US-09-800-729-79	Sequence 79, Appl
44	243.4	56.0	381	12	US-10-268-883-4	Sequence 4, Appl
45	241.8	55.6	381	14	US-10-084-139-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-861-294-1
; Sequence 1, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMGF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(435)
; NAME/KEY: sig_peptide
; LOCATION: (1)...(60)
; NAME/KEY: mat_peptide
; LOCATION: (61)...(435)
US-09-861-294-1

Query Match 100.0%; Score 435; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.7e-136;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGGGCCCCGCTCAGATCTTGGTCTTGTGCTCTGTTCAGGTACCATGT 60
|||||
Db 1 ATGGGGCCCCGCTCAGATCTTGGTCTTGTGCTCTGTTCAGGTACCATGT 60
|||||

Qy	61	GACATCCAGATGACCCAGTCTCCATCTCTCTTATCTGCCCTCTCTGGGACAAAGATCTAGT	120
Db	61	GACATCCAGATGACCCAGTCTCCATCTCTCTTATCTGCCCTCTCTGGGACAAAGATCTAGT	120
Qy	121	CTCAGTCTCTGGGCAAGTCTCAGGACATTTGGTATTAACTTACATTTGGCTTTCAGCAGGACCA	180
Db	121	CTCAGTCTCTGGGCAAGTCTCAGGACATTTGGTATTAACTTACATTTGGCTTTCAGCAGGACCA	180
Qy	181	GATGGAACATTTAAACGGCTGATCTACGCCACATCCAGTTTAGTTTCTGGTGTCCCAAA	240
Db	181	GATGGAACATTTAAACGGCTGATCTACGCCACATCCAGTTTAGTTTCTGGTGTCCCAAA	240
Qy	241	AGGTTTCAGTGGCAGTAGGCTCTGGGTCAGATTTATTTCTCTACCATCAGCAGCCTTGAGTCT	300
Db	241	AGGTTTCAGTGGCAGTAGGCTCTGGGTCAGATTTATTTCTCTACCATCAGCAGCCTTGAGTCT	300
Qy	301	GAAGATTTGTAGCCATTATTTACTGCTACATATGCTAGTTCTCCGTACACGTTCCGAGGG	360
Db	301	GAAGATTTGTAGCCATTATTTACTGCTACATATGCTAGTTCTCCGTACACGTTCCGAGGG	360
Qy	361	GGGACCAAGCTGGAAATAAAAGGGCTGATGCTGCACCAACTGTATCCCATCTTCCCAACCA	420
Db	361	GGGACCAAGCTGGAAATAAAAGGGCTGATGCTGCACCAACTGTATCCCATCTTCCCAACCA	420
Qy	421	TCCAGTAAGCTTTGGG	435
Db	421	TCCAGTAAGCTTTGGG	435

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RESULT 2
US-10-367-506-1
; Sequence 1, Application US/10367506
; Publication NO. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMGF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(435)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(60)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (61)...(435)
; US-10-367-506-1

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Query Match	100.0%	Score 435;	DB 12;	Length 435;
Best Local Similarity	100.0%;	Pred. No. 2.7e-136;		
Matches 435;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGGGGGGCCCTGCTCAGATTC	TGGGGTCTCTGTGCTTGTTC	CCAGGTACCCAGATG	60
Db	1	ATGGGGGGCCCTGCTCAGATTC	TGGGGTCTCTGTGCTTGTTC	CCAGGTACCCAGATG	60
QY	61	GACATCCAGATGACCCAGTC	CTCCATCTCTCTATCTGCC	CTCTGGGACAAAGAGTCAGT	120

Db	61		GACATCCAGATGACCAGCTCCATCCCTCCCTATCTGCCCTCTGGGACAAAGAGTCAGT	120
Qy	121		CTCAGCTTGTGGGCAAGTCAGGACATTGGTATTAACTTACATTTGGCTTCAGCAGGAACCA	180
Db	121		CTCAGCTTGTGGGCAAGTCAGGACATTGGTATTAACTTACATTTGGCTTCAGCAGGAACCA	180
Qy	181		GATGGAACCTATTAAACGCCTGATCTACGCCACATCCAGTTTGGTGTGCCCAAA	240
Db	181		GATGGAACCTATTAAACGCCTGATCTACGCCACATCCAGTTTGGTGTGCCCAAA	240
Qy	241		AGGTTTCAGTGGCAGTAGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCCTTGAGTCT	300
Db	241		AGGTTTCAGTGGCAGTAGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCCTTGAGTCT	300
Qy	301		GAAGATTTTGTAGCCTATTACTTGCTCAATATGCTAGTTCTCCGTACAGCTTCGGAGGG	360
Db	301		GAAGATTTTGTAGCCTATTACTTGCTCAATATGCTAGTTCTCCGTACAGCTTCGGAGGG	360
Qy	361		GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA	420
Db	361		GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA	420
Qy	421		TCCAGTAAGCTTGGG	435
Db	421		TCCAGTAAGCTTGGG	435

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RESULT 3
US-09-924-099-27
; Sequence 27, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takao
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KORIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 27

```

```

? SEQ ID NO 27
? LENGTH: 407
? TYPE: DNA
? ORGANISM: Mus musculus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)...(407)
? NAME/KEY: sig peptide
? LOCATION: (1)...(60)
? US-09-924-099-27

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Query Match 88.4%; Score 384.6; DB 10; Length 407;
Best Local Similarity 96.6%; Pred. No. 2.6e-119;
Matches 393; Conservative 0; Mismatches 14; Indels 0; Gaps 0

Qy	1	ATGGGGGGCCCTGCCTCAGATTCCTTGGGTTCTTGTGCTTGTGTTCCAGGTACCAATGT	60
Db	1	ATGGGGGGCCCTGCCTCAGATTTTGGGTTCTTGTGCTTGTGTTCCAGGTACCAATGT	60
Qy	61	GACATCCAGATGACCCGCTCCATCTCCTTATCTGCCTCTCTGGGACAAAGATCAGT	120
Db	61	GACATCCAGATGACCCGCTCCATCTCCTTATCTGCCTCTCTGGGAAAGAGATCAGT	120
Qy	121	CTCACTTGTTCGGGCAAGTCAGGACATTTGGTATTAACTTACATTGGCTTCAGCAGGAACCA	180

Db 187 GATGGAACATATAAACCGCTGATCTACGCCCATCCACTTTAGATTCTGGTGTCCTCCAAAA 246
Qy 241 AGGTTTCAGTCAGTAGTCTGGCTCAGATTATCTCTCACCATCAGCAGCTTTGAGTCT 300
Db 247 AGGTTTCAGTCAGTAGTCTGGCTCAGATTATCTCTCACCATCAGCAGCTTTGAGTCT 306
Qy 301 GAAGATTTTGTAGCTATTACTGCTCTACAATATGCTAGTCTTCGGTACACGTTCCGAGGG 360
Db 307 GAAGATTTTGCAGACTATTACTGCTCTACAATATGCTAGTCTTCGGTACACGTTCCGAGGG 366
Qy 361 GGGACCAAGCTGGAATAAACGG 384
Db 367 GGCACCAAGCTGGAATAAACGG 390

RESULT 6

US-09-007-093-1
; Sequence 1, Application US/09007093
; Patent No. US2002025315A1
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,093
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/483,576
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-765
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-007-093-1

Query Match 74.3%; Score 323.4; DB 9; Length 387;
Best Local Similarity 90.6%; Pred. No. 1.1e-96;
Matches 345; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1 ATGGGGCCCTGCTCAGATCTGGCTTCTTGTCTCTTGTTCAGGTACAGATGT 60
Db 7 ATGAGGGTCTCTGCTCAGTTTGTGGCTTCTTGTCTCTTGTTCAGGTACAGATGT 66
Qy 61 GACATCCAGATGACCCAGTCTCCATCTCTATCTGCTCTCTGGGACAAAGAGTCACT 120
Db 67 GACATCCAGATGACCCAGTCTCCATCTCTATCTGCTCTCTGGGACAAAGAGTCACT 126

Qy 121 CTCACTTCTCGGCAAGTCAGGACATTTGGTATTAACTTACATTGCTTCAGCAGAACCA 180
Db 127 CTCACCTTGTGCGGCAAGTCAGGAAATAGTGGTTACTTAACTTGCCTTCAGCAGAACCA 186
Qy 181 GATGGAACATATAAACCGCTGATCTACGCCCATCCAGTTTATGTTCTGGTGTCTCCAAA 240
Db 187 GATGGAACATATAAACCGCTGATCTACGCCCATCCAGTTTATGTTCTGGTGTCTCCAAA 246
Qy 241 AGGTTTCAGTCAGTAGTCTGGCTCAGATTATCTCTCACCATCAGCAGCTTTGAGTCT 300
Db 247 AGGTTTCAGTCAGTAGTCTGGCTCAGATTATCTCTCACCATCAGCAGCTTTGAGTCT 306
Qy 301 GAAGATTTTGTAGCTATTACTGCTCTACAATATGCTAGTCTTCGGTACACGTTCCGAGGG 360
Db 307 GAAGATTTTGCAGACTATTACTGCTCTACAATATGCTAGTCTTCGGTACACGTTCCGAGGG 366
Qy 361 GGGACCAAGCTGGAATAAAAA 381
Db 367 GGGACCAAGCTGGAGCTGAA 387

RESULT 7

US-08-779-784-17
; Sequence 17, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiro
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1694
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
US-08-779-784-17


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TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 739 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..729
; OTHER INFORMATION: /product= "520C9 sfv polypeptide
; sequence"
; US-09-887-853-5
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Query Match 71.1%; Score 309.4; DB 10; Length 739;
Best Local Similarity 95.2%; Pred. No. 7.7e-94;
Matches 319; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 56 GATGTGATCCAGATGACCCAGTCTCCATCCCTCTTATCTGCTCTCTCTGGGACAAAGAG 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 395 GATCCGATATCCAGATGACCCAGTCTCCATCCCTCTTATCTGCTCTCTCTGGGAGAAAG 454

QY 116 TCAGTCTCACTTGTGGGCAAGTCAGGACATTTGGTATTAACTTACATTGCTTCAGCAGG 175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 TCAGTCTCACTTGTGGGCAAGTCAGGACATTTGGTATTAACTTACATTGCTTCAGCAGG 514

QY 176 AACGAGTGAACATATTAAACGGCTGATCTACGCCACATCCAGTTAGTTCTGGTGTC 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 515 ACCGAGTGAACATATTAAACGGCTGATCTACGCCACATCCAGTTAGTTCTGGTGTC 574

QY 236 CCAAAAGTTTCAGTGGCAGTAGTCTGGTGCAGATATTCTCTCACCATCAGCAGCCTTG 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 575 CCAAAAGTTTCAGTGGCAGTAGTCTGGTGCAGATATTCTCTCACCATCAGTAGCCTTG 634

QY 296 AGTCTGAAGATTTGTAGCTATTACTGTCTACAATAGTGTCTCCGTACAGCTTG 355
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 635 AGTCTGAAGATTTGTAGCTATTACTGTCTACAATAGTGTCTCCGTACAGCTTG 694

QY 356 GAGGGGGACCAAGCTGGAATAAAACGGCTGAT 390
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 695 GAGGGGGACCAAGCTGGAATAAAACGGCTGAT 729

RESULT 10
; US-09-924-099-20
; Sequence 20, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 20
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of
; OTHER INFORMATION: SEQ
; OTHER INFORMATION: ID NO:10

US-09-924-099-19
; Sequence 19, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 19
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of
; OTHER INFORMATION: SEQ
; OTHER INFORMATION: ID NO:9

US-09-924-099-19
Query Match 70.7%; Score 307.4; DB 10; Length 711;
Best Local Similarity 95.2%; Pred. No. 3.6e-93;
Matches 317; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 49 GGTACCAGATGTGACATCCAGATGACCCAGTCTCCATCCCTCTTATCTGCTCTCTGGGA 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 GGTGGCGGATCGGACATCCAGATGACCCAGTCTCCATCCCTCTTATCTGCTCTCTGGGA 438

QY 109 CAAAGAGTCACTTCTGCGGCAAGTCAGGACATTTGGTATTAACTTACATTAGTGTCT 168
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 439 GAAAGAGTCACTTCTGCGGCAAGTCAGGACATTTGGTATTAACTTACATTAGTGTCT 498

QY 169 CAGCAGGAACAGATGGAACATATTAAACGGCTGATCTACGCCACATCCAGTTAGTGTCT 228
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 499 CACAGGAACAGATGGAACATTTTAAACGGCTGATCTACGCCACATCCAGTTAGTGTCT 558

QY 229 GGTGTCCCAAGAGTTTCAGTGGCAGTAGTCTGGGTGAGATTTCTCTCACCATCAGC 288
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 559 GGTGTCCCAAGAGTTTCAGTGGCAGTAGTCTGGGTGAGATTTCTCTCACCATCAGC 618

QY 289 AGCCTTGAGTCTGAAGATTTTGTAGCTATTACTGTCTACAATAGTGTCTCCGTAC 348
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 619 AGCCTTGAGTCTGAAGATTTTGTAGCTATTACTGTCTACAATAGTGTCTCCGTAC 678

QY 349 ACCTTGGGAGGGGGACCAAGCTGGAATAAAAC 382
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 679 ACCTTGGGAGGGGGACCAAGCTGGAATAAAAC 712

RESULT 11
; US-09-924-099-19
; Sequence 19, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 19
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of
; OTHER INFORMATION: SEQ
; OTHER INFORMATION: ID NO:9

US-09-924-099-19
Query Match 70.7%; Score 307.4; DB 10; Length 711;
Best Local Similarity 95.2%; Pred. No. 3.6e-93;
Matches 317; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 49 GGTACCAGATGTGACATCCAGATGACCCAGTCTCCATCCCTCTTATCTGCTCTCTGGGA 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 GGTGGCGGATCGGACATCCAGATGACCCAGTCTCCATCCCTCTTATCTGCTCTCTGGGA 438

QY 109 CAAAGAGTCACTTCTGCGGCAAGTCAGGACATTTGGTATTAACTTACATTAGTGTCT 168
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 439 GAAAGAGTCACTTCTGCGGCAAGTCAGGACATTTGGTATTAACTTACATTAGTGTCT 498
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169	QY	CAGCAGGAACACGATGGAACTATTAAAGCGCTGATCTACGCCACATCCAGTTTAGTGTTCT	228
170			
171			
499	Db	CAACAGGAACACGATGGAACTTTTAAACGGCTGATCTACGCCACATCCAGTTTAGATTCT	558
500			
229	QY	GGTGTCGCCAAAAGGTTCCAGTGGCAGTAGTGCTGGGTACAGATTATTCTCTCACCATCAGC	288
230			
231			
559	Db	GGTGTCGCCCAAGAGGTTCCAGTGGCAGTAGTGCTGGGTACAGATTATTCTCTCACCATCAGC	618
560			
289	QY	AGCCTTGAGTCTGGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTAC	348
290			
291			
619	Db	AGCCTTGAGTCTGAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTAC	678
620			
349	QY	AGTTTCGAGGGGGGACCAAGCTGGAAATAAA	381
350			
351			
679	Db	AGTTTCGAGGGGGGACCAAGCTGGCAATAAA	711
680			
681			

RESULT 12

US-09-924-099-11

; Sequence 11, Application US/09924099
; Patent No. US20020128450A1

; GENERAL INFORMATION:

APPLICANT: NISHIDA, Yoshihiro

APPLICANT: OKURA, Takanori

APPLICANT: TANIMOTO, Tadao

APPLICANT: KURIMOTO, Masashi

: TITLE OF INVENTION: PEPTIDES

FILE OF INVENT
: FILE REFERENCE:

; FILE REFERENCE: : CURRENT APPLICATION NUMBER: US/09/924,099

: CURRENT APPLICATION NUMBER: US/0
 : CURRENT FILING DATE: 2001-08-08

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; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER. 00/238 511

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; PRIOR APPLICATION NUMBER: 09/338,511
 : PRIOR FILING DATE: 1000-05-22
 : PRIOR FILING DATE: 1000-05-22

;	PRIOR FILING DATE: 1999-06-23	
:	PRIOR APPLICATION NUMBER: 000 044 '00	

; PRIOR APPLICATION NUMBER: JP 289,044/98

1 ; PRIOR FILING DATE: 1998-10-12

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER

; PRIOR FILING DATE: EARLI
NUMBER OF SEQ. IN NO. 33

; NUMBER OF SEQ

; SEQ ID NO 11

; LENGTH: 32

; TYPE: DNA

; ORGANISM: Mu:

Query Match 70.4%; Score 305.4; DB 10; Length 324;
Best Local Similarity 96.6%; Pred. No. 5.5e-93;
Matches 313; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY	61	GACATCCAGATGACCCAGCTGCCATCTCCTTATCTGCGCTCTCTGGGACAAAGAGTCACT	120
Db	1	GACATCCAGATGACCCAGCTGCCATCTCCTTATCTGCGCTCTCTGGGACAAAGAGTCACT	60
QY	121	CTCAGCTTGTCTGGGCAAGTCAGGACATTGGTATTAACTTACATTTGGCTTCAGCGAAGCA	180
Db	61	CTCAGCTTGTCTGGGCAAGTCAGGACATTGGTAGTAAATTTACTTGGCTTCAACAGGAACCA	120
QY	181	GATGGAACATTATTAACGCCTGATCTACGCCACATCCAGTTTAGTTCTGGTGTCCCCAA	240
Db	121	GAITGGAACTTTTTAACGCCTGATCTACGCCACATCCAGTTTAGTTCTGGTGTCCCCAA	180
QY	241	AGGTTCACTGGCAGTAGTCTGGGTCAAGATTATTTCTCACCATCAGCAGCCTTAGTCT	300
Db	181	AGGTTCACTGGCAGTAGTCTGGGTCAAGATTATTTCTCACCATCAGCAGCCTTAGTCT	240
QY	301	GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACAGTTTCGGAGG	360
Db	241	GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACAGTTTCGGAGG	300
QY	361	GGGACCAAGCTGGAAATTAACCG	384
Db	301	GGGACCAAGCTGGCAATTAACCG	324

RESULT 13

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US-09-797-481-1
; Sequence 1, Application US/09797481
; Patent No. US20010047083A1
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
Kohler, Heinz
Foop, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: MURINE ANTI-IDIOTYPE ANTIBODY 3H1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/797,481
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/361,772
FILING DATE: 27-JUL-1999
APPLICATION NUMBER: US 08/579,940
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/365,484
FILING DATE: 28-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 22..447
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
PS-09-797-481-1

```

	Query Match	61.5%	Score 267.6	DB 9	Length 447
	Best Local Similarity	76.8%	Pred. No. 7.7e-80		
	Matches 327	Conservative	0	Mismatches 99	Indels 0
	Gaps	0			
Qy	1	ATGGGGCCCGCTGCTCAGATTCTTGGGTTCTTGTGTCTCTGTTCCTGGTATCCAGATGT	60		
Db	22	ATGGTATCCACAGCTCAGTTCCTTGGTATCTTGTGTCTGGTTCAGGATATCAAACT	81		
Qy	61	GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT	120		
Db	82	GACATCAAGATGACCCAGTCTCCATCTTCCATGTATGCATCTCTAGGAGAGAGAGTCACG	141		
Qy	121	CTCAGTTGTGGGCAAGTCAGGACATTTGGTATTAACCTTACATTTGGCTTCAGCAGGAACCA	180		
Db	142	ATCATTGCAAGGGAGTCAGGACATTAATGGTTATTTAAATTGGTTCCAACAGAACCA	201		
Qy	181	GATGGAACTATTAAACGCCCTGATCTACGGCCACATCCAGTTTAGTGTCTGGTGTCCCCAAA	240		
Db	202	GGGAAATCTCCTTAAGACCCCTGATCTATCGTGTGCAATAGATTGATAGATGGGTGCCCATCA	261		

QY 241 AGGTTGAGTGGCAGTAGGCTGGGTCAGATTATTTCTCACCACATCAGCAGCCCTTGAGTCT 300
Db 262 AGGTTGAGTGGCAGTAGGCTGGGCAAGTTTACTCTCTCACCACATCAGCAGCCCTGGAATAT 321
QY 301 GAAGATTTGTAGCCTTACTCTCTACAAATATGCTAGTTCCTCGGTACAGGTTGAGGG 360
Db 322 GAAGATATGGAACTTATTATTCTCTACAGTTTGTAGTTCCTCGGTGATGTTGCGTGA 381
QY 361 GGGACCAAGCTGGAATAAAACGGCTGATGCTGCGACCAACTGTATCCATCTTCCACCA 420
Db 382 GGCACCAAGCTGGAATAAAACGGCTGATGCTGCGACCAACTGTATCCATCTTCCACCA 441
QY 421 TCCAGT 426
Db 442 TCCAGT 447

RESULT 14
US-09-844-736-3
; Sequence 3, Application US/09844736
; Patent No. US20020041872A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; Foon, Kenneth A.
; Chatterjee, Sunil K.
; TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
; CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/844,736
; FILING DATE: 09-Apr-1997
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,692
; FILING DATE: April 9, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Polizzi, Catherine M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 30414-20004.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-844-736-3
Query Match 61.5%; Score 267.6; DB 9; Length 447;
Best Local Similarity 76.8%; Pred. No. 7.7e-80;
Matches 327; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Db 142 ATCATTGGAAGCGAGTCAGGACATTAATGGTTATTAAATGGTTCCAAAGAACCA 201
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QY 241 AGGTTGAGTGGCAGTAGGCTGGGTCAGATTATTTCTCACCACATCAGCAGCCCTTGAGTCT 300
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QY 301 GAAGATTTGTAGCCTTACTCTCTACAAATATGCTAGTTCCTCGGTACAGTTCGGAGGG 360
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QY 361 GGGACCAAGCTGGAATAAAACGGCTGATGCTGCGACCAACTGTATCCATCTTCCACCA 420
Db 382 GGCACCAAGCTGGAATAAAACGGCTGATGCTGCGACCAACTGTCTCCATCTTCCACCA 441
QY 421 TCCAGT 426
Db 442 TCCAGT 447

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US-10-162-396-3
; Sequence 3, Application US/10162396
; Publication No. US20030077274A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; Foon, Kenneth A.
; Chatterjee, Sunil K.
; TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
; CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,396
; FILING DATE: 31-Jul-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/844,736
; FILING DATE: April 27, 2001
; APPLICATION NUMBER: US 08/838,692
; FILING DATE: April 9, 1997
; APPLICATION NUMBER: US 60/044,455
; FILING DATE: April 12, 1996
; APPLICATION NUMBER: US 08/631,085
; FILING DATE: April 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Polizzi, Catherine M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 304142000402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:

Search completed: August 30, 2003, 19:50:20
Job time : 161.241 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2003, 16:08:05 ; Search time 1512.79 seconds
(without alignments)
6988.707 Million cell updates/sec

Title: US-08-836-455-1

Perfect score: 435

Sequence: 1 ATGGGGGCCCTGCTCAGAT.....CACCATCCAGTAAGCTTGGG 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_esti:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	362.8	83.4	926	12	BG962572 602829953
3	334	76.8	714	12	BG963548 602831226
4	320.2	73.6	374	13	BY083003 BY083003

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8	285.2	65.6	626	10	BF582283
9	285.2	65.6	725	10	BF580940
10	282.8	65.0	1459	13	BQ18407
11	278.8	64.1	762	10	BF144806
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13	276.4	63.5	772	10	BF581992
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16	274.8	63.2	669	10	BI123422
17	274.8	63.2	708	12	BI103114
18	273.2	62.8	886	10	BG756818
19	268.8	61.8	685	10	BG518543
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22	265.2	61.0	764	14	CB956251
23	265.2	61.0	1019	12	BM914405
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35	260.4	59.9	763	14	CB985168
36	260.4	59.9	770	14	CB987520
37	260.4	59.9	776	14	CB986151
38	260.4	59.9	805	14	CB955618
39	260.4	59.9	807	14	CB958795
40	260.4	59.9	888	13	BQ881840
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ALIGNMENTS

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DEFINITION
601780387F1 NCI_CGAP_Lu30 Mus musculus cdna clone IMAGE:4008404 5',
mRNA sequence.
EST.
BF138788.1 GI:10977828
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 630)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LIAW9242 row: n column: 21
High quality sequence stop: 628.

BF138788 630 bp mRNA linear EST 24-OCT-2000
601780387F1 NCI_CGAP_Lu30 Mus musculus cdna clone IMAGE:4008404 5',
mRNA sequence.

BF138788.1 GI:10977828

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 630)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LIAW9242 row: n column: 21

High quality sequence stop: 628.

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FEATURES          Location/Qualifiers
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/clone="IMAGE:4008404"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DHI0B"
/clone_lib="NCI_CGAP_Lu30"
Site:2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dt. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT      162 a 158 c 150 g 160 t
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Query Match      85.8%; Score 373.2; DB 10; Length 630;
Best Local Similarity 92.3%; Pred. No. 4.3e-106;
Matches 393; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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QY 365 CCAAGCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATCCATCTTCCACCAATCCA 424
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LOCUS             60282953F1 NCI_CGAP_Co24 Mus musculus cdna clone IMAGE:4984788 5',
DEFINITION        mRNA sequence.
ACCESSION         BG962572
VERSION           BG962572.1 GI:14350209
KEYWORDS          EST.
SOURCE            Mus musculus (house mouse)
ORGANISM          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE         1 (bases 1 to 926)
AUTHORS           NIH-MGC .
TITLE             National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL           Unpublished
COMMENT           Contact: Robert Strausberg, Ph.D.
                  Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10991 row: 1 column: 13
High quality sequence stop: 685.

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/clone_lib="NCI_CGAP_Co24"
/site="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      230 a 259 c 205 g 232 t
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Best Local Similarity 90.2%; Pred. No. 9.4e-103;
Matches 388; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
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QY 361 GGGACCAAGCTGGAAATAAAGCGGCTGATCTGCACCAACTGTATCCATCTTCCACCA 420
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Db 435 TCCAGTAAAGC 444

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DEFINITION        mRNA sequence.
ACCESSION         BG963548
VERSION           BG963548.1 GI:14351185
KEYWORDS          EST.
SOURCE            Mus musculus (house mouse)
ORGANISM          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

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etc. Mus musculus cDNA clone K630040M06 5', mRNA sequence.

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 374)

A., A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Giasi, C., Godzik, A., Gough, J., Grimmond, S., Gustinch, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, V., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G.

Jarvis, E. D., Kanaji, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sadelain, A., Schneider, C., Simple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verdaro, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavalova, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawaji, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Ichino, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851

22354683
12466851
Contact: Yoshihide Hayashizaki

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

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Tel: 81-45-503-9222

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@cs.riken.go.jp

Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: <http://genome-gsc.riken.go.jp/>
Aizawa, K., Akimura, T., Arakawa, T.,
Carninci, P., Fukuda, S., Hirozane

URL: <http://genome.gsc.riken.go.jp/>
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, K., Numazaki, R., Ohno, M., Sakai, K.

T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Havaishizaki, Y. Direct

, Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Substitution
Computational Analysis of Full-length Mouse cDNAs Compared with

Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10(10), 1617-1630 (2000)

prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10(10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library Genome Res 11 (2): 281-289 (2001)

encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

cdNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to

Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
please visit our website (<http://genome.qsc.riken.ac.jp/>) for

prepare mouse tissues.
please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

further details.

FEATURES source Location/Qualifiers

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(dev_stage=adult,tissue_type=liver,sex=male),
(dev_stage=13 days embryo,tissue_type=whole body,sex=mix),
(dev_stage=14 days embryo,tissue_type=whole body,sex=mix),
(dev_stage=16 days embryo,tissue_type=whole body,sex=mix),
(dev_stage=17 days embryo,tissue_type=whole body,sex=mix),
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sex=female),(dev_stage=10 days neonate,tissue_type=brain,
sex=mix),(dev_stage=10 days neonate,tissue_type=thymus,
sex=mix),(dev_stage=10 days neonate,tissue_type=heart,
sex=mix)"
88 a 89 c 85 g 111 t 1 others

BASE COUNT 88 a 89 c 85 g 111 t 1 others

Query Match 73.6%; Score 320.2; DB 13; Length 374;
Best Local Similarity 95.9%; Pred. No. 1.7e-89;
Matches 326; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGGGGCCCTGCTCAGATCTTGGGTCTTGTGCTCTTGTTCAGGTACACAGTGT 60
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DB 153 CTCATCTGTCGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGCTTCAGCAGAACCA 212
QY 181 GATGGAATATTAAACGCTGATCTACGCCACATFCCAGTTAGTCTTGTGTCGCCCAA 240
DB 213 GATGGAATATTAAACGCTGATCTACGCCACATFCCAGTTAGTCTTGTGTCGCCCAA 272
QY 241 AGGTTCAAGTGGCAGTCTGGGTCAAGATTATCTCTCACCATCAGCAGCCTTGAGTCT 300
DB 273 AGGTTCAAGTGGCAGTCTGGGTCAAGATTATCTCTCACCATCAGCAGCCTTGAGTCT 332
QY 301 GAAGATTTGTAGCTATTACTGTCTACAATATGCTAGTCT 342
DB 333 GAACATTTGTAGCTATTACTGTCTACAATATGCTAGTCT 374

RESULT 5
BI152061
LOCUS 602916512f1 NCI_CGAP_Lu29 Mus musculus cdna clone IMAGE:5066931 5',
DEFINITION mRNA sequence.
EST.
VERSION BI152061.1 GI:14612062
KEYWORDS
SOURCE Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 827)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11180 row: h column: 04
High quality sequence stop: 827.
Location/Qualifiers

FEATURES source

1. 827
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5066931"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 235 a 219 c 180 g 193 t

Query Match 66.2%; Score 287.8; DB 12; Length 827;
Best Local Similarity 80.7%; Pred. No. 3.5e-79;
Matches 348; Conservative 0; Mismatches 82; Indels 1; Gaps 1;
QY 1 ATGGGGCCCTGCTCAGATCTTGGGTCTTGTGCTCTTGTTCAGGTACACAGTGT 59
DB 13 ATGATGCTCTGTTCACTTCTTGGTCTCTGCTCTGTTTCAAGGTACACAGTGT 72
QY 60 TGACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGTCACT 119
DB 73 TGATATCCAGATGACACAGACTACATCTCTGCTCTCTCTGGGACAGAGTCACT 132
QY 120 TCTCATTGTCGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGCTTCAGCAGAACCA 179
DB 133 CATCAGTTGAGGCAAGTCAGGACATTTAGATTTAACTGGTATCAGCAGAACCA 192
QY 180 AGATGGAATATTAAACGCTGATCTACGCCACATCAGTTAGTCTTGTGTCGCCCAA 239
DB 193 AGATGGAATATTAAACGCTGATCTACGCCACATCAGTTAGTCTTGTGTCGCCCAA 252
QY 240 AGGTTCAAGTGGCAGTCTGGGTCAAGATTATCTCTCACCATCAGCAGCCTTGAGTCT 299
DB 253 AGGTTCAAGTGGCAGTCTGGGTCAAGATTATCTCTCACCATCAGCAGCCTTGAGTCT 312
QY 300 TGAAGATTTGTAGCTATTACTGTCTACAATATGCTAGTCTTCTCCGTACACGTTGGGAGG 359
DB 313 AGAAGATATTGCCACATTTACTTTTCCCAACAGGATAGTAACTCCGTATAGTTCGATC 372
QY 360 GGGGACCAAGCTGGAATAAAACGGGCTGATGTCACCACTGTATCCATCTTCCCACT 419
DB 373 GGGGACCAAGCTGGAATAAAACGGGCTGATGTCACCACTGTATCCATCTTCCCACT 432
QY 420 ATCCAGTAAAC 430
DB 433 ATCCAGTAAAC 443

RESULT 6
BG518527
LOCUS 6025782261f1 NCI_CGAP_Lu29 Mus musculus cdna clone IMAGE:3491798 5',
DEFINITION mRNA sequence.
ACCESSION BG518527
VERSION BG518527.1 GI:13513491

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KEYWORDS  EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus

REFERENCE   1 (bases 1 to 874)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LAM8536 row: i column: 15
            High quality sequence stop: 843.
            Location/Qualifiers
              1..874
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                /mol_type="mRNA"
                /strain="CZECH I"
                /db_xref="taxon:10090"
                /clone="IMAGE:3491798"
                /tissue_type="spontaneous tumor, metastatic to mammary.
                Stem cell origin."
                /lab_host="DH10B"
                /clone_lib="NCI_CGAP_Lu29"
                /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                Library constructed by Life Technologies. Investigator
                providing samples: Gilbert Smith, NIH"

BASE COUNT 234 a 232 c 205 g 203 t
ORIGIN

Query Match      66.1%; Score 287.6; DB 10; Length 874;
Best Local Similarity 79.3%; Pred. No. 4.2e-79;
Matches 341; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY  1 ATGGGGGCCCTGCTCAGATCTTGGGTTCTTGGTCTTGTGCTTGTTCAGGTACCAGATGT 60
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Db  35 ATGAGGGCCCTGCTCAGTCTTGGGATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 94

QY  61 GACATCCAGATGACCCAGTCTCCATCCCTTATCTGCTCTCTGCTGCTGCTGCTGCTGCT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  95 GACATCAAGATGACCCAGTCTCCATCCCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 154

QY  121 CTCACCTTCTCGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGCTTCCAGCAGGAACCA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  155 ATCACTTGCAGGCGAGTCAGGACATTTAAAGCTATTAAAGCTGGTACGACGAGGAACCA 214

QY  181 GATGGAATATTAAACGCTGATCTACGCCACATCCAGTTTGGTTCCTGCTGCTGCTGCTGCT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  215 TGGAAATCTCTTAAGACCTGATCTATTATGCAACAAGCTTGGCAGATGGGGTCCCATCA 274

QY  241 AGGTTTCAGTGCAGTGGTGGTGCAGATTTCTCTCACCACATCAGCAGCCTTCAGTCT 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  275 AGATTTCAGTGCAGTGGTGGGCAAGATTTCTCTTAACCATCAGCAGCCTGGAGTCT 334

QY  301 GAAGATTTTGTAGCTATTACTGTCTACAATATGCTAGTTCTTCGCTACACGTTGGGAGGG 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  335 GACGACAGCAACTTATTACTGTCTACAGATGGTGAGAGCCGCTATACGTTCCGATCG 394

QY  361 GGGACCAAGCTGGAAATAAAGCGCTGATGCTGCACCACTGATTCATCTTCCACCA 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  395 GGGACCAAGCTGGAAATAAAGCGCTGATGCTGCACCACTGATTCATCTTCCACCA 454

QY  421 TCCAGTAGC 430
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Db  455 TCCAGTAGC 464

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RESULT 7
LOCUS     BF579422
DEFINITION BF579422 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:420814 5',
            mRNA sequence.
ACCESSION BF579422
VERSION    BF579422.1 GI:11653134
KEYWORDS   EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 891)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LAM9772 row: a column: 09
            High quality sequence stop: 711.
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                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:420814"
                /lab_host="DH10B (T1 phage-resistant)"
                /clone_lib="NCI_CGAP_Co24"
                /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 1.6 kb. Constructed by Life
                Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 246 a 226 c 204 g 215 t
ORIGIN

Query Match      65.9%; Score 286.8; DB 10; Length 891;
Best Local Similarity 80.7%; Pred. No. 7.5e-79;
Matches 347; Conservative 0; Mismatches 82; Indels 1; Gaps 1;

QY  1 ATGGGGGCCCTGCTCAGATCTTGGGTTCTTGGTCTTGTGCTTGTTCAGGTACCAGATGT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  13 ATGAGGACCCCTGCTCAGTCTTCTTGGATCTTGTGCTCTGCTGCTGCTGCTGCTGCTGCT 72

QY  61 GACATCCAGATGACCCAGTCTCCATCCCTTATCTGCTCTCTGCTGCTGCTGCTGCTGCTGCT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  73 GACATCAAGATGACCCAGTCTCCATCTTCCATCTTCCATCTCTAGGAGAGAGTCACT 132

QY  121 CTCACCTTCTCGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGCTTCCAGCAGGAACCA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  133 ATCACTTGCAGGCGAGTCAGGACATTTAAAGCTATTAAAGCTGGTTCGACGAGGAACCA 192

QY  181 GATGGAATATTAAACGCTGATCTACGCCACATCCAGTTTGGTTCCTGCTGCTGCTGCTGCT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  193 G-GAAATCTCTTAAGACCTGATCTATCGTACAAAGATGATAGTGGGTCCCGTCA 251

QY  241 AGGTTTCAGTGCAGTGGTGGTGCAGTATTCTCTCACCACATCAGCAGCCTTCAGTCT 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  252 AGGTTTCAGTGCAGTGGTGGTGGCAAGATTTCTCTCACCACATCAGCAGTCTGAGTAT 311

QY  301 GAAGATTTTGTAGCTATTACTGTCTACAATATGCTAGTTCTTCCCTCAGCAGTTCGAGGG 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  312 GAAGATGCGGAATTTATTATTGCTACAGTATGATGAGTTTCCCTCAGCAGTTCGAGGG 371

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QY 361 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA 420
Db 372 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA 431
QY 421 TCCAGTAAGC 430
Db 432 TCCAGTGAGC 441

RESULT 8
BF582283 602101109F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224267 5', EST 12-DEC-2000
LOCUS mRNA sequence.
DEFINITION
ACCESSION BF582283
VERSION BF582283.1 GI:11655995
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9814 row: a column: 04
High quality sequence stop: 624.
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Location/Qualifiers
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/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4224267"
/lab_host="DHI0B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/lab_host="DHI0B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/site="Organ: colon; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 178 a 153 c 137 g 158 t
ORIGIN

Query Match 65.6%; Score 285.2; DB 10; Length 626;
Best Local Similarity 80.5%; Pred. No. 2.1e-78;
Matches 346; Conservative 0; Mismatches 83; Indels 1; Gaps 1;

QY 1 ATGGGGGCCCCCTGCATCAGATCTTGGGTTCTTGTGCTCTGTTCCAGGTACAGATGT 60
Db 1 ATGATGTCCTCTGCTCAGTTCCTTGGTCTCTGCTGCTGCTCTGTTTCAAGGTACAGATGT 59
QY 61 GACATCCAGATGACCCAGTCTCCATCCCTATCTGCTCTCTGGGACAAAGATCAGT 120
Db 60 GATATCCAGATGACACAGACTACATCCCTCTGCTGCTCTCTGCGGAGACAGATCACC 119
QY 121 CTCACTTGTGCGGCAAGTCAGGACATGGTATTAACTTACATTTGCTTTCAGCAGGAACCA 180
Db 120 ATCAATTGCGCAAGTCAGGACATTTAGCAATTTTAAATTTGTTATCAGCAGGAACCA 179
QY 181 GATGGAATTAATACGCTGATCTACGCCACATCCAGTTAGTTCTGTGTTGCCCAAA 240
Db 180 GATGGAATGTTAACTCCTGATTAATACACATCAAAATTTACATTCAGGAGTCCCATCA 239
QY 241 AGGTTCACTGCGCAGTAGTCTGGGTCAGATTTATCTCTCACCATCAGCAGGCTTGAAGTCT 300

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Db 240 AGGTTCACTGCGCAGTAGTCTGGGACAGATTTATCTCTCACCATCAGCAACTGGAACCT 299
QY 301 GAAGATTTTGTAGCTTATTACTGCTACAATATGCTTCTCCGTACACGTTCCGAGGG 360
Db 300 GAAGATATTTGCCACTTACTATTGTGACAGATATTTAAGCTTCCATTGACGCTCGGCTCG 359
QY 361 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA 420
Db 360 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA 419
QY 421 TCCAGTAAGC 430
Db 420 TCCAGTGAGC 429

RESULT 9
BF580940 602100636F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224032 5', EST 12-DEC-2000
LOCUS mRNA sequence.
DEFINITION
ACCESSION BF580940
VERSION BF580940.1 GI:11654652
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9813 row: g column: 09
High quality sequence stop: 694.
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Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4224032"
/lab_host="DHI0B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/site="Organ: colon; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 207 a 183 c 159 g 176 t
ORIGIN

Query Match 65.6%; Score 285.2; DB 10; Length 725;
Best Local Similarity 80.5%; Pred. No. 2.2e-78;
Matches 346; Conservative 0; Mismatches 83; Indels 1; Gaps 1;

QY 1 ATGGGGGCCCCCTGCATCAGATCTTGGGTTCTTGTGCTCTGTTTCCAGGTACCAAGATGT 60
Db 20 ATGATGTCCTCTGCTCAGTTCCTTGGTCTCTGCTGCTGCTGTTTCAAGGTACCAAGATGT 78
QY 61 GACATCCAGATGACCCAGTCTCCATCCCTATCTGCTCTCTGGGACAAAGATCAGT 120
Db 79 GATATCCAGATGACACAGACTACATCCCTCTGCTGCTCTCTGCGGAGACAGATCACC 138
QY 121 CTCACTTGTGCGGCAAGTCAGGACATGGTATTAACTTACATTTGCTTTCAGCAGGAACCA 180

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Db      139 ATCAGTTGCGAGTGAAGTCAGGCACTAGTAATTAATTAACAGGTATACAGCAAAACCA 198
Qy      181 GATGGAACTATTAAACCCCTGATCTAGCCACATCCAGTTTAGTCTCTGGTGCCCCAAA 240
Db      199 GATGGAACTTTAACTCTGATCTATTACACATCAAGTTTACACTCAGGAGTCCCATCA 258
Qy      241 AGGTTACAGTGGCAGTGGTCTGGGTGAGATTTATCTCTACCATCAGCAGCCCTTGAGTCT 300
Db      259 AGGTTACAGTGGCAGTGGTCTGGGACACATTTATCTCTACCATCAGCAACCTGGAACCT 318
Qy      301 GAAGATTTTACGCTTACTCTTACAAATATAGTCTCGGTACAGCTTCGGAGGG 360
Db      319 GAAGATTTTCCCACTTACTATTGACAGTATAGTCTTCCATTCACGTTCCGGCTCG 378
Qy      361 GGACCAAGCTGGAATAAAACGGGTGATGCTGCACCAACTGTATCATCTTCCCAACCA 420
Db      379 GGACAAAGTTGGAATAAAACGGGTGATGCTGCACCAACTGTATCATCTTCCCAACCA 438
Qy      421 TCCAGTAAGC 430
Db      439 TCCAGTGAGC 448

RESULT 10
BQ918407
LOCUS      1459 bp mRNA linear EST 20-AUG-2002
DEFINITION AGENCOURT_8885602 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6397382 5', mRNA sequence.
ACCESSION BQ918407
VERSION BQ918407.1 GI:22333105
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Cloning Strategy: Agencourt Bioscience Corporation
Cloning Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM13895 row: c column: 15
High quality sequence start: 165
High quality sequence stop: 634.
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6397382"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 393 a 441 c 306 g 315 t 4 others
ORIGIN
Query Match 65.0%; Score 282.8; DB 13; Length 1459;
Best Local Similarity 78.6%; Pred. No. 1.6e-77;
Matches 338; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
Qy      1 ATGGGGCCCCCTGCTAGATCTCTGGTCTTGTCTGCTCTGTTTCCAGTACAGATGT 60

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Db      190 ATGATGTCTCTGCTCAGTTCTCTGGTCTCTCTGTTCTGTTTCTAGGTTCCAGATGT 249
Qy      61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGCGACAAAGAGTCAGT 120
Db      250 GAATCCAGATGACACAGACTACATCTCTGCTCTGCTCTCTGCGACAGAGTCCACC 309
Qy      121 CTCACTTGTCTGGCAGTCTGAGTCTAGTATTAACATTTACATTTGGTCTTCCAGCAACCA 180
Db      310 ATCATTGTCAGGTCAGTCTAGTATTAATTTAACTGGTATCAGCAAAACCA 369
Qy      181 GATGGAACTATTAAACCCCTGATCTAGCCACATCCAGTTTAGTCTCTGGTGTCCCCAAA 240
Db      370 GATGGAACTATTAAACCTCTGATCTACTACACATCAAAATACACTCAGAGTCCCATCA 429
Qy      241 AGGTTACAGTGGCAGTCTGGTCTGATGCTGCACCAACTGTATCCATCTTCCCAACCA 489
Db      430 AGGTTACAGTGGCAGTGGTCTGGAACAGATTTCTCTCACCATTACCAACTGTCGAGCA 489
Qy      301 GAAGATTTTGTAGCTTACTGTCTACAATATGCTTCTCCGTACAGCTTCGGAGGG 360
Db      490 GAGGATATTGCCACTTACTTTTGCCAAACAGGGTAATACACTTCGCTGGACGTTCCGTTGA 549
Qy      361 GGACCAAGCTGGAATAAAACGGGTGATGCTGCACCAACTGTATCCATCTTCCCAACCA 420
Db      550 GGCACCAAACTAGAAAGTCAATCGGCTGATGCTGCACCAACTGTATCCATCTTCCCAACCA 609
Qy      421 TCCAGTAAGC 430
Db      610 TCCAGTGAGC 619

RESULT 11
BQ144806
LOCUS      762 bp mRNA linear EST 24-OCT-2000
DEFINITION BQ144806F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4022181 5',
mRNA sequence.
ACCESSION BQ144806
VERSION BQ144806.1 GI:10983846
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Cloning Strategy: Incyte Genomics, Inc.
Cloning Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9278 row: 1 column: 22
High quality sequence stop: 677.
FEATURES
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1. .762
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4022181"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu30"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; transgenic model WNT-1, expression driven by
MTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dt. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

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BASE COUNT      215 a      182 c      183 g      182 t
ORIGIN

Query Match      64.1%; Score 278.8; DB 10; Length 762;
Best Local Similarity 78.4%; Pred. No. 2.3e-76;
Matches 334; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Qy 5 GGGCCCTGCTCAGATCTGGGCTTCTTGGTCTTGTTCCTGCTTGTTCAGGATGTGACA 64
Db 1 GGACCCCTGCTCAGTGGGCTTGGGATCTTGTGCTCTGTGCTTGTTCAGGATGTGACA 60
Qy 65 TCCAGATGACCCAGCTCTCCATCTCTTATCTCTCTCTGCGGACAAAGATGCTCA 124
Db 61 TCAAGATGACCCAGCTCTCCATCTTCCATGTATGCTCTCTAGGGAGAGATGCTACTCA 120
Qy 125 CTTCTGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGCTTCAGCAGGAACAGATG 184
Db 121 CTTGCAAGGCGAGTCAGGACATTAATAGCTATTATACACTGGTACCAGCAAGACGAA 180
Qy 185 GAATCTATAAGCGCTGATCTACGCCACATCCAGTTTAGTTCTGGTGTCCCAAAAGGT 244
Db 181 AATCTCTAAGACCTGATCTATGTTGCAACAGCTTGGTAGATGGGTGCCATCAAGGT 240
Qy 245 TCAGTGCAGTAGCTCTGGGTCAGATTTCTCTCACCATCAGCAGCTTGGAGTCTGAAG 304
Db 241 TCAGTGCAGTAGATCTGGGCAAGATTATTTCTCACCATCAGCAGCTTGGAGTCTGAAG 300
Qy 305 ATTTTGTAGCCTTACTGCTACAAATATGCTAGTTCTCTCCATCAGCAGCTTGGAGTCTGAAG 364
Db 301 ATATAGGAATTTATTTATGCTACAGTATGATGATTTCCGTATACGTTCCGATCGGGGA 360
Qy 365 CCAAGCTGGAATAAAGCGGCTGATGCTGCACCACTGATATCCATCTTCCCAACATCCA 424
Db 361 CCAAGCTGGAATAAAGCGGCTGATGCTGCACCACTGATATCCATCTTCCCAACATCCA 420
Qy 425 GTAGGC 430
Db 421 GTAGGC 426

RESULT 12
LOCUS      B0943305      901 bp      mRNA      linear      EST 21-AUG-2002
DEFINITION AGENCOURT_8880809 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6397142 5', mRNA sequence.
ACCESSION  B0943305
VERSION    B0943305.1 GI:22358783
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     NIH-MGC http://mgi.nci.nih.gov/
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: The Cepko Laboratory
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1AM13894 row: i column: 15
          High quality sequence stop: 670.
          Location/Qualifiers
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              /organism="Mus musculus"
              /mol_type="mRNA"
              /strain="FVB/N"
              /db_xref="taxon:10090"

/clone="IMAGE:6397142"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site: 1; NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      231 a      243 c      199 g      227 t      1 others
ORIGIN

Query Match      63.9%; Score 278; DB 13; Length 901;
Best Local Similarity 77.9%; Pred. No. 4.4e-76;
Matches 335; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Qy 1 ATGGGGCCCTGCTCAGATCTTGGGCTTCTTGTGCTTGTTCAGGATGTGACA 60
Db 14 ATGAGGACCCCTGCTCAGATCTTGGGATCTTGTGCTTGTTCAGGATGTGACA 73
Qy 61 GACATCCAGATGACCCAGCTTCCATCTCTCTCTCTCTGCGGACAAAGATGCTCA 120
Db 74 GACATCAAGATGACCCAGCTTCCATCTTCCATGTATGATCTCTAGGAGGCGGTCACT 133
Qy 121 CTCATCTTGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGCTTCAGCAGGAACCA 180
Db 134 ATCACTTGCAGGCGAGTCAGGACATTTATTCCTTATTAATGTTCCAGCAGAAACCA 193
Qy 181 GATGGAATATTAACGCCCTGATCTACGCCACATCCAGTTTAGTTCTGGTGTCCCAAAA 240
Db 194 GGAAGCCTCTTAAGACCCCTGATCTATCATCAACAACAGATGATGGGTCCTCTCA 253
Qy 241 AGTTTCAGTGGCAGTAGTCTGGGTCAGATTTATTCCTCACCATCAGCAGCTTGGTCT 300
Db 254 AGTTTCAGTGGCAGTAGTCTGGGCAAGATTATTTCTCACCATCAACAGCTGGAGTGT 313
Qy 301 GAAGATTTGTAGCCTATTACTGCTACAAATATGCTAGTTCTCGGTACACCTTGGAGGG 360
Db 314 GAAGATATGGAATTTATTTATGCTACAGTATGATGATTTCCGCTCAGCTCGGTGGT 373
Qy 361 GGGACCAAGCTGGAATAAAGCGGCTGATGCTGCACCACTGATCCATCTTCCCAACCA 420
Db 374 GGGACCAAGCTGGAAGTGGAGCGGCTGATGCTGCACCACTGATCCATCTTCCCAACCA 433
Qy 421 TCCAGTAAAGC 430
Db 434 TCCAGTAAAGC 443

RESULT 13
LOCUS      BF581992      772 bp      mRNA      linear      EST 12-DEC-2000
DEFINITION 602099448F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219618 5',
mRNA sequence.
ACCESSION  BF581992
VERSION    BF581992.1 GI:11655613
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     NIH-MGC http://mgi.nci.nih.gov/
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Jeffrey E. Green, M.D.
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1AM9801 row: o column: 11

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High quality sequence stop: 715.

FEATURES

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/organism="Mus musculus"
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4219618"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCL_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 216 a 204 c 175 g 176 t 1 others
ORIGIN

Query Match 63.5%; Score 276.4; DB 10; Length 772;
Best Local Similarity 80.7%; Pred. No. 1.3e-75;
Matches 322; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 32 TGTGCTCTGTTCCAGGTACCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCT 91
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Db 30 TGTGCTCTGTTTCAAGTTCAGATGTGATATCCAGATGACACAGACTACATCTCC 89
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QY 92 TATCTGCCCTCTGGGACAAAGAGTCAGTCTCACTTGTGCGGCAAGTCAGGACATTGGTA 151
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Db 90 TGTCTGCCCTCTCTGGGAGACAGATCACCATCAGTTGCAGTGAAGTCAGGGCATTGCCA 149
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QY 152 TTAACATTACATGGCTTCAGCAGGACACAGATGAACATTAACGCCCTGATCTAGCCCA 211
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 150 ATTATTAACTGGTATCAGCAAGAACACAGATGGAACTGTAAACCTCTGATCTATTACA 209
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 212 CATCCAGTTAGTCTTGTGTCGCCAAAGTTTCAGTGGCAGTAGGTCTGGGTCAAGATT 271
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 210 CATCAAGTTTACACTCAGGATGCCATCAAGTTTCAGTGGCAGTGGTCTGGGACAGATT 269
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QY 272 ATTCTCTACCATCAGCAGCTTGAGTCTGAAGATTTTGTAGCCTATTACTGCTCAAT 331
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Db 270 ATTCTCTACCATCAGCAACCTGGAACCTGAAGATATNGCCACTTACTATTGTCCAGCAGT 329
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QY 332 ATGCTAGTTCTCGTACAGTTCGGAGGGGGGACCAAGCTGGGAATTAACAGGGCTGATG 391
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Db 330 ATGCTTACCTTCGTGGAGCTTCGGTGGAGGGACCAAGTTGGAAATCAACAGGGCTGATG 389
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QY 392 CTGCACCAACTGTATCCATCTTCCACCATCCAGTAAGC 430
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Db 390 CTGCACCAACTGTATCCATCTTCCACCATCCAGTGAGC 428
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RESULT 14

BI455041 830 bp mRNA linear EST 21-AUG-2001
LOCUS 60317343F1 NCI_CGAP_Mam5 Mus musculus cdna clone IMAGE:5252723 5',
DEFINITION mRNA sequence.

ACCESSION BI455041

VERSION BI455041.1 GI:15245697

KEYWORDS EST.

SOURCE Mus musculus

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 830)

NIH-MGC <http://mgc.ncl.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgaps-femail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11638 row: e column: 12

High quality sequence stop: 820.

FEATURES

source

1. .830
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5252723"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCL_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 227 a 230 c 172 g 201 t

ORIGIN

Query Match 63.5%; Score 276.4; DB 12; Length 830;
Best Local Similarity 77.7%; Pred. No. 1.4e-75;
Matches 334; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 1 ATGGGGGCCCTCCTCAGATTCCTGGTCTCTCTGCTCTGTTTCCAGGTACCAGATGT 60
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QY 61 GACATCCAGATGACCCAGTCTCCATCTCTCTTATCTGCTCTCTGGGACAAAGAGTCAGT 120
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QY 121 CTCACITTCGGCAGTCCAGGACATTCGTTATTAATTCATTCATTCAGTGGCTTCAGCAGGAACCA 180
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Db 126 ATCAATTCGAGGCAAGTCAGGACATTAACCAATTTATTAATTTGGTATCAGCAGAAACCA 185
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QY 181 GATGGAACTATTAAACGCTGTACGCCACATCCAGTTTAGTCTGCTGTCCTCCCAAA 240
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Db 186 AATGGAACCTTTAACTCTCTGATCTCTACACTTCCATATTCACACTCAGAGAGTCCCATCA 245
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QY 241 AGGTTTCAGTGGCAGTAGGTCTGGGTGAGATTTATCTCTCACCATCAGCAGCCTTGAGTCT 300
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Db 246 AGGTTTCAGTGGCAGTGGTCTGGAACAGATTTATCTCTCACCATTAGCAACCTGGAACGA 305
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QY 301 GAAGATTTGTAGCCTATTACTGTCTACAAATATGCTCTCGGTACACAGTTCGGAGGG 360
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Db 306 GAAGATATTGCCACTTACTTTTCCCAACAGGGTAATTCGCTTCTCTCAGCTTCGGGTGCT 365
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QY 361 GGGACCAAGCTGGAATAAAACGGGTGATGCTGCACCACTGTATCTCATCTTCCCAACCA 420
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Db 366 GGGACCAAACTGGAATGAACGGGTGATGCTGCACCACTGTATCTCATCTTCCCAACCA 425
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QY 421 TCCAGTAAGC 430
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Db 426 TCCAGTGAGC 435
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RESULT 15

BE284224

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 695)

BE284224 695 bp mRNA linear EST 13-JUL-2000
LOCUS 601099161F1 NCI_CGAP_Lu29 Mus musculus cdna clone IMAGE:3491798 5',
DEFINITION mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 695)

AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cqabbs-r@mail.nih.gov

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FEATURES
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/db_xref="taxon:10090"
/clone="IMAGE:3491798"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo d
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
184 a 182 c 172 g 157 t
BASE COUNT
ORIGIN

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Query Match	63.4%	Score 275.6	DB 10	Length 695
Best Local Similarity	79.1%	Prod. No. 2.3e-75		
Matches 340	Conservative 0	Mismatches 89	Indels 1	Gaps 1
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15	ATGAGGGCCCTGCTCAGTTTTTGGGATCTTG-TGCTCTGGTTTCCAGGTATCAGATGT	73		
61	GACATCAGATGACCCAGTCTCCATCCTCTTATCTGCTCTCTCTGGGACAAAGAGTCAGT	120		
74	GACATCAAGATGACCCAGTCTCCATCCTCCATGTATGCATCGCTGGGAGAGAGTCACT	133		
121	CTCAGTCTGCGGCAAGTCAGGACATTTGTTATTAACCTATTTGGCTTTCAGCAGGAACCA	180		
134	ATCAGTTGCAAGCGAGTCAGGACATTAAGAACTATTTAAGCTGGTACCAGCAGAAACCA	193		
181	GATGGAACTATTAAAGCCCTGATCTACGCCACATCCAGTTTAGGTTTGGTGTCCCAAA	240		
194	TGGAAATCTCTTAAGACCCCTGATCTATTATGCAACAAGCTTGGCAGATGGGGTCCCATCA	253		
241	AGGTTACAGTGGCAGTAGGTCCTGGTCAGATTAATCTCTCAGCATCAGCAGGCTTGAGTCT	300		
254	AGATTAGTGGCAGTGGATCTGGGCAAGATTAATCTCTAACCATCAGCAGGCTTGGAGTCT	313		
301	GAAGATTTGTAGCCTATTACTGTCTACAAATATGCTAGTTCTCCGTACACAGTTCCGAGGG	360		
314	GAGCATACAGCAACTATTACTGTCTACAGCATGGTGAGAGGCCGTATACGTTCCGATCG	373		
361	GGAGCAACGCTGGAATAAAGCGGCTGATCTGCACCAACTGTATTCATCTTCCACCA	420		
374	GGAGCCNAGCTGGAATAAAGCGGCTGATCTGCACCAACTGTATTCATCTTCCACCA	433		
421	TCCAGTAAGC	430		
434	TCCAGTGAGC	443		

Search completed: August 30, 2003; 19:44:46
Job time : 1519.79 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2003, 22:04:11 ; Search time 24.8154 Seconds
(without alignments)
927.461 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 145

Sequence: 1 MGAPAQILGFLLLFPGTRC.....IKRDAAPTVSIFPPSSKLG 145

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size :

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	145	100.0	145	18	AAW27119	Murine monoclonal
2	145	100.0	145	24	AAO16292	Mouse 1D10 anti-bo
3	90	62.1	145	20	AAW87593	Antibody 1D10 119
4	33	22.8	129	18	AAW22537	Murine anti-human
5	33	22.8	129	23	AAE20200	Murine 44H104 mab
6	33	22.8	129	23	AAE20204	Murine 44H104 mab
7	30	20.7	146	16	AAW4966	Anti-idiotypic anti
8	30	20.7	206	20	AAW39452	Antibody ABX-CBL 1
9	29	20.0	92	20	AAW95480	Mouse derived RT3

ALIGNMENTS

RESULT 1

RESOLUT
AAW27119
ID AAW27119 standard: Protein: 145 AA.

XX
AC AAW27119.

25-MAR-2003 (updated)

DT	23 MAR 2003	(updated)
DT	04 -JAN-1998	(first entry)

DE Murine monoclonal anti-idiotypic antibody 11D10 VL region.

XX
XX

KW Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;

[illegible]

OS Mus musculus.

XX

FH	Key	Location
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3	3	3
4	4	4
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FT	Protein	21..145
FT	Protein	21..145

FT	Mat_protein
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FT . Region 21..43

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FRT /note= "framework region 1"

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FT	region	/note="framework region I"
FT	region	44 54

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FT Region 55-69

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11 region
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FT /label= FRZ  
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FT	Region	70..76
FT	Region	70..76

FT	/label= CDR2
FT	

```

FT FT /note= "complementarity determining region 2"
FT FT 77..108
FT FT /label= FR3
FT FT /note= "framework region 3"
FT FT 109..117
FT FT /label= CDR3
FT FT 118..127
FT FT /note= "complementarity determining region 3"
FT FT /label= FR1
FT FT /note= "framework region 4"
XX XX
FN W09722699-A2.
XX XX
XX PD 26-JUN-1997.
XX XX
XX PF 19-DEC-1996; 96WO-US20757.
XX XX
PR 20-DEC-1995; 95US-0575762.
PR 26-JAN-1996; 96US-0591965.
PR 13-DEC-1996; 96US-0766350.
XX XX
PA (KENT ) UNIV KENTUCKY.
XX XX
XX Chatterjee M, Chatterjee SK, Foon KA;
XX XX
XX WPI; 1997-341690/31.
XX DR N-PSDB; AAT85149.
XX XX
XX Monoclonal anti-idiotype antibody 11D10 - elicits immune response
XX PT against human milk fat globule disease associated tumours,
XX PT especially breast cancer
XX PS
XX Claim 9; Page 94; 130pp; English.
XX XX
XX This polypeptide sequence comprises the light chain variable region
XX CC (VL) of monoclonal anti-idiotype antibody 11D10 produced by
XX CC hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
XX CC naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype
XX CC response. It elicits an immune response against a specific epitope
XX CC of a high mol.wt. mucin of human milk fat globule (HMFG). It
XX CC induces an immunological response to HMFG in mice, rabbits, monkeys
XX CC and patients with advanced HMFG-associated tumours. Pharmaceutical
XX CC compositions and vaccines comprising 11D10, 11D10 polypeptides
XX CC and/or 11D10 polynucleotides (see also AAT85149-50) are claimed.
XX CC Also claimed are diagnostic kits and methods of using 11D10, 11D10
XX CC polypeptides and/or 11D10 polynucleotides, including methods of
XX CC treating HMFG-associated tumours. 11D10 is also used in a claimed
XX CC method of palliating HMFG-associated disease and in claimed kits to
XX CC detect or quantify anti-HMFG antibody.
XX CC (Updated on 25-MAR-2003 to correct PR field.)
XX XX
SQ Sequence 145 AA;
Query Match 100.0%; Score 145; DB 18; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.7e-125;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPAIQLGFLLLFPGTRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQEP 60
DB 1 MGAPAIQLGFLLLFPGTRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQEP 60
QY 61 DGTIKRLIYATSSLGSGVPRKFRSGSDYSLTIFSSLESDFVAYYCLQYASSPYTFGG 120
DB 61 DGTIKRLIYATSSLGSGVPRKFRSGSDYSLTIFSSLESDFVAYYCLQYASSPYTFGG 120
QY 121 GTKLEIKRADAAPTVSIFFPPSSKLG 145
DB 121 GTKLEIKRADAAPTVSIFFPPSSKLG 145
RESULT 2
AAO16292
ID AAO16292 standard; Protein; 145 AA.
XX AC AAO16292;
XX DT 20-MAR-2003 (first entry)
XX DE Mouse 11D10 antibody light chain variable region.
XX KW Mouse; murine; vaccine; tumour; human milk fat globules; HMFG;
XX KW carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour;
XX KW CEA-associated tumour; anti-idiotype antibody.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
XX FT Peptide 1..20
XX FT /label= signal_peptide
XX FT Protein 21..145
XX FT /note= "Mature murine 11D10 antibody light chain variable
XX FT region"
XX FN W0200292012-A2.
XX XX
XX PD 21-NOV-2002.
XX XX
XX PF 17-MAY-2002; 2002WO-US15840.
XX XX
XX PR 17-MAY-2001; 2001US-0861294.
XX XX
XX PA (KENT ) UNIV KENTUCKY RES FOUND.
XX PI Chatterjee M, Foon KA;
XX XX
XX WPI; 2003-129216/12.
XX DR N-PSDB; AAL51273.
XX XX
XX Use of anti-idiotypic antibodies for human milk fat globules (HMFG)- or
XX PT carcinoembryonic antigen (CEA)-associated tumor for delaying the
XX PT development of, or treating a HMFG- or CEA-associated tumor (e.g.
XX PT breast tumor) in humans
XX PS Claim 2; Fig 1; 98pp; English.
XX XX
XX The invention comprises a method for delaying the development of, or
XX CC treating a tumor that is associated with human milk fat globules (HMFG)
XX CC or carcinoembryonic antigen (CEA). The method of the invention involves
XX CC administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an
XX CC anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for
XX CC delaying the development, of or treating HMFG/CEA-associated tumours. The
XX CC present amino acid sequence represents the light chain variable region of
XX CC the mouse 11D10 anti-idiotype antibody.
XX XX
SQ Sequence 145 AA;
Query Match 100.0%; Score 145; DB 24; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.7e-125;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPAIQLGFLLLFPGTRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQEP 60
DB 1 MGAPAIQLGFLLLFPGTRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQEP 60
QY 61 DGTIKRLIYATSSLGSGVPRKFRSGSDYSLTIFSSLESDFVAYYCLQYASSPYTFGG 120
DB 61 DGTIKRLIYATSSLGSGVPRKFRSGSDYSLTIFSSLESDFVAYYCLQYASSPYTFGG 120
QY 121 GTKLEIKRADAAPTVSIFFPPSSKLG 145
DB 121 GTKLEIKRADAAPTVSIFFPPSSKLG 145
RESULT 3
AAW87593
ID AAW87593 standard; Protein; 145 AA.

```

XX AC AAW87593;
XX DT 16-MAR-1999 (first entry)
XX DE Antibody 11D10 light chain variable region.
XX KW Murine; mouse; antibody; light chain; variable region; anti-idiotypic;
KW human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
XX OS Mus sp.
XX PH Location/Qualifiers
FT Peptide 1..20
FT Protein /note= "signal peptide"
FT Region 21..999
FT Region 21..43 /note= "mature protein"
FT Domain 44..54 /label= framework_1
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 55..69 /label= framework_2
FT Misc-difference 55 /note= "encoded by TGG"
FT Domain 70..76 /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 77..108 /label= framework_3
FT Domain 109..117 /label= CDR3
FT /note= "complementarity determining region 3"
FT Region 118..127 /label= framework_4
XX WO9856419-A1.
XX PN 17-DEC-1998.
XX PD 12-JUN-1998; 98WO-US12250.
XX PF 11-JUN-1998; 98US-0096244.
XX PR 13-JUN-1997; 97US-0049540.
XX PS (KENT) UNIV KENTUCKY RES FOUND.
XX PI Chatterjee M, Poon KA;
XX WP; 1999-060029/05.
XX N-PSDB; AAV83772.
XX Delaying development of, or treating, HMFG-associated tumours -
XX using anti-idiotypic antibody 11D10 raised against antibodies to
XX human milk fat globule protein
XX Disclosure; Fig 1; 54pp; English.
XX This sequence represents the light chain variable region of the murine
XX antibody 11D10. This anti-idiotypic antibody is used to delay the
XX development of, or treat, a human milk fat globule (HMFG) associated
XX tumour in an individual having low tumour burden. The antibody 11D10
XX is used to prevent the recurrence of HMFG-associated tumours e.g.
XX ovarian, non-small cell lung and pancreatic carcinoma, especially for
XX treating breast tumours.
XX Sequence 145 AA;
XX Query Match 62.1%; Score 90; DB 20; Length 145;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-74;
XX Matches 90; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 56 LQEPDGTIKRLIYATSSLSGSGVPRKPSGSRSGDYSLTSSLESSEDFVAYYCIQYASSP 115
DB 56 LQEPDGTIKRLIYATSSLSGSGVPRKPSGSRSGDYSLTSSLESSEDFVAYYCIQYASSP 115
QY 116 YTEGGGTKEIKRADAAPTVSIIPPSSKLG 145
DB 116 YTEGGGTKEIKRADAAPTVSIIPPSSKLG 145
RESULT 4
AAW22537
ID AAW22537 standard; Protein; 129 AA.
XX AC AAW22537;
XX DT 03-NOV-1997 (first entry)
XX DE Murine anti-human class II monoclonal antibody 44H104 VL chain.
XX KW Antibody; light chain; variable region; hybridoma cell line 44H104;
KW immune response; enhance; stimulate; vaccine; immunodiagnosis;
KW antigen delivery.
XX OS Mus musculus.
XX PN WO9640941-A1.
XX PD 19-DEC-1996.
XX PF 07-JUN-1996; 96WO-CA00400..
XX PR 07-JUN-1995; 95US-0483576.
XX PA (CONN-) CONNAUGHT LAB LTD.
XX PI Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH;
XX WP; 1997-077271/07.
XX N-PSDB; AAT77851.
XX Recombinant conjugate antibody mol., modified for delivering an
XX antigen - elicits enhanced immune response without the use of
XX adjuvant to generate antibodies which are useful in vaccines or
XX immuno:diagnosis
XX Example 1; Fig 1A; 64pp; English.
XX Novel recombinant conjugate antibody molecules comprise a monoclonal
XX antibody specific for a surface structure of antigen presenting
XX cells (APC), genetically modified to contain at least one antigen
XX exclusively at one or more preselected sites. The conjugate is capable
XX of delivering the antigen to APC and eliciting an immune response to
XX the antigen. The new conjugates are useful as vaccines and are able
XX to elicit an enhanced immune response without the use of an adjuvant.
XX In a specific example, a conjugate was constructed using the murine
XX anti-human class II monoclonal antibody secreted by hybridoma
XX 44H104. The peptide CLTB36 was chosen as antigen; it consists of
XX a tandemly linked T and B cell epitope derived from HIV MN strain.
XX The present sequence represents the light chain variable region
XX from 44H104 which was used in the preparation of a conjugate with
XX antigen CLTB36.
XX Sequence 129 AA;
XX Query Match 22.8%; Score 33; DB 18; Length 129;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-22;
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 FPGTRCDIQMTQSPSSLSASISGQRVSLTCRASQ 47
DB 17 FPGTRCDIQMTQSPSSLSASISGQRVSLTCRASQ 49

RESULT 5

AAE20200
ID AAE20200 standard; Protein: 129 AA.

XX AC AAE20200;

XX DT 18-JUN-2002 (first entry)

XX DE Murine 44H104 mab variable light chain (VL).

XX KW Murine; mab; light chain; VL; conjugate antibody; antigen delivery;
XX KW immune system; vaccine; detecting agent; antibacterial.

XX OS Mus sp.

XX PN US2002025315-A1.

XX PD 28-FEB-2002.

XX PF 14-JAN-1998; 98US-0007093.

XX PR 14-JAN-1998; 98US-0007093.

XX PA (ANAN/) ANAND N N.

XX PA (BARB/) BARBER B H.

XX PA (CATE/) CATES G A.

XX PA (CATE/) CATERINI J E.

XX PA (KLEI/) KLEIN M H.

XX PI Anand NN, Barber BH, Cates GA, Caterini JE, Klein MH;

XX DR WPI; 2002-267519/31.

XX DR N-PSDB; AAD32138.

XX PT Novel recombinant conjugate antibody, useful as a vaccine against
XX PT pathogens having a specific antigen, comprises a monoclonal antibody
XX PT specific for an antigen presenting cell surface structure -

XX PS Example 1; Fig 1A; 28pp; English.

XX CC The invention relates to a recombinant conjugate antibody, comprising
XX CC a monoclonal antibody specific for a surface structure of antigen
XX CC presenting cells genetically modified to contain an antigen moiety
XX CC for the purpose of delivery of the antigen moiety to antigen-
XX CC presenting cells of the immune system. The conjugate antibody is
XX CC formulated as a vaccine to protect a host against a disease caused
XX CC by a pathogen expressing the antigen. The antibody is useful as a
XX CC detecting agent. The present sequence is murine 44H104 mab variable
XX CC light chain (VL).

XX CC Note: This sequence SEQ.ID.NO:2 is stated to be similar to the
XX CC sequence shown in page 11-12 of the specification (AAE20204).

XX CC However these sequences differ.

XX SQ Sequence 129 AA;

Query Match

Best Local Similarity 22.8%; Score 33; DB 23; Length 129;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 FPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQ 47

DB 17 FPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQ 49

RESULT 6

AAE20204
ID AAE20204 standard; Protein: 129 AA.

XX AC AAE20204;

XX DT 18-JUN-2002 (first entry)

XX DE Murine 44H104 mab variable light chain (VL), alternative version.

XX

KW Murine; mab; light chain; VL; conjugate antibody; antigen delivery;
KW immune system; vaccine; detecting agent; antibacterial.

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX FT Misc-difference 93.

XX FT /note= "Encoded by TAT"

XX PN US2002025315-A1.

XX PD 28-FEB-2002.

XX PF 14-JAN-1998; 98US-0007093.

XX PR 14-JAN-1998; 98US-0007093.

XX PA (ANAN/) ANAND N N.

XX PA (BARB/) BARBER B H.

XX PA (CATE/) CATES G A.

XX PA (CATE/) CATERINI J E.

XX PA (KLEI/) KLEIN M H.

XX PI Anand NN, Barber BH, Cates GA, Caterini JE, Klein MH;

XX DR WPI; 2002-267519/31.

XX DR N-PSDB; AAD32138.

XX PT Novel recombinant conjugate antibody, useful as a vaccine against
XX PT pathogens having a specific antigen, comprises a monoclonal antibody
XX PT specific for an antigen presenting cell surface structure -

XX PS Example 1; Page 11-12; 28pp; English.

XX CC The invention relates to a recombinant conjugate antibody, comprising
XX CC a monoclonal antibody specific for a surface structure of antigen
XX CC presenting cells genetically modified to contain an antigen moiety
XX CC for the purpose of delivery of the antigen moiety to antigen-
XX CC presenting cells of the immune system. The conjugate antibody is
XX CC formulated as a vaccine to protect a host against a disease caused
XX CC by a pathogen expressing the antigen. The antibody is useful as a
XX CC detecting agent. The present sequence is murine 44H104 mab variable
XX CC light chain (VL), alternative version.

XX CC Note: This sequence SEQ.ID.NO:2 is stated to be similar to the
XX CC sequence shown in fig 1A (AAE20200). However these sequences differ.

XX SQ Sequence 129 AA;

Query Match

Best Local Similarity 22.8%; Score 33; DB 23; Length 129;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 FPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQ 47

DB 17 FPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQ 49

RESULT 7

AAE20204

ID AAE20204 standard; Protein: 146 AA.

XX AC AAE20204;

XX DT 02-FEB-1996 (first entry)

XX DE Anti-idiotype antibody Idiol7 clone 17KB1.

XX KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
XX KW complementarity determining region.

XX OS Mus sp.

```

FH Key      Location/Qualifiers
FT Peptide  1..13
PT /label= signal_peptide
XX
PN JP07101999-A.
XX
XX 18-APR-1995.
PD
XX 06-OCT-1993; 93JP-0272950.
PF
XX 06-OCT-1993; 93JP-0272950.
PR
XX (HAGI/) HAGIWARA Y.
PA
XX WPI; 1995-182987/24.
DR N-PSDB; AAQ90431.
DR
XX
XX Novel anti-idiotype antibody against an human anticancer monoclonal
PT antibody - and DNA sequences encoding the antibody, useful in
PT pharmacology, medicine and biochemical fields.
PT
XX Example 5; Page 19; 28pp; Japanese.
PS
XX AAR74960-R74969 are clones of the anti-idiotype antibodies Idio3,
CC Idio17, Idio20, Idio27 and Idio33 against a human anticancer monoclonal
CC antibody. These antibodies and DNA encoding them are useful in
CC pharmacological, medical and biochemical fields of research.
XX
XX Sequence 146 AA;
SQ
Query Match 20.7%; Score 30; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 116 YTFGGGKLEIKRADAAPTIVSIFPPSSKLG 145
Db |||||
112 YTFGGGKLEIKRADAAPTIVSIFPPSSKLG 141
RESULT 8
AAV39452
ID AAY39452 standard; Protein; 206 AA.
XX
AC AAY39452;
XX
DT 19-NOV-1999 (first entry)
DE
XX Antibody ABX-CBL light chain sequence.
XX
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
XX Homo sapiens.
XX
XX WO9945031-A2.
PN
PD 10-SEP-1999.
XX
XX 03-MAR-1999; 99WO-US04583.
PF
XX 03-MAR-1998; 98US-0034607.
PR
XX 03-FEB-1999; 99US-0244253.
XX
XX (ABGE-) ABGENIX INC.
PA
XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
PI
XX WPI; 1999-540816/45.
DR
XX New monoclonal antibody, used for treating e.g. graft versus host
PT

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```

PT disease, cancers, autoimmune diseases and inflammatory diseases -
XX
PS Disclosure; Page 58; 245pp; English.
XX
CC This sequence represents the light chain of the antibody ABX-CXL. The
CC invention relates to a monoclonal antibody (MAB) with an isotype
CC that fixes complement and a variable region that binds to the epitope on
CC CD147 bound by the IgM MAB ABX-CBL, providing that the antibody is not
CC CBL1. The MAB can selectively kill activated T-cells, activated B-cells
CC or resting or activated monocytes. The products and methods can be used
CC for treating diseases involving activated T-cells or B-cells or
CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
CC rejection diseases (e.g. renal transplant, ocular transplant), cancers
CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
CC (e.g. arthritis).
XX
SQ Sequence 206 AA;
Query Match 20.7%; Score 30; DB 20; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 113 SSPYTFGGGKLEIKRADAAPTIVSIFPPSS 142
Db |||||
85 SSPYTFGGGKLEIKRADAAPTIVSIFPPSS 114
RESULT 9
AAW95480
ID AAW95480 standard; Protein; 92 AA.
XX
AC AAW95480;
XX
DT 29-MAR-1999 (first entry)
DE
XX Mouse derived RT3 phage antibody light chain pattern C genetic sequence.
XX
KW Catalytic; antibody; phage display; immunising; phage expression vector;
KW prodrug; scfv.
XX
XX Mus sp.
OS
XX US5855885-A.
PN
XX 05-JAN-1999.
PD
XX 14-JUL-1994; 94US-0273146.
PF
XX 22-JAN-1993; 93US-0007684.
PR
XX 14-JUL-1994; 94US-0273146.
XX
XX (CHIS/) CHISWELL D.
PA (DARS/) DARSLEY M J.
PA (FITZ/) FITZGERALD K.
PA (KENT/) KENTEN J H.
PA (MART/) MARTIN M T.
PA (MCCA/) MCCAFFERTY J.
PA (SMIT/) SMITH R.
PA (TITM/) TITMAS R C.
PA (WILL/) WILLIAMS R O.
XX
XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;
PI
XX WPI; 1999-105036/09.
DR N-PSDB; AAX00879.
XX
XX Production of catalytic antibodies displayed on bacteriophages -
PT comprises generating a gene library of antibody-derived domains
PT inserting coding into a phage expression vector and isolating the
PT catalytic antibodies
XX

```

PS Example 4; Fig 11; 117pp; English.

XX The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene library of antibody-derived domains; (b) inserting coding for the domains into a phage expression vector; and (c) isolating the catalytic antibodies. The phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The catalytic antibodies can be isolated by preparing an antigen; optionally immunising an animal with the antigen; generating a library of VH and VL domains from the immunised animal; cloning the VH and VL domains into a phage expression vector to generate phage display antibodies; selecting phage display antibodies which bind specifically to the antigen; screening the selected phage display antibodies for catalytic activity to substrate; and isolating the catalytic antibodies, where the phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The processes are used to produce catalytic antibodies, which can be used for in vivo activation of a prodrug. The present sequence represents a genetic sequence of light chain PCR pattern C from mouse derived RT3 phage antibodies.

XX Sequence 92 AA;

SQ Query Match 20.0%; Score 29; DB 20; Length 92;
Best Local Similarity 100.0%; Pred. No. 8e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPRFSGSRGSDYSLTISSEDFV 104
|||||

Db 48 SGVPRFSGSRGSDYSLTISSEDFV 76
|||||

RESULT 10

AAW95476

ID AAW95476 standard; Protein; 92 AA.

AC AAW95476;

XX 29-MAR-1999 (first entry)

DE Mouse derived RT3 phage antibody light chain pattern A genetic sequence.

KW Catalytic; antibody; phage display; immunising; phage expression vector; prodrug; scFv.

OS Mus sp.

XX US5855885-A.

PN 05-JAN-1999.

PD 14-JUL-1994; 94US-0273146.

PF 22-JAN-1993; 93US-0007684.

PR 14-JUL-1994; 94US-0273146.

XX (CHIS/) CHISWELL D.

PA (DARS/) DARSLEY M J.

PA (FITZ/) FITZGERALD K.

PA (KENT/) KENTEN J H.

PA (MART/) MARTIN M T.

PA (MCCA/) MCCAFFERTY J.

PA (SMIT/) SMITH R.

PA (TITM/) TITMAS R C.

PA (WILL/) WILLIAMS R O.

XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;

PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;

XX WPI; 1999-105036/09.

DR N-PSDB; AAX00875.

XX Production of catalytic antibodies displayed on bacteriophages - comprises generating a gene library of antibody-derived domains

PT

inserting coding into a phage expression vector and isolating the catalytic antibodies

Example 4; Fig 9A-F; 117pp; English.

The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene library of antibody-derived domains; (b) inserting coding for the domains into a phage expression vector; and (c) isolating the catalytic antibodies. The phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The catalytic antibodies can be isolated by preparing an antigen; optionally immunising an animal with the antigen; generating a library of VH and VL domains from the immunised animal; cloning the VH and VL domains into a phage expression vector to generate phage display antibodies; selecting phage display antibodies which bind specifically to the antigen; screening the selected phage display antibodies for catalytic activity to substrate; and isolating the catalytic antibodies, where the phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The processes are used to produce catalytic antibodies, which can be used for in vivo activation of a prodrug. The present sequence represents a genetic sequence of light chain pattern A from mouse derived RT3 phage antibodies.

XX Sequence 92 AA;

SQ Query Match 20.0%; Score 29; DB 20; Length 92;
Best Local Similarity 100.0%; Pred. No. 8e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPRFSGSRGSDYSLTISSEDFV 104
|||||

Db 48 SGVPRFSGSRGSDYSLTISSEDFV 76
|||||

RESULT 11

AAW70954

ID AAW70954 standard; protein; 95 AA.

AC AAW70954;

XX 14-OCT-1998 (first entry)

DE Light chain of monoclonal antibody RS-255.

KW Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody; respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;

KW viral infection; inhibit; fusion; protection; transcription;

KW antiviral agent; prophylaxis; diagnosis; infection; contamination.

OS Mus sp.

XX FR2758331-A1.

PN 17-JUL-1998.

PD 14-JAN-1997; 97FR-0000300.

PF 14-JAN-1997; 97FR-0000300.

PR (UYBO-) UNIV BOURGOGNE.

PA Bourgeois C, Kohli E, Pothier P;

PI WPI; 1998-390320/34.

XX New peptide(s) recognising viral epitope with tropism to mucosa - useful for, e.g. diagnosing, preventing and treating viral infection(s)

XX Disclosure; Fig 2; 51pp; French.

XX The present sequence represents the light chain of monoclonal antibody RS-255, which is directed against the respiratory syncytial virus (RSV).

CC

CC The specification describes peptides which recognise, by
 CC antigen-antibody type reactions, at least 1 epitope of a pathogenic virus
 CC having tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous
 CC to CDR regions of monoclonal antibodies specific for RSV. AAW70917-28 are
 CC analogous to CDR regions of monoclonal antibodies specific for site III
 CC or IV of the VP6 protein of rota virus (RV). The peptides can neutralise
 CC viral infections and may also inhibit fusion between infected and
 CC uninfected cells or cells and viruses. They provide passive or active
 CC antiviral agents or for prophylaxis, in human or veterinary medicine. The
 CC peptides can be labelled and used to diagnose infection or contamination
 CC by the virus. The peptides are particularly directed against RSV or RS
 CC but may also be used against papilloma, adeno, entero, polio, influenza
 CC or immune deficiency viruses.

XX
 SQ Sequence 95 AA;

Query Match 20.0%; Score 29; DB 19; Length 95;
 Best Local Similarity 100.0%; Pred. No. 8.2e-19;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPRFSGRSGSDYSLTISSEDFV 104
 |||||
 DB 43 SGVPRFSGRSGSDYSLTISSEDFV 71

RESULT 12
 AAY90824

ID AAY90824 standard; Protein; 107 AA.

XX
 AC AAY90824;

XX
 DT 29-AUG-2000 (first entry)

XX
 DE 520C9 hybridoma VL domain SEQ ID NO:26.

XX Antigen binding site; immunoglobulin; cancer antigen; immunological;
 KW antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;
 KW specific binding assay; affinity purification; drug targeting;
 KW toxin targeting; imaging; genetic; therapeutic.

XX Homo sapiens.

XX
 PN US6054561-A.

XX
 PD 25-APR-2000.

XX
 PF 07-JUN-1995; 95US-0483749.

XX
 PR 21-MAR-1986; 86US-0842476.

XX
 PR 08-MAY-1988; 88US-0190778.

XX
 PR 08-FEB-1984; 84US-0577976.

XX
 PR 11-JAN-1985; 85US-0690750.

XX
 PR 11-AUG-1994; 94US-0288981.

XX
 PA (CHIR) CHIRON CORP.

XX
 PI Ring DB;

XX
 DR WPI: 2000-338508/29.

XX
 DR N-PSDB; AAA38908.

XX
 PT Monoclonal antibody capable of binding to human breast cancer antigen

XX
 PT useful for affinity purification, drug or toxin targeting, imaging, and

XX
 PT treating cancer

XX
 PS Disclosure; Fig 13; 57pp; English.

XX The present invention describes a monoclonal antibody (MAB) (I) that

XX binds to a human breast cancer antigen that is also bound by MAB 454C11

XX and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also

XX described is a hybridoma that produces (I). (I) is useful in specific

CC and genetic or immunological therapeutics for various cancers. The
 CC present sequence represents a VL domain derived from a 520C9 hybridoma,
 CC which is used in the exemplification of the present invention.

XX
 SQ Sequence 107 AA;

Query Match 20.0%; Score 29; DB 21; Length 107;
 Best Local Similarity 100.0%; Pred. No. 9e-19;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPRFSGRSGSDYSLTISSEDFV 104
 |||||
 DB 56 SGVPRFSGRSGSDYSLTISSEDFV 84

RESULT 13
 AAR21310

ID AAR21310 standard; Protein; 108 AA.

XX
 AC AAR21310;

XX
 DT 21-MAY-1992 (first entry)

XX
 DE Light chain of M1f clone.

XX
 KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;

XX KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;

XX KW specific binding pairs; replicable genetic display package.

XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers

XX
 FT Region 25..34

XX
 FT Region /label= CDR1

XX
 FT Region 50..56

XX
 FT Region /label= CDR2

XX
 FT Region 89..96

XX
 FT Region /label= CDR3

XX
 PN WO9201047-A.

XX
 PD 23-JAN-1992.

XX
 PF 10-JUL-1991; 91WO-GB01134.

XX
 PR 15-MAY-1991; 91GB-0010549.

XX
 PR 10-JUL-1990; 90GB-0015198.

XX
 PR 19-OCT-1990; 90GB-0022845.

XX
 PR 12-NOV-1990; 90GB-0024503.

XX
 PR 06-MAR-1991; 91GB-0004744.

XX
 PA (CMB-) CAMBRIDGE ANTIBODY.

XX
 PA (MEDI-) MED RES COUNCIL.

XX
 PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;

XX
 PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;

XX
 PI Winter GP, Bonnett TP;

XX
 DR WPI; 1992-056862/07.

XX
 DR Producing members of specific binding pairs - by expression in

XX
 PT recombinant host cells with a secreting replicable genetic

XX
 PT display package.

XX
 PS Example 46; Fig 52; 109pp; English.

XX The sequence is the light chain of clone M1f encoding an scFv frag-

XX ment specific for both hen and turkey egg lysozyme (HEL and TEL).

XX The DNA encoding the chain was amplified from a cDNA library prepd.

XX from the spleen of an unimmunised mouse. The corresponding heavy

XX chain was also amplified from an existing construct, pSWI-VHDI.3

XX (ward et al, 1989). The two fragments were assembled via a linker

XX to prepare an scFv construct which was ligated into the fdCAT2

CC vector for expression on the surface of fd bacteriophage. In this
 CC way, the VL domain was replaced by a library of VL domains to allow
 CC for selection of a broader range of antibody specificities. Several
 CC clones were isolated which bound to TEL (the parent antibody D1.3
 CC binds exclusively to HEL). The sequences of the light chains of
 CC two of these clones, WF1 and M21 are given in AAR21310 and AAR21311
 CC respectively. The D1.3 light chain is given in AAR21309.
 CC See also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81.
 XX
 SQ Sequence 108 AA;

Query Match 20.0%; Score 29; DB 13; Length 108;
 Best Local Similarity 100.0%; Pred. No. 9.1e-19;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPKFRSGSGSDYSLTISSEDFV 104
 |||||
 DB 56 SGVPKFRSGSGSDYSLTISSEDFV 84

RESULT 14
 AAY44587
 ID AAY44587 standard; Protein; 108 AA.

XX AAY44587;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE Mouse anti-IL-18 antibody light chain variable region.

XX Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
 KW hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18;
 KW antiinflammatory; immunosuppressive; leucocytopenic; antiallgic;
 KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
 KW immunopathy; inflammatory disorder; immunoreaction.

XX Mus musculus.

XX EP974600-A2.

XX 26-JAN-2000.

XX 24-JUN-1999; 99EP-0304977.

XX 24-JUN-1998; 98JP-0177580.

XX 12-OCT-1998; 98JP-0289044.

XX 22-DEC-1998; 98JP-0365023.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX WPI; 2000-118341/11.

XX N-PSDB; AAZ49534.

XX New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases -
 XX
 XX

PS Claim 5; Page 17; 36pp; English.

XX The present protein sequence is the mouse anti-Interleukin-18 antibody
 CC light chain variable region (VL) encoded by cDNA derived from hybridoma
 CC #125-2H. The nucleotide sequence is used in the production of recombinant
 CC monoclonal antibody #125-2HmAb, which is capable of neutralising
 CC biological activities of interleukin-18. The antibody has antiallgic,
 CC antiinflammatory, immunosuppressive, leucocytopenic, antipyretic,
 CC antiallergic and hepatotropic activity and can be used for prevention and
 CC treatment of autoimmune diseases, immunopathies and inflammatory
 CC disorders caused by excessive immunoreaction.

XX Sequence 108 AA;

Query Match 20.0%; Score 29; DB 21; Length 108;
 Best Local Similarity 100.0%; Pred. No. 9.1e-19;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPKFRSGSGSDYSLTISSEDFV 104
 |||||
 DB 56 SGVPKFRSGSGSDYSLTISSEDFV 84

RESULT 15
 AAE34366
 ID AAE34366 standard; Protein; 130 AA.

XX AAE34366;

XX 14-MAY-2003 (first entry)

XX Escherichia coli light chain variable region.

XX S-surface antigen; Hepatitis B virus; HBV; therapy; infection; virucide;
 KW hepatotropic.

XX Escherichia coli.

XX Key Location/Qualifiers
 FT Region 24..40
 FT /note= "CDR1"
 FT Region 56..62
 FT /note= "CDR2"
 FT Region 95..102
 FT /note= "CDR3"

XX WO200292819-A1.

XX 21-NOV-2002.

XX 15-MAY-2002; 2002WO-KR00905.

XX 16-MAY-2001; 2001KR-0026634.

XX (YUHA-) YUHAN CORP.

XX Lee JW, Ko IY, Kang HK, Song MY, Song TH, Kim CS;

XX WPI; 2003-140281/13.

XX N-PSDB; AAD52607.

XX New light and heavy chain variable regions of a monoclonal antibody
 PT against the S-surface antigen of the hepatitis B virus (HBV), useful
 PT for neutralizing or removing HBV, or for preventing or treating HBV
 PT infection -
 XX

PS Claim 2; Page 16; 20pp; English.

XX The invention relates to light and heavy chain variable regions of a
 CC monoclonal antibody against S-surface antigen of the hepatitis B virus
 CC (HBV). The variable regions of the antibodies are useful against HBV
 CC S-surface antigens, e.g. adr, adw, ayr or ayw, particularly for
 CC neutralising or removing HBV. They may also be employed to treat or
 CC prevent HBV infection. The present sequence is Escherichia coli light
 CC chain variable region.

XX Sequence 130 AA;

Query Match 20.0%; Score 29; DB 24; Length 130;
 Best Local Similarity 100.0%; Pred. No. 1.1e-18;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TFGGKTLEIKRADAPTVSIFPPSSKLG 145
 |||||
 DB 102 TFGGKTLEIKRADAPTVSIFPPSSKLG 130

Search completed: August 30, 2003, 22:09:54
Job time : 25.8154 secs



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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2003, 22:08:56 ; Search time 15.5705 Seconds
(without alignments)
1273.781 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 145

Sequence: 1 MGAPAQILGFLLLFPGRNC.....IKRDAAPVTSIFPPSSKLG 145

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 510680 seqs, 136781880 residues

Word size : 0

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA.*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pap.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pap.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pap.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pap.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pap.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pap.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	145	100.0	145	9	US-08-861-294-2
2	145	100.0	145	12	US-10-367-506-2
3	33	22.8	129	9	US-09-007-093-2
4	29	20.0	108	10	US-09-924-099-1
5	29	20.0	130	8	US-08-779-784-35
6	29	20.0	130	14	US-10-146-305-7
7	29	20.0	149	10	US-09-990-205-2
8	29	20.0	149	15	US-10-153-401-2
9	29	20.0	237	10	US-09-924-099-9
10	29	20.0	243	10	US-09-924-099-10
11	29	20.0	243	10	US-09-887-853-6
12	28	19.3	108	12	US-10-268-883-12
13	28	19.3	112	12	US-10-355-780-1
14	28	19.3	130	12	US-10-268-883-11
15	27	18.6	109	12	US-09-943-906-74

16	17.9	124	9	US-09-802-077-4	Sequence 4, Appli
17	17.9	124	9	US-09-802-096-4	Sequence 4, Appli
18	17.9	124	11	US-09-925-179-4	Sequence 4, Appli
19	17.9	142	10	US-09-840-459-102	Sequence 102, App
20	17.9	234	12	US-10-281-479A-24	Sequence 24, Appl
21	17.9	238	10	US-09-903-327A-4	Sequence 4, Appli
22	17.9	238	15	US-10-216-484-11	Sequence 11, Appl
23	17.9	672	11	US-09-900-766-1	Sequence 1, Appli
24	17.2	33	9	US-09-861-294-9	Sequence 9, Appli
25	17.2	33	12	US-10-367-506-9	Sequence 9, Appli
26	17.2	142	9	US-09-797-481-2	Sequence 2, Appli
27	17.2	142	9	US-09-844-736-4	Sequence 4, Appli
28	17.2	142	15	US-10-162-396-4	Sequence 4, Appli
29	16.6	95	10	US-09-943-906-72	Sequence 72, Appl
30	15.9	23	9	US-09-861-294-5	Sequence 5, Appli
31	15.9	23	12	US-10-367-506-5	Sequence 5, Appli
32	14.5	121	11	US-09-929-665-11	Sequence 11, Appl
33	14.5	121	11	US-09-929-546-11	Sequence 11, Appl
34	13.8	269	14	US-10-027-770-2	Sequence 2, Appli
35	13.8	269	14	US-10-027-770-5	Sequence 5, Appli
36	13.1	129	9	US-09-839-447A-2	Sequence 2, Appli
37	13.1	129	15	US-10-153-271-2	Sequence 2, Appli
38	11.7	19	9	US-09-839-447A-25	Sequence 25, Appl
39	11.7	19	15	US-10-153-271-25	Sequence 25, Appl
40	11.0	16	9	US-09-756-899A-3	Sequence 3, Appli
41	11.0	23	11	US-09-563-222-130	Sequence 130, App
42	11.0	108	9	US-09-329-200A-17	Sequence 17, Appl
43	11.0	109	9	US-09-329-200A-7	Sequence 7, Appli
44	11.0	109	11	US-09-929-665-21	Sequence 21, Appl
45	11.0	109	11	US-09-929-546-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1									
US-09-861-294-2									
; Sequence 2, Application US/09861294									
; Patent No. US20020098190A1									
; GENERAL INFORMATION:									
; APPLICANT: Malaya CHATTERJEE									
; APPLICANT: Kenneth A. FOON									
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING									
; TITLE OF INVENTION: TUMORS BEARING HMF AND CEA ANTIGENS									
; FILE REFERENCE: 304142000620									
; CURRENT APPLICATION NUMBER: US/09/861,294									
; CURRENT FILING DATE: 2001-05-17									
; PRIOR APPLICATION NUMBER: 60/049,540									
; PRIOR FILING DATE: 1997-06-13									
; PRIOR APPLICATION NUMBER: 09/096,244									
; PRIOR FILING DATE: 1998-06-11									
; NUMBER OF SEQ ID NOS: 38									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 2									
; LENGTH: 145									
; TYPE: PRT									
; ORGANISM: Mus musculus									
; FEATURE:									
; NAME/KEY: SIGNAL									
; LOCATION: (1)...(20)									
US-09-861-294-2									
Query Match 100.0%; Score 145; DB 9; Length 145;									
Best Local Similarity 100.0%; Pred. No. 6.4e-122;									
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MGAPAQILGFLLLFPGRNC	1	MGAPAQILGFLLLFPGRNC	1				
Db	1	MGAPAQILGFLLLFPGRNC	1	MGAPAQILGFLLLFPGRNC	1				
QY	61	DGTIKRLIYATSSILGSGVPRFSGRSGSDYSLTISLSEDFVAYCLOAYSSPYTFGG	120	DGTIKRLIYATSSILGSGVPRFSGRSGSDYSLTISLSEDFVAYCLOAYSSPYTFGG	120				
Db	61	DGTIKRLIYATSSILGSGVPRFSGRSGSDYSLTISLSEDFVAYCLOAYSSPYTFGG	120	DGTIKRLIYATSSILGSGVPRFSGRSGSDYSLTISLSEDFVAYCLOAYSSPYTFGG	120				

Qy 121 GTKLEIKRADAAPTVSIFPPSSKLG 145
|
Db 121 GTKLEIKRADAAPTVSIFPPSSKLG 145

RESULT 2

US-10-367-506-2
; Sequence 2, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMGF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-367-506-2

Query Match 100.0%; Score 145; DB 12; Length 145;
Best Local Similarity 100.0%; Pred. No. 6.4e-122; Indels 0; Gaps 0;
Matches 145; Conservative 0; Mismatches 0;
Qy 1 MGAPAQILGFLLLFPQTRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEP 60
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Db 1 MGAPAQILGFLLLFPQTRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEP 60
Qy 61 DGTIKRLIYATSSLGSGVPRKFRSGSGSDYSLTISSEDFVAYYCLQYASSPYTFGG 120
|
Db 61 DGTIKRLIYATSSLGSGVPRKFRSGSGSDYSLTISSEDFVAYYCLQYASSPYTFGG 120
Qy 121 GTKLEIKRADAAPTVSIFPPSSKLG 145
|
Db 121 GTKLEIKRADAAPTVSIFPPSSKLG 145

RESULT 3

US-09-007-093-2
; Sequence 2, Application US/09007093
; Patent No. US2002025315A1
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,093
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/483,576
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-765
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-007-093-2

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Best Local Similarity 100.0%; Pred. No. 6.4e-22;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 FPGTRCDIQMTQSPSSLSASLGQVSLTCRASQ 47
|
Db 17 FPGTRCDIQMTQSPSSLSASLGQVSLTCRASQ 49

RESULT 4

US-09-924-099-1
; Sequence 1, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-1

Query Match 20.0%; Score 29; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 SGVPKFRSGSGSDYSLTISSEDFV 104
|
Db 56 SGVPKFRSGSGSDYSLTISSEDFV 84

RESULT 5

US-08-779-784-35
; Sequence 35, Application US/08779784

Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-08-779-784-35

Query Match 20.0%; Score 29; DB 8; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPRFSGSRGSDYSLTISSESEDFV 104
Db 78 SGVPRFSGSRGSDYSLTISSESEDFV 106

RESULT 6
US-10-146-305-7
; Sequence 7, Application US/10146305
; Publication No. US20020173035A1
; GENERAL INFORMATION:
; APPLICANT: YUHAN CORPORATION
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
; FILE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME
; REFERENCE: OVI1740
; CURRENT APPLICATION NUMBER: US/10/146,305
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16

NUMBER OF SEQ ID NOS: 14
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-146-305-7

Query Match 20.0%; Score 29; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TFGGGTKLEIKRADAAPTIVSIFPPSSKLG 145
Db 102 TFGGGTKLEIKRADAAPTIVSIFPPSSKLG 130

RESULT 7
US-09-990-205-2
; Sequence 2, Application US/09990205
; Patent No. US20020150572A1
; GENERAL INFORMATION:
; APPLICANT: FOON, Kenneth A.
; APPLICANT: CHATTERJEE, Malaya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000501
; CURRENT APPLICATION NUMBER: US/09/990,205
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: U.S. 09/192,838
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/065,774
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-990-205-2

Query Match 20.0%; Score 29; DB 10; Length 149;
Best Local Similarity 100.0%; Pred. No. 2.7e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TFGGGTKLEIKRADAAPTIVSIFPPSSKLG 145
Db 121 TFGGGTKLEIKRADAAPTIVSIFPPSSKLG 149

RESULT 8
US-10-153-401-2
; Sequence 2, Application US/10153401
; Publication No. US20030114398A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:


```
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6
Query Match 20.0%; Score 29; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 4.2e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPKRFSGSRGSDYSLTISSEDFV 104
Db 189 SGVPKRFSGSRGSDYSLTISSEDFV 217

RESULT 12
US-10-268-883-12
; Sequence 12, Application US/10268883
; Publication No. US20030138862A1
; GENERAL INFORMATION:
; APPLICANT: TSO, J. Yun
; APPLICANT: Green, Jennifer Macphate
; TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
; FILE REFERENCE: 05882.0062.NPUS01
; CURRENT APPLICATION NUMBER: US/10/268,883
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: USSN 60/329,178
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: USSN 60/331,965
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse
US-10-268-883-12
Query Match 19.3%; Score 28; DB 12; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPKRFSGSRGSDYSLTISSEDF 103
Db 56 SGVPKRFSGSRGSDYSLTISSEDF 83

RESULT 13
US-10-355-780-1
; Sequence 1, Application US/10355780
; Publication No. US20030143224A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley
; APPLICANT: Safar, Jiri
; APPLICANT: Williamson, Anthony
; APPLICANT: Burton, Dennis
; TITLE OF INVENTION: Antibodies Specific for Ungulate Prp
; FILE REFERENCE: UCAL-194
; CURRENT APPLICATION NUMBER: US/10/355,780
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US/09/627,218B
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized peptide
US-10-355-780-1
Query Match 19.3%; Score 28; DB 12; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.7e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPKRFSGSRGSDYSLTISSEDF 103
Db 56 SGVPKRFSGSRGSDYSLTISSEDF 83

RESULT 14
US-10-268-883-11
; Sequence 11, Application US/10268883
; Publication No. US20030138862A1
; GENERAL INFORMATION:
; APPLICANT: TSO, J. Yun
; APPLICANT: Green, Jennifer Macphate
; TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
; FILE REFERENCE: 05882.0062.NPUS01
; CURRENT APPLICATION NUMBER: US/10/268,883
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: USSN 60/329,178
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: USSN 60/331,965
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mouse
US-10-268-883-11
Query Match 19.3%; Score 28; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPKRFSGSRGSDYSLTISSEDF 103
Db 78 SGVPKRFSGSRGSDYSLTISSEDF 105

RESULT 15
US-09-943-906-74
; Sequence 74, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE Prp
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
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;
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-09-943-906-74

Query Match 18.6%; Score 27; DB 10; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 SGVPRFSGSRGSDYSLTISLSEED 102
Db 56 SGVPRFSGSRGSDYSLTISLSEED 82

Search completed: August 30, 2003, 22:12:32
Job time : 16.5705 secs

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OM protein - protein search, using sw model

Run on: August 30, 2003, 22:07:01 ; Search time 10.2181 Seconds
(without alignments)
1364.679 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 145

Sequence: 1 MGAPAQILGFLLLFPGR.....IKRADAAPTVSIFPPPSKLG 145

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	29	20.0	88	2	PL0261
2	29	20.0	106	2	PL0260
3	29	20.0	106	2	PL0259
4	29	20.0	130	1	KVMSM4
5	28	19.3	91	2	S17622
6	28	19.3	98	2	PH1062
7	28	19.3	108	4	B47271
8	28	19.3	197	2	S29593
9	28	19.3	214	2	S68212
10	27	18.6	225	2	S37484
11	26	17.9	219	2	PC4203
12	26	17.9	219	2	S38865
13	24	16.6	225	2	JL0029
14	22	15.2	128	2	PN0445
15	22	15.2	140	2	PN0446
16	22	15.2	217	2	S42772
17	22	15.2	234	2	S14237
18	20	13.8	106	2	PL0262
19	19	13.1	210	2	A56169
20	19	13.1	219	2	S16112
21	19	13.1	219	2	S52028
22	18	12.4	101	2	K28840
23	18	12.4	117	1	KVMS3B
24	17	11.7	107	2	S40366
25	17	11.7	129	2	S32513
26	16	11.0	94	2	PH1063
27	16	11.0	94	2	E33730
28	16	11.0	97	2	PH1064
29	16	11.0	101	2	C28840

RESULT 1

PL0261

Ig kappa chain V region (anti-DNA, DP1SVK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

A:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997

C:Accession: PL0261

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0261

A:Molecule type: mRNA

A:Residues: 1-88 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:1-5/Region: framework 1

F:6-16/Region: complementarity-determining 1

F:17-31/Region: framework 2

F:32-38/Region: complementarity-determining 2

F:39-70/Region: framework 3

F:71-79/Region: complementarity-determining 3

F:80-88/Region: framework 4

Query Match

Best Local Similarity 20.0%; Score 29; DB 2; Length 88;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPRFSGSRSGSYSLTISLSSEDFV 104

Db 38 SGVPRFSGSRSGSYSLTISLSSEDFV 66

RESULT 2

PL0260

Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

A:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

C:Accession: PL0260

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0260

A:Molecule type: mRNA

A:Residues: 1-106 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 20.0%; Score 29; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 9.7e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPKRFSGSGSDYSLTISSEDFV 104
|||||
DB 56 SGVPKRFSGSGSDYSLTISSEDFV 84
|||||

RESULT 3
PL0259
Ig kappa chain V region (anti-DNA, Dp11VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0259
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-287, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0259
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 20.0%; Score 29; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 9.7e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPKRFSGSGSDYSLTISSEDFV 104
|||||
DB 56 SGVPKRFSGSGSDYSLTISSEDFV 84
|||||

RESULT 4
KVMSM4
Ig kappa chain precursor V region (MOPC 41) - mouse
N:Contains: Ig kappa chain precursor V region VK41
C:Species: Mus musculus (house mouse)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 28-May-1999
C:Accession: A93211; A93211; A93815; A94239; A01922; A01923
R:Seidman, J.G.; Max, E.E.; Leder, P.
Nature 280, 370-375, 1979
A:Title: A kappa-immunoglobulin gene is formed by site-specific recombination without fu
A:Reference number: A93211; MUID:79221900; PMID:111146
A:Accession: A93211
A:Molecule type: DNA
A:Residues: 1-130 <PC41>
A:Accession: B93211
A:Molecule type: DNA
A:Residues: 1-117 <VK41>
A:Cross-references: GB:V00804; GB:J00566; NID:952127; PID:CAA24186.1; PID:g575660
A:Note: The sequences were determined from the differentiated gene MOPC 41 and the germ
R:Burststein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A:Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors
A:Reference number: A93815; MUID:77148916; PMID:403522
A:Accession: A93815
A:Molecule type: protein
A:Residues: 1-33 <BUR>
A:Note: Met-3 is apparently used as an alternative initiator in 25% of the chains

R:Gray, W.R.; Dreyer, W.J.; Hood, L.
Science 155, 465-467, 1967
A:Title: Mechanism of antibody synthesis: size differences between mouse kappa chains
A:Reference number: A94239; MUID:67056897; PMID:4162931
A:Accession: A94239
A:Molecule type: protein
A:Residues: 23-49, 'B', '51-53, 'LSB', '57-58, '22', '61-62, 'B2', '65-76, 'B', '78-108, 110-130 <GRA
A:Experimental source: Bence Jones protein MOPC 41
C:Genetics:
A:Introns: 19/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (h
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: alternative initiators; heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status experimental <SIG1>
F:23-22/Domain: signal sequence #status experimental <SIG2>
F:23-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>
F:38-112/Domain: immunoglobulin homology <IMM>
F:43-110/Disulfide bonds: #status predicted

Query Match 20.0%; Score 29; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPKRFSGSGSDYSLTISSEDFV 104
|||||
DB 78 SGVPKRFSGSGSDYSLTISSEDFV 106
|||||

RESULT 5
S17622
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17622
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17622
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-91 <CIA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-82/Domain: immunoglobulin homology <IMM>

Query Match 19.3%; Score 28; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 8e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPKRFSGSGSDYSLTISSEDFV 103
|||||
DB 48 SGVPKRFSGSGSDYSLTISSEDFV 75
|||||

RESULT 6
PH1062
Ig light chain V region (clone 202.105) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1062
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1062
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-98 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 19.3%; Score 28; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.5e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPRFSGSRGSDYSLTISSEDF 103
|||||
Db 56 SGVPRFSGSRGSDYSLTISSEDF 83

RESULT 7

B47271
nitrophenyl phosphonate-specific antibody 48G7 light chain VJ - synthetic (fragment)
C;Species: synthetic
A;Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli
C;Date: 21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change 11-Aug-1995
C;Accession: B47271

R;Lesley, S.A.; Patten, P.A.; Schultz, P.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993
A;Title: A genetic approach to the generation of antibodies with enhanced catalytic activity
A;Reference number: A47271; MUID:93165660; PMID:8094556
C;Accession: B47271

A;Molecule type: DNA; protein

A;Residues: 1-108 <LES>

A;Note: sequence extracted from NCBI backbone (NCBI:124856, NCBIP:124859)

A;Note: parts of this sequence were determined by protein sequencing

F;24-89/Disulfide bonds: #status predicted

Query Match 19.3%; Score 28; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 9.2e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPRFSGSRGSDYSLTISSEDF 103
|||||
Db 57 SGVPRFSGSRGSDYSLTISSEDF 84

RESULT 8

S29593
Ig kappa chain (W65) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000

C;Accession: S29593

R;Seymour, R.

submitted to the EMBL Data Library, February 1991

A;Reference number: S29593

A;Accession: S29593

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-197 <SEY>

A;Cross-references: EMBL:X57856; NID:g52588; PIDN:CAA40991.1; PID:g52589

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

Query Match 19.3%; Score 28; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 PYTFGGTGLEIKRADAAPTIVSIFPPSS 142
|||||
Db 115 PYTFGGTGLEIKRADAAPTIVSIFPPSS 142

RESULT 9

S68212

Ig kappa chain (Mab03-1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000

C;Accession: S68212

R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.

FEBS Lett. 375, 273-276, 1995

A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin

A;Reference number: S68211; MUID:96085223; PMID:7498516

A;Accession: S68212

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-214 <YAK>

A;Cross-references: EMBL:D29668

C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 19.3%; Score 28; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.6e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 PYTFGGTGLEIKRADAAPTIVSIFPPSS 142
|||||
Db 101 PYTFGGTGLEIKRADAAPTIVSIFPPSS 128

RESULT 10

S37484

Ig kappa chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000

C;Accession: S37484

R;Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A;Reference number: S37483

A;Accession: S37484

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-225 <DUC>

A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

Query Match 18.6%; Score 27; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 YTFGGTGLEIKRADAAPTIVSIFPPSS 142
|||||
Db 107 YTFGGTGLEIKRADAAPTIVSIFPPSS 133

RESULT 11

PC4203

Ig kappa chain (monoclonal antibody MAbA34) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000

C;Accession: PC4203

R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.

Gene 173, 257-259, 1996

A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a

A;Reference number: PC4202; MUID:97082978; PMID:8964510

A;Accession: PC4203

A;Molecule type: mRNA

A;Residues: 1-219 <KWA>

A;Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226

C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;1-112/Domain: V region #status predicted <VRG>

F;113-219/Domain: C region #status predicted <CRG>

Query Match 17.9%; Score 26; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TFGGGTGLEIKRADAAPTIVSIFPPSS 142
|||||
Db 102 TFGGGTGLEIKRADAAPTIVSIFPPSS 127

RESULT 12

S38865

Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C:Accession: S38865
R:Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of an
A:Reference number: S38864
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <KIP>
A:Cross-references: EMBL:227396; NID:q416538; PIDN:CA81787.1; PID:q416539
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 17.9%; Score 26; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.5e-17; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

Qy 117 TFGGGTKLEIKRADAAPTTSIFPPSS 142
|||||
Db 102 TFGGGTKLEIKRADAAPTTSIFPPSS 127

RESULT 13
JL0029
Ig kappa chain precursor (RP93) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C:Accession: JL0029
R:Chien, N.C.; Pollock, R.R.; Desaynard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A:Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphospho
A:Reference number: JL0029; MUID:88171315; PMID:3127529
A:Accession: JL0029
A:Molecule type: mRNA
A:Residues: 1-225 <CHI>
A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A:Note: the authors translated the codon CGG for residue 106 as pro, ACC for residue 132
A:Note: the nucleotide sequence shown is inconsistent with authors' translation because
ect except for four positions shown above
C:Comment: The protein is an anti-phosphorylcholine antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:7-225/Product: Ig kappa chain #status predicted <ILC>
F:7-106/Domain: V region #status predicted <VAR>
F:107-119/Domain: J region #status predicted <JIR>
F:120-225/Domain: C region #status predicted <COR>

Query Match 16.6%; Score 24; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 TFGGGTKLEIKRADAAPTTSIFPP 140
|||||
Db 108 TFGGGTKLEIKRADAAPTTSIFPP 131

RESULT 14
PN0445
Ig kappa chain precursor V-I region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PN0445
R:Kaluza, B.; Betzel, G.; Shao, H.; Diamantsehn, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A:Title: A general method for chimerization of monoclonal antibodies by inverse polymera
A:Reference number: PN0444; MUID:93138402; PMID:1339379
A:Accession: PN0445
A:Molecule type: mRNA
A:Residues: 1-128 <KAL>
A:Cross-references: GB:L02347

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-10/Domain: signal sequence #status predicted <SIG>
F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 15.2%; Score 22; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.3e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 TFGGGTKLEIKRADAAPTTSIF 138
|||||
Db 107 TFGGGTKLEIKRADAAPTTSIF 128

RESULT 15
PN0446
Ig kappa chain precursor V-II region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PN0446
R:Kaluza, B.; Betzel, G.; Shao, H.; Diamantsehn, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A:Title: A general method for chimerization of monoclonal antibodies by inverse polym
A:Reference number: PN0444; MUID:93138402; PMID:1339379
A:Accession: PN0446
A:Molecule type: mRNA
A:Residues: 1-140 <KAL>
A:Cross-references: GB:L02345
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-140/Product: Ig light chain kappa-2 V region #status predicted <MAT>
F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 15.2%; Score 22; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 TFGGGTKLEIKRADAAPTTSIF 138
|||||
Db 119 TFGGGTKLEIKRADAAPTTSIF 140

Search completed: August 30, 2003, 22:11:49
Job time : 10.2181 secs

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OM protein - protein search, using sw model

Run on: August 30, 2003, 22:04:41 ; Search time 8.75839 Seconds
(without alignments)
778.553 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 145

Sequence: 1 MGAPAQILGFLLLFPQTRC.....IKRADAAPTVISFPSSKLG 145

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	29	20.0	130	1 KV5G_MOUSE	P01639 mus musculus
2	18	12.4	117	1 KV5H_MOUSE	P01641 mus musculus
3	16	11.0	117	1 KV1L_HUMAN	P01601 homo sapien
4	16	11.0	129	1 KV1W_HUMAN	P04431 homo sapien
5	16	11.0	129	1 KV1X_HUMAN	P04432 homo sapien
6	14	9.7	106	1 KAC_MOUSE	P01837 mus musculus
7	14	9.7	108	1 KV1A_HUMAN	P01593 homo sapien
8	14	9.7	108	1 KV1B_HUMAN	P01594 homo sapien
9	14	9.7	108	1 KV1G_HUMAN	P01599 homo sapien
10	14	9.7	108	1 KV1H_HUMAN	P01600 homo sapien
11	14	9.7	108	1 KV1O_HUMAN	P01607 homo sapien
12	14	9.7	108	1 KV1P_HUMAN	P01608 homo sapien
13	14	9.7	108	1 KV1Q_HUMAN	P01609 homo sapien
14	14	9.7	108	1 KV1R_HUMAN	P01610 homo sapien
15	14	9.7	108	1 KV1Y_HUMAN	P08362 homo sapien
16	14	9.7	108	1 KV5Q_MOUSE	P01650 mus musculus
17	14	9.7	108	1 KV5S_MOUSE	P01652 mus musculus
18	14	9.7	108	1 KV5T_MOUSE	P01653 mus musculus
19	14	9.7	113	1 KV2E_MOUSE	P03976 mus musculus
20	14	9.7	113	1 KV2F_MOUSE	P01630 mus musculus
21	13	9.0	106	1 KACA_RAT	P01836 rattus norv
22	13	9.0	106	1 KACB_RAT	P01835 rattus norv
23	13	9.0	111	1 KV3D_MOUSE	P03977 mus musculus
24	13	9.0	111	1 KV3H_MOUSE	P01660 mus musculus
25	13	9.0	111	1 KV3J_MOUSE	P01662 mus musculus
26	13	9.0	111	1 KV3L_MOUSE	P01664 mus musculus
27	13	9.0	112	1 KV1U_HUMAN	P01613 homo sapien
28	13	9.0	112	1 KV2D_MOUSE	P01629 mus musculus
29	13	9.0	112	1 KV3B_MOUSE	P01655 mus musculus
30	13	9.0	136	1 KV5B_MOUSE	P01634 mus musculus
31	12	8.3	107	1 KV6A_MOUSE	P01675 mus musculus
32	12	8.3	107	1 KV6D_MOUSE	P01678 mus musculus
33	12	8.3	108	1 KV1M_HUMAN	P01605 homo sapien

ALIGNMENTS

RESULT 1

ID	KV5G_MOUSE	STANDARD;	PRT;	130 AA.
AC	P01639; P01640;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-V region MOPC 41 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			P01643 mus musculus
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			P01644 mus musculus
OX	NCBI_TaxID=10090;			P01645 mus musculus
RN	[1]			P01646 mus musculus
RP	SEQUENCE FROM N.A.			P01647 mus musculus
RX	MEDLINE=79221900; PubMed=111146;			P01648 mus musculus
RA	Seldman J.G., Max E.E., Leder P.;			P01649 mus musculus
RT	"A kappa-immunoglobulin gene is formed by site-specific recombination			P01612 homo sapien
RT	without further somatic mutation.";			P01631 mus musculus
RL	Nature 280:370-375(1979).			P01597 homo sapien
RN	[2]			P01651 mus musculus
RP	SEQUENCE OF 1-33.			
RX	MEDLINE=77148916; PubMed=403522;			
RA	Burstein Y., Schechter I.;			
RT	"Amino acid sequence of the NH2-terminal extra piece segments of the			
RT	precursors of mouse immunoglobulin lambda1-type and kappa-type light			
RL	chains.";			
[3]	Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).			
RP	SEQUENCE OF 23-130.			
RX	MEDLINE=67056897; PubMed=4162931;			
RA	Gray W.R., Dreyer W.J., Hood L.;			
RT	"Mechanism of antibody synthesis: size differences between mouse			
RT	kappa chains.";			
RL	Science 155:465-467(1967).			
CC	-1- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE			
CC	SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.			
CC	-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
DR	PIR: A93211; KVM5M4.			
DR	HSSP; P01607; IREI.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; Igv; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Immunoglobulin V region; Signal; Bence-Jones protein.			
FT	SIGNAL	1	22	
FT	CHAIN	23	130	IG KAPPA CHAIN V-V REGION MOPC 41.
FT	DOMAIN	23	45	FRAMEWORK-1.
FT	DOMAIN	46	56	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	57	71	FRAMEWORK-2.
FT	DOMAIN	72	78	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	79	110	FRAMEWORK-3.
FT	DOMAIN	111	119	COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN	120	129	FRAMEWORK-4.
FT	DISULFID	45	110	BY SIMILARITY.

```

FT VARIANT      1      2      MISSING (IN 25% OF THE MOLECULES).
FT NON_TER     130     130
SQ SEQUENCE    130 AA; 14311 MW; 5EPE0FE71D5F1BEC CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 1; Length 130;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SGVPRFSGSRGSDYSLTISSEDFV 104
DB 78 SGVPRFSGSRGSDYSLTISSEDFV 106

RESULT 2
KV5H_MOUSE
ID KV5H_MOUSE STANDARD; PRT; 117 AA.
AC P01641;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 173B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81064681; PubMed=6777049;
RA Max E.E., Seidman J.G., Miller H., Leder P.;
RT "Variation in the crossover point of kappa immunoglobulin gene V-J
recombination: evidence from a cryptic gene.";
RL Cell 21:793-799(1980).
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DR EMBL; K00880; AAA39031.1; -
DR PIR; A01924; KVM3B.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL      1      22
FT CHAIN       23     117 IG KAPPA CHAIN V-V REGION MOPC 173B.
FT DOMAIN      23     45 FRAMEWORK-1.
FT DOMAIN      46     56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN      57     71 FRAMEWORK-2.
FT DOMAIN      72     78 FRAMEWORK-3.
FT DOMAIN      79     110 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN      111    >117 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID    45     110 BY SIMILARITY.
FT NON_TER     117     117
SQ SEQUENCE    117 AA; 12954 MW; 24B3D4B9AC2E4D6C CRC64;

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 117;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 RCDIQMTQSPSSLSASLG 36
DB 21 RCDIQMTQSPSSLSASLG 38

RESULT 3
KV11_HUMAN
ID KV11_HUMAN STANDARD; PRT; 117 AA.

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AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
kappa genes and a pseudogene.";
RL Nature 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129397; PubMed=6402305;
RA Bentley D.L., Rabbitts T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
recently duplicated human V kappa sequences have diverged by gene
conversion.";
RL Cell 32:181-189(1983).
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-----
DR EMBL; K01322; AAA58930.1; -
DR EMBL; K01324; AAA58932.1; -
DR EMBL; V00558; CAA23824.1; -
DR PIR; A01881; K1HU11.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL      1      22
FT CHAIN       23    >117 IG KAPPA CHAIN V-I REGION HK101.
FT DOMAIN      23     45 FRAMEWORK-1.
FT DOMAIN      46     56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN      57     71 FRAMEWORK-2.
FT DOMAIN      72     78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN      79     110 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN      111    >117 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID    45     110 BY SIMILARITY.
FT NON_TER     117     117
SQ SEQUENCE    117 AA; 12799 MW; D7D0FF3718CEF587 CRC64;

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 117;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 RCDIQMTQSPSSLSAS 34
DB 21 RCDIQMTQSPSSLSAS 36

RESULT 4
KV1W_HUMAN
ID KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;

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RN RP SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
RX MEDLINE=79084137; PubMed=103625;
RA Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;
RT "Complete sequence of constant and 3' noncoding regions of an
FT immunoglobulin mRNA using the dideoxynucleotide method of RNA
RT sequencing.";
RL Cell 15:1067-1075(1978).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
FT and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [5]
RN SEQUENCE FROM N.A.
RX MEDLINE=81191915; PubMed=6262318;
RA Max E.E., Maizel J.V. Jr., Leder P.;
RT "The nucleotide sequence of a 5.5-kilobase DNA segment containing the
FT mouse kappa immunoglobulin J and C region genes.";
RL J. Biol. Chem. 256:5116-5120(1981).
RN [6]
RN SEQUENCE FROM N.A.
RX MEDLINE=81198949; PubMed=6785724;
RA Altenburger W., Neumater P.S., Steinmetz M., Zachau H.G.;
RT "DNA sequence of the constant gene region of the mouse immunoglobulin
FT kappa chain.";
RL Nucleic Acids Res. 9:971-981(1981).
RN [7]
RN SEQUENCE FROM N.A.
RX MEDLINE=88329081; PubMed=3138116;
RA de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.;
RT "Expression in non-lymphoid cells of mouse recombinant immunoglobulin
FT directed against the tumour marker human placental alkaline
FT phosphatase.";
RL Eur. J. Biochem. 176:287-295(1988).
RN CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL: V00807; CAA24189.1; --
DR PIR: B90262; KIMS.
DR PDB: 1AIF; 01-FEB-97.
DR PDB: 1FSK; 02-OCT-00.
DR PDB: 1IGC; 03-JUN-95.
DR PDB: 1KB5; 08-APR-98.
DR PDB: 1KCR; 11-MAY-02.
DR PDB: 1KCS; 11-MAY-02.
DR PDB: 1KCU; 11-MAY-02.
DR PDB: 1KCV; 11-MAY-02.
DR PDB: 25C8; 09-JUL-99.
DR MGD: MGI:96495; Iqk-C.
DR InterPro: IPR007110; Iq-like.
DR InterPro: IPR003597; Iq_ch.
DR InterPro: IPR003006; Iq_MHC.
DR Pfam: PF00047; Iq; 1.
DR SMART: SM00407; IGCL; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON_TER 1 1
FT DOMAIN 5 102 IG-LIKE.
FT DISULFID 26 86
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
SQ SEQUENCE 106 AA; 11778 MW; 4B51FF5EF49BAEB5 CRC64;

Query Match 9.7%; Score 14; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 129 ADAAPTYSIFPPSS 142
Db 1 ADAAPTYSIFPPSS 14
RESULT 7
KV1A_HUMAN
ID KV1A_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
FT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01861; KIHUAG.
DR HSP; P01607; IREI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Iq-like.
DR InterPro: IPR003006; Iq_MHC.
DR Pfam: PF00047; Iq; 1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;
Query Match 9.7%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 DIQMTQSPSSLSAS 34
Db 1 DIQMTQSPSSLSAS 14
RESULT 8
KV1B_HUMAN
ID KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


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FT  DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 57 88 FRAMEWORK-3.
FT  DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN 98 107 FRAMEWORK-4.
FT  DISULFID 23 88 BY SIMILARITY.
FT  NON_TER 108 108
SQ  SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 9.7%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 DIQMTQSPSSLSAS 34
Db 1 DIQMTQSPSSLSAS 14

RESULT 11
KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-1 region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=8093329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
and characterization of the tryptic peptides; the complete amino acid
sequence of the protein; a contribution to the elucidation of the
three-dimensional structure of antibodies, in particular their
combining site."
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RP MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
of the Bence-Jones protein REI refined at 2.0-A resolution."
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A91663; KIHURE.
DR PDB; IREI; 17-FEB-84.
DR PDB; IAR2; 12-NOV-97.
DR PDB; 1BWV; 29-DEC-99.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 98 107 FRAMEWORK-4.
FT STRAND 23 88
FT 24 7

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FT  STRAND 10 13
FT  TURN 15 16
FT  STRAND 19 25
FT  TURN 30 31
FT  STRAND 33 38
FT  TURN 40 41
FT  STRAND 44 49
FT  TURN 50 52
FT  STRAND 53 54
FT  TURN 56 57
FT  TURN 60 61
FT  STRAND 62 67
FT  TURN 68 69
FT  STRAND 70 75
FT  HELIX 80 82
FT  STRAND 85 90
FT  STRAND 97 98
FT  STRAND 102 106
FT  NON_TER 108 108
SQ  SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 9.7%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 DIQMTQSPSSLSAS 34
Db 1 DIQMTQSPSSLSAS 14

RESULT 12
KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-1 region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
Cum.)."
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A91638; KIHURY.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

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FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDESA313DF3A CRC64;

Query Match 9.7%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 DIQQTSPSSLSAS 34
Db 1 DIQQTSPSSLSAS 14

RESULT 13

KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P01609;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Sw.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059271; PubMed=4435756;
RA Eulitz M., Hilschmann N.;
RT "The primary structure of a human immunoglobulin L-chain of
kappa-type (Bence-Jones protein Scw.), II: The chymotryptic peptides
and the complete amino acid sequence.",
RL Hoppe-Seyler's Z. Physiol. Chem. 353:842-866(1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01875; KIHUS.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11764 MW; 32CECD9F644414 CRC64;

Query Match 9.7%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 DIQQTSPSSLSAS 34
Db 1 DIQQTSPSSLSAS 14

Query Match 9.7%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 DIQQTSPSSLSAS 34
Db 1 DIQQTSPSSLSAS 14

RESULT 14
KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.",
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A01876; KIHWE.
DR HSP; P80362; IWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 9.7%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 DIQQTSPSSLSAS 34
Db 1 DIQQTSPSSLSAS 14

RESULT 15

KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:

Query Match 9.7%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 DIQQTSPSSLSAS 34
Db 1 DIQQTSPSSLSAS 14

RT structural origin of altered domain interactions in immunoglobulin
RL light-chain dimers.;
RL Biochemistry 33:14848-14857(1994).
RN [2]

RP SEQUENCE OF 1-35.
RX MEDLINE-81267384; PubMed-6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
related fragment of the human KI Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PDB: 1WTL; 01-NOV-94.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT CONFLICT 30 31 TN -> SD (IN REF. 2).
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 9.7%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 21 DIQMTQSPSSLSAS 34
| | | | | | | | | |
Db 1 DIQMTQSPSSLSAS 14

Search completed: August 30, 2003, 22:10:22
Job time : 9.75839 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2003, 22:06:06 ; Search time 22.3825 Seconds
(without alignments)
1671.732 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 145

Sequence: 1 MGAPQILGFLLLFPQTRC.....IKRDAAPTVISFPSSKLG 145

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- SPTREMBL_23:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	86.2	127	11	Q925S9 mus musculus
2	28	19.3	239	11	O8VC55 mus musculus
3	28	19.3	239	11	O8K0F8 mus musculus
4	26	17.9	233	11	O91WS9 mus musculus
5	26	17.9	238	11	O8VC16 mus musculus
6	22	15.2	214	11	O9RIA5 mus musculus
7	22	15.2	234	11	O8R062 mus musculus
8	22	15.2	234	11	O8VCP0 mus musculus
9	22	15.2	238	11	O99M37 mus musculus
10	19	13.1	112	11	O8K1F3 mus musculus
11	17	11.7	112	11	O8K1F0 mus musculus
12	17	11.7	114	11	O8K1F1 mus musculus
13	17	11.7	134	11	O8VDD0 mus musculus
14	16	11.0	234	11	O8R028 mus musculus
15	16	11.0	234	11	O91WF8 mus musculus
16	16	11.0	235	11	O91W12 mus musculus

17	15	10.3	298	11	Q9QYF0	Q9QYF0 mus musculus
18	14	9.7	107	4	Q9UL81	Q9UL81 homo sapien
19	14	9.7	107	4	Q96SA9	Q96SA9 homo sapien
20	14	9.7	108	4	Q9UL70	Q9UL70 homo sapien
21	14	9.7	108	4	Q9UL77	Q9UL77 homo sapien
22	14	9.7	108	11	Q8VIJ0	Q8VIJ0 mus musculus
23	14	9.7	116	4	Q96PF6	Q96PF6 homo sapien
24	13	9.0	104	11	Q9JL82	Q9JL82 mus musculus
25	13	9.0	109	11	Q920E6	Q920E6 mus musculus
26	13	9.0	111	11	Q920E9	Q920E9 mus musculus
27	12	8.3	97	11	Q9JL76	Q9JL76 mus musculus
28	12	8.3	101	11	Q9JL78	Q9JL78 mus musculus
29	12	8.3	241	11	Q921A6	Q921A6 mus musculus
30	11	7.6	99	11	Q9JL74	Q9JL74 mus musculus
31	11	7.6	103	11	Q9JL80	Q9JL80 mus musculus
32	11	7.6	107	11	Q9JL84	Q9JL84 mus musculus
33	10	6.9	170	11	Q925S2	Q925S2 mus musculus
34	9	6.2	527	16	Q8DBN7	Q8DBN7 vibrio vuln
35	8	5.5	15	11	Q9QV17	Q9QV17 rattus sp.
36	8	5.5	107	11	Q9ER29	Q9ER29 mus musculus
37	8	5.5	162	6	Q9NLG8	Q9NLG8 salmieri bol
38	8	5.5	220	16	O8DS60	O8DS60 streptococc
39	8	5.5	236	16	Q9XA92	Q9XA92 streptomyce
40	8	5.5	239	4	Q8TCD0	Q8TCD0 homo sapien
41	8	5.5	246	8	Q9XPG4	Q9XPG4 leiocassis
42	8	5.5	246	8	Q9XPG5	Q9XPG5 leiocassis
43	8	5.5	261	16	Q8COT1	Q8COT1 staphylococ
44	8	5.5	316	12	Q9QMH4	Q9QMH4 parvo-like
45	8	5.5	345	11	Q8CLH2	Q8CLH2 mus musculus

ALIGNMENTS

RESULT 1

Q925S9	PRELIMINARY;	PRT;	127 AA.
ID	Q925S9		
AC	Q925S9;		
DT	01-DEC-2001 (TReMBLrel. 19, Created)		
DT	01-DEC-2001 (TReMBLrel. 19, Last sequence update)		
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)		
DE	Immunoglobulin light chain (Fragment).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BALB/c;		
RX	MEDLINE=99306687; PubMed=10380019;		
RA	Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,		
RA	Foon K.A., Chatterjee S.K.;		
RT	"Construction and characterization of a chimeric fusion protein		
RT	consisting of an anti-idiotypic antibody mimicking a breast cancer-		
RL	Hybridoma 18:193-202(1999)."		
DR	EMBL; AF124721; AAK55120.1;		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
FT	NON_TER 127		
SQ	SEQUENCE 127 AA; 13794 MW; 13F61BEBB981FA5 CRC64;		

Query Match 86.2%; Score 125; DB 11; Length 127;
Best Local Similarity 100.0%; Pred. No. 6.4e-122;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 APAQILGFLLLFPQTRCDTQMTQSPSSLSASLCQRVSLTCRASQDIGINLHWLQQEPPDG 62
Db 3 APAQILGFLLLFPQTRCDTQMTQSPSSLSASLCQRVSLTCRASQDIGINLHWLQQEPPDG 62

DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 17.9%; Score 26; DB 11; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.3e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TFGGKLEIKRADAAPTIVSIFPPSS 142
|||||
DB 121 TFGGKLEIKRADAAPTIVSIFPPSS 146

RESULT 6

Q9RIA5 ID Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; RAD40242.1; -
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 15.2%; Score 22; DB 11; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GTKLEIKRADAAPTIVSIFPPSS 142
|||||
DB 101 GTKLEIKRADAAPTIVSIFPPSS 122

RESULT 7

Q8R062 ID Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 15.2%; Score 22; DB 11; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GTKLEIKRADAAPTIVSIFPPSS 142
|||||
DB 121 GTKLEIKRADAAPTIVSIFPPSS 142

RESULT 8

Q8VCP0 ID Q8VCP0 PRELIMINARY; PRT; 234 AA.
AC Q8VCP0
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019474; AAH19474.1; -
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 15.2%; Score 22; DB 11; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GTKLEIKRADAAPTIVSIFPPSS 142
|||||
DB 121 GTKLEIKRADAAPTIVSIFPPSS 142

RESULT 9

Q99M37 ID Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.

DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 238 AA; FB2B06A0B801330A CRC64;

Query Match 15.2%; Score 22; DB 11; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GTKLEIKRAADAPTIVSIFPPSS 142
 |||||
 DB 125 GTKLEIKRAADAPTIVSIFPPSS 146

RESULT 10

Q8K1F3 PRELIMINARY; PRT; 112 AA.
 AC Q8K1F3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
 RT "Innate proteolytic antibodies: Failed D-Vipase response to the D-
 RT entantioner of VIP and identification of L-Vipase VL domains.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF16282; AAM64200.1;
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00409; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 112
 SQ SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

Query Match 13.1%; Score 19; DB 11; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 PYTFGGGKLEIKRAADAP 133
 |||||
 DB 94 PYTFGGGKLEIKRAADAP 112

RESULT 11

Q8K1F0 PRELIMINARY; PRT; 112 AA.
 AC Q8K1F0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;

RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
 RT "Innate proteolytic antibodies: Failed D-Vipase response to the D-
 RT entantioner of VIP and identification of L-Vipase VL domains.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF16285; AAM64203.1;
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00409; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 112
 SQ SEQUENCE 112 AA; 11901 MW; F6644663201AA239 CRC64;

Query Match 11.7%; Score 17; DB 11; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TFGGGTKLEIKRAADAP 133
 |||||
 DB 96 TFGGGTKLEIKRAADAP 112

RESULT 12

Q8K1F1 PRELIMINARY; PRT; 114 AA.
 AC Q8K1F1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
 RT "Innate proteolytic antibodies: Failed D-Vipase response to the D-
 RT entantioner of VIP and identification of L-Vipase VL domains.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF16284; AAM64202.1;
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00409; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 114
 SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3EEFD1 CRC64;

Query Match 11.7%; Score 17; DB 11; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TFGGGTKLEIKRAADAP 133
 |||||
 DB 98 TFGGGTKLEIKRAADAP 114

RESULT 13

Q8VDD0 PRELIMINARY; PRT; 134 AA.
 AC Q8VDD0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)


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DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Anti-MOG z12 variable light chain (Fragment).
GN ANTI-MOG KAPPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c;
RA Sembi P.;
RL "targeting T cells to the CNS.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416331; CAC94866.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14525 MW; CDF8E2236E2D0CF CRC64;

Query Match 11.78; Score 17; DB 11; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 117 TFGGGTKLEIKRADAAP 133
    |||||
Db 118 TFGGGTKLEIKRADAAP 134

RESULT 14
Q8R028
ID Q8R028 PRELIMINARY; PRT; 234 AA.
AC Q8R028;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028540; AAH28540.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 148377F9C1CD0AEE CRC64;

Query Match 11.0%; Score 16; DB 11; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 KRADAAPTVSIFPPSS 142
    |||||
Db 127 KRADAAPTVSIFPPSS 142

RESULT 15
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Q91WF8
ID Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 11.0%; Score 16; DB 11; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 KRADAAPTVSIFPPSS 142
    |||||
Db 127 KRADAAPTVSIFPPSS 142

Search completed: August 30, 2003, 22:11:18
Job time : 23.3825 secs
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GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 30, 2003, 22:10:26 ; Search time 2967.15 Seconds
(without alignments)
1999.191 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 740

Sequence: 1 MGAQAIGLILLFPGRRC.....IKRADAAPTIVSIFPPSKLG 145

Scoring table:

BLASUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-O=/cpn2.1/USPTO.spool/US08836455/runat_29082003.132901.22281/app_query.fasta_1.654
-DB=GenEmbl -QFMT=fastap -SURFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08836455.ecgn.1.1.3608 -runat_29082003.132901.22281 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*

29: em.vi.*
30: em.htg_hum.*
31: em.htg_inv.*
32: em.htg_other.*
33: em.htg_mus.*
34: em.htg_pin.*
35: em.htg_rod.*
36: em.htg_mam.*
37: em.htg_vrt.*
38: em.sy.*
39: em.higo_hum.*
40: em.htgo_mus.*
41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	740	100.0	435	6	AR164505	AR164505	Sequence
2	740	100.0	435	6	BD085737	BD085737	Methods o
3	642	86.8	381	10	AF124721	AF124721	Mus muscu
4	633	85.5	407	6	E54981	E54981	Peptide. 1/
5	601	81.2	390	10	MUSIKCC	L41880	Mus musculu
6	599	80.9	381	10	AF045508	AF045508	Mus muscu
7	599	80.9	384	10	AB017434	AB017434	Mus muscu
8	592	80.0	381	10	AF045495	AF045495	Mus muscu
9	581	78.5	381	10	AF045510	AF045510	Mus muscu
10	551	74.5	405	10	AB016620	AB016620	Mus muscu
11	547	73.9	684	10	MUSIGKAC1	J00565	Mus musculu
12	542	73.2	685	10	MMIGK7	V00808	Part of the
13	541	73.1	380	10	MMIGGVJ1	X02177	M.musculus
14	539	72.8	381	10	MMIGGVJ2	X02178	M.musculus
15	533	72.0	354	10	AB089681	AB089681	Mus muscu
16	527	71.2	387	6	AR169918	AR169918	Sequence
17	514	69.5	324	6	AX722008	AX722008	Sequence
18	513	69.3	1019	10	BC027418	BC027418	Mus muscu
19	512	69.2	642	10	AF178454	AF178454	Mus muscu
20	511	69.1	321	10	AF163749	AF163749	Mus muscu
21	511	69.1	383	10	MUSIGKCM	M12191	Mouse Ig ac
22	511	69.1	972	10	AF466770	AF466770	Mus muscu
23	507	68.5	739	6	AR007981	AR007981	Sequence
24	507	68.5	739	6	AR058996	AR058996	Sequence
25	507	68.5	739	6	I23446	I23446	Sequence 5
26	506	68.4	324	6	E54967	E54967	Peptide. 1/
27	506	68.4	324	6	I03643	I03643	Sequence 4
28	506	68.4	324	6	I07835	I07835	Sequence 4
29	506	68.4	348	10	MMVJIG	X54755	Mouse reari
30	506	68.4	959	10	BC015292	BC015292	Mus muscu
31	505	68.2	321	10	MUSIGRAA3	M59920	Mouse IG ge
32	505	68.2	756	6	AX256284	AX256284	Sequence
33	505	68.2	1497	6	AX256302	AX256302	Sequence
34	503	68.0	432	6	AI7965	AI7965	Variable re
35	503	68.0	438	6	BD015544	BD015544	Human mon
36	503	68.0	438	6	BD094922	BD094922	Human mon
37	502	67.8	432	6	AI7963	AI7963	Variable re
38	502	67.8	711	6	E54975	E54975	Peptide. 1/
39	502	67.8	729	6	E54976	E54976	Peptide. 1/
40	502	67.8	771	6	AX256296	AX256296	Sequence
41	501	67.7	324	10	MUSX	L48667	Mus musculu
42	501	67.7	998	9	S65921	S65921	anti-colore
43	499	67.4	203877	10	AC122260	AC122260	Mus muscu
44	497	67.2	570	10	AF003293	AF003293	Mus muscu
45	496	67.0	330	10	MMIGGIVL	X82890	M.musculus

ALIGNMENTS

RESULT 1

AR164505 LOCUS AR164505 435 bp DNA linear PAT 17-OCT-2001
 DEFINITION Sequence 1 from patent US 6274143.
 ACCESSION AR164505
 VERSION AR164505.1 GI:16237555
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 435)
 AUTHORS Chatterjee, M. and Foon, K.A.
 TITLE Methods of delaying development of HMFg-associated tumors using anti-idiotypic antibody 11D10
 JOURNAL Patent: US 6274143-A 1 14-AUG-2001;
 FEATURES
 source 1..435
 BASE COUNT 100 a 111 c 102 g 122 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 7,64e-66 Length: 435
 Score: 740.00 Matches: 145
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-08-836-455-2 (1-145) x AR164505 (1-435)
 QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 DB 1 ATGGGGGCCCTCTCAGATTCTGGGTTCTTGTGCTTGTTCAGGTACCATGATGT 60
 QY 21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGATCAGT 120
 QY 41 LeuThrCysArgAlaSerGlnAspIleGlyLeuAsnLeuHisTrpLeuGlnGluPro 60
 DB 121 CTCACCTGTGCGGCAAGTCAGGACATGGTATTAACTTACATTTGCTTCCAGCAGGAACCA 180
 QY 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 DB 181 GATGGAACTATTAAACGCCCTGATCTAGCCACATCCAGTTAGGTTCTGCTGCTCCCAAA 240
 QY 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 DB 241 AGGTTGAGTGGCAGTAGGTTGGTCCAGATTATCTCTCACCATCAGCACCTTGAGTCT 300
 QY 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 DB 301 GAAGATTTTGTAGCCTATTACTCTCTACAAATATGCTAGTTCCTCCGACACGTTCCGAGGG 360
 QY 121 GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
 DB 361 GGGACCAAGCTGGAATAAAACGGCTGATGCTGCACCAACTGATCCATCTTCCCAACCA 420
 QY 141 SerSerLysLeuGly 145
 DB 421 TCCAGTAAGCTTGGG 435
 RESULT 2
 BD085737 LOCUS BD085737 435 bp DNA linear PAT 27-AUG-2002
 DEFINITION Methods of delaying development of HMFg-associated tumors using anti-idiotypic antibody 11D10.
 ACCESSION BD085737
 VERSION BD085737.1 GI:22631347
 KEYWORDS JP 2001523269-A/1.
 SOURCE unidentified
 ORGANISM unclassified.

1 (bases 1 to 435)
 Chatterjee, M. and Foon, K.A.
 TITLE Methods of delaying development of HMFg-associated tumors using anti-idiotypic antibody 11D10
 JOURNAL Patent: JP 2001523269-A 1 20-NOV-2001;
 COMMENT THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
 OS Unidentified
 PN JP 2001523269-A/1
 PD 20-NOV-2001
 PF 12-JUN-1998 JP 199503252
 PR 13-JUN-1997 US 60/049540, 11-JUN-1998 US 09/096244 PI
 PC MALAYA CHATTERJEE; KENNETH A FOON
 PC A61K39/395; A61K39/39//C07K16/42
 CC Strandedness: Single;
 CC Topology: Linear;
 CC Methods of delaying development of HMFg-associated tumors CC
 using
 CC anti-idiotypic antibody 11D10
 FH Key Location/Qualifiers
 FT CDS 1..435
 FT mat peptide 61.
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 BASE COUNT 100 a 111 c 102 g 122 t
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 Pred. No.: 7,64e-66 Length: 435
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 Percent Similarity: 100.00% Conservatives: 0
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 RESULT 3
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DEFINITION   Mus musculus immunoglobulin light chain mRNA, partial cds.
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VERSION      AF124721.1  GI:14164546
KEYWORDS     Mus musculus (house mouse)
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    1 (bases 1 to 381)
AUTHORS      Chatteerjee,S.K. and Tripathi,P.K.
TITLE        Direct Submission
JOURNAL      Submitted (29-JAN-1999) Internal Medicine, University of Kentucky,
MEDLINE      800 Rose Street, Lexington, KY 40536, USA
PUBMED       10380019
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LOCUS      E54981
DEFINITION Peptide.
ACCESSION  E54981
VERSION    E54981.1  GI:18629719
KEYWORDS   JP 2000236884-A/15.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 407)
AUTHORS    Nishida,T., Okura,T., Tanimoto,T. and Kurimoto,M.
TITLE      Peptide
JOURNAL    Patent: JP 2000236884-A 15 05-SEP-2000;
            HAYASHIBARA BIOCHEM LAB INC
COMMENT    OS Mus musculus (mouse)
            PN JP 2000236884-A/15
            PD 05-SEP-2000
            PF 24-JUN-1999  JP 1999177846
            PR
            PI TAKEHIRO NISHIDA,TAKANORI OKURA,TADAO TANIMOTO, PI MASASHI
            KURIMOTO
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BASE COUNT 96 a   99 c   96 g   116 t
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Alignment Scores:
Pred. No.: 1.15e-51 Length: 381
Score: 599.00 Matches: 118
Percent Similarity: 96.06% Conservative: 4
Best Local Similarity: 92.91% Mismatches: 5
Query Match: 80.95% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-2 (1-145) x AF045508 (1-381)

QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
DB 1 ATAGGGCCCTCCACAGATTTTGGCTTCTTGGCTTCTTGGCTTCCAGGTACAGATGT 60
QY 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCCCTCTGGGAGAAAGAGTCAGT 120
QY 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGluPro 60
DB 121 CTCACCTGTGGGCAAGTCAGGACATTTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 180
QY 61 AspGlyThrIleLysArgLeuIleTyAlaThrSerSerLeuThrIleSerSerLeuGluSer 80
DB 181 GATGGAACTATTAAAGCCCTGATCTAGCCACATCCAGTTATCTCACCATCAGCAGCCTTGAGTCT 240
QY 81 ArgPheSerGlySerArgSerGlySerAspTyAlaThrSerSerLeuThrIleSerSerLeuGluSer 100
DB 241 AGCTTCAGTGGCAGTAGTCTGGTGCAGATTTATCTCACCATCAGCAGCCTTGAGTCT 300
QY 101 GluAspPheValAlaTyTyCysLeuGlnTyAlaSerSerProTyThrPheGlyGly 120
DB 301 GAAGATTTGTAGACTATTACTCTACATATGCTAGTCTCCGTTGAGTCTCCGTTGGA 360
QY 121 GlyThrLysLeuGluIleLys 127
DB 361 GGCACCAAGCTGGCAATCAAA 381

RESULT 7
AB017434 384 bp mRNA linear ROD 08-JAN-2000
LOCUS Mus musculus mRNA for anti-IL-18 IgG Light chain, clone 125-2H,
DEFINITION partial cds.
ACCESSION AB017434.1 GI:6683473
VERSION Mus musculus (house mouse)
KEYWORDS IgG Light chain.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Nishida,Y.
JOURNAL Variable region of anti Human IL-18 IgG Light(kappa) chain
REFERENCE Published Only in Database (2000)
AUTHORS Nishida,Y.
TITLE Direct Submission
JOURNAL Submitted (02-Sep-1998) Yoshihiro Nishida, Hayashibara Biochemical
Laboratories, Inc., Fujisaki Institute; 675-1, Fujisaki, Okayama,
Okayama 702-8006, Japan [E-mail:fujihgo.harenet.or.jp,
Tel:+81-86-276-3141, Fax:+81-86-276-6885]
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="125-2H"
/cell_type="Hybridoma"
1..>384
/codon_start=1
/product="variable region precursor of anti-IL-18 IgG

Light chain"
/protein_id="BAA89228.1"
/db_xref="GI:6683474"
/translation="MRAPQIFGFLLLPPTGTRCDIQMTQSPSSLSASLGERVSLTCR
ASDIDGSKLYWLOQEDPGCFKRLIYATSSLDGVPKRFSGSRGSGSYSLTISSESD
FVDIYCLQYASSPYTFGGGTKLAIR"
sig_peptide 1..60
mat_peptide 61..>384
BASE COUNT 91 a 92 c 91 g 110 t
ORIGIN
Alignment Scores:
Pred. No.: 1.15e-51 Length: 384
Score: 599.00 Matches: 118
Percent Similarity: 93.75% Conservative: 2
Best Local Similarity: 92.19% Mismatches: 8
Query Match: 80.95% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-2 (1-145) x AB017434 (1-384)
QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
DB 1 ATAGGGCCCTCCACAGATTTTGGCTTCTTGGCTTCTTGGCTTCCAGGTACAGATGT 60
QY 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCCCTCTGGGAGAAAGAGTCAGT 120
QY 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGluPro 60
DB 121 CTCACCTGTGGGCAAGTCAGGACATTTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 180
QY 61 AspGlyThrIleLysArgLeuIleTyAlaThrSerSerLeuThrIleSerSerLeuGluSer 80
DB 181 GATGGAACTATTAAAGCCCTGATCTAGCCACATCCAGTTATCTCACCATCAGCAGCCTTGAGTCT 240
QY 81 ArgPheSerGlySerArgSerGlySerAspTyAlaThrSerSerLeuThrIleSerSerLeuGluSer 100
DB 241 AGCTTCAGTGGCAGTAGTCTGGTGCAGATTTATCTCACCATCAGCAGCCTTGAGTCT 300
QY 101 GluAspPheValAlaTyTyCysLeuGlnTyAlaSerSerProTyThrPheGlyGly 120
DB 301 GAAGATTTGTAGACTATTACTCTACATATGCTAGTCTCCGTTGAGTCTCCGTTGGA 360
QY 121 GlyThrLysLeuGluIleLys 128
DB 361 GGCACCAAGCTGGCAATCAAA 384

RESULT 8
AF045495 381 bp mRNA linear ROD 28-FEB-1998
LOCUS Mus musculus dC4 anti-poly(dC) monoclonal antibody kappa light
DEFINITION chain variable region, (IgK) mRNA, partial cds.
ACCESSION AF045495
VERSION AF045495.1 GI:2906073
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
JOURNAL Anti-DNA antibodies of normal mice immunized with poly(dC) are
REFERENCE structurally similar to natural autoantibodies
AUTHORS Unpublished
TITLE 2 (bases 1 to 381)
JOURNAL O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
REFERENCE Direct Submission
AUTHORS O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
TITLE Submitted (02-FEB-1998) Biochemistry, Tufts University School of
JOURNAL Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
FEATURES Location/Qualifiers

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Db      241 AGGTTCAAGTGGCAGTAGGCTGGGTCTAGATTATTTCTCACCATCAGCAGCCTTGAGTCT 300
QY      101 GluAspPheValAlaIaIaTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
        |||||
Db      301 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTTCCATTACGCTGGGCTCG 360
QY      121 GlyThrLysLeuGluIleLys 127
        |||||
Db      361 GGCACAAAGTTGGAATAAAA 381

RESULT 10
LOCUS   AB016620                405 bp mRNA linear ROD 27-MAR-2002
DEFINITION Mus musculus mRNA for Immunoglobulin light chain variable region, partial cds.
ACCESSION AB016620
VERSION   AB016620.1 GI:3395670
KEYWORDS Immunoglobulin light chain variable region.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS  Arakawa,F., Yamamoto,T., Kanda,H., Watanabe,T. and Kuroki,M.
TITLE    cDNA sequence analysis of monoclonal antibody FU-MK-1 specific for a transmembrane carcinoma-associated antigen, and construction of a mouse/human chimeric antibody
JOURNAL  Hybridoma 18 (2), 131-138 (1999)
MEDLINE  9305680
PUBMED   10380012
REFERENCE 2 (bases 1 to 405)
AUTHORS  Arakawa,F.
TITLE    Direct Submission
JOURNAL  Submitted (30-JUL-1998) Fumiko Arakawa, School of Medicine, Fukuoka University, First Department of Biochemistry; 7-45-1 Nanakuma, Jonan-ku, Fukuoka, Fukuoka 814-80, Japan (E-mail:farakawa@emsat.fukuoka-u.ac.jp, Tel:092-801-1011(ex.3246), Fax:092-801-3600)
FEATURES             Location/Qualifiers
     source           1..405
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /cell_line="FU-MK-1 hybridoma"
     exon             1..392
     primer_bind      1..43
                     /note="PCR primer region"
     CDS              11..>392
                     /codon_start=1
                     /product="Immunoglobulin light chain variable region"
                     /protein_id="BA332080.1"
                     /db_xref="GI:3395671"
                     /translaltion="MRAPAQLGLFLIMFPGIRCDIKMTQSPSSLSASLGERVSLTCR ASQEISGLSWLQKQPDGTVKRLIYAATSLHSGVPRFRSGRSGSDYSLTISLESDD FADYICLOYASDPWTFGGTQKLEIK"
     sig_peptide      11..70
     intron            393..405
     primer_bind      393..405
                     /note="PCR primer region"
     BASE COUNT      98 a 100 c 97 g 110 t
     ORIGIN
Alignment Scores:
Pred. No.:          8.65e-47          Length:          405
Score:              551.00           Matches:         108
Percent Similarity: 90.08%           Conservative:    10
Best Local Similarity: 82.44%         Mismatches:      13
Query Match:        74.46%           Indels:          0
DB:                  10              Gaps:            0

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US-08-836-455-2 (1-145) x AB016620 (1-405)
QY      1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCys 20
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Db      11 ATAGGGCCCTGCTCAGATTCTGGCTTCTTGCTCTGGTTTCCAGGTATAGATGT 70
QY      21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
        |||
Db      71 GACATCAAGATGACCCAGTCGCCATCTCTCTTATCTGCTCTCTGGGAGAAAGAGTCACT 130
QY      41 LeuThrCysArgAlaSerGlnAspIleGlyIleasnLeuHisTrpLeuGlnGlnGluPro 60
        |||
Db      131 CTCACCTGTCTGGCAAGTCAGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAAAACCA 190
QY      61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
        |||
Db      191 GATGGAACCTGTTAAACGCCCTGATCTAGCCGCATCCACTTACATCTGGTGTCCCAAAA 250
QY      81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
        |||
Db      251 AGGTTCAAGTGGCAGTAGGCTGGTCTGAGTCTATCTCTCACCATCAGCAGCCTTGAGTCT 310
QY      101 GluAspPheValAlaIaTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
        |||
Db      311 GAGCATTTTGCAGACTATTACTGTCTACAGTATGCTAGTGTATCGTGGACGTTCCGGTGA 370
QY      121 GlyThrLysLeuGluIleLysArgAlaAspAla 131
        |||
Db      371 GGCACCAAGCTGGNAATCAACGTAAGAATTCG 403

RESULT 11
LOCUS   MUSIGKAC1                684 bp DNA linear ROD 19-JUN-2002
DEFINITION Mus musculus immunoglobulin kappa chain variable region (Igh) gene, exons 1 and 2.
ACCESSION J00565
VERSION   J00565.1 GI:196531
KEYWORDS 1 of 3
SEGMENT  Mus musculus (house mouse)
SOURCE   Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 684)
AUTHORS  Seidman,J.G., Max,E.E. and Leder,P.
TITLE    A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation
JOURNAL  Nature 280 (5721), 370-375 (1979)
MEDLINE  79221900
PUBMED   111146
REFERENCE 2 (bases 1 to 684)
AUTHORS  Gough,N.M., Cory,S. and Adams,J.M.
TITLE    Identical 3' non-coding sequences in five mouse Ig kappa chain mRNAs favour a unique C kappa gene
JOURNAL  Nature 281 (5730), 394-396 (1979)
MEDLINE  80011674
PUBMED   113684
REFERENCE 3 (sites)
AUTHORS  Queen,C. and Baltimore,D.
TITLE    Immunoglobulin gene transcription is activated by downstream sequence elements
JOURNAL  Cell 33 (3), 741-748 (1983)
MEDLINE  83259260
PUBMED   6409419
COMMENT  [2] sites; comment.
         this sequence is a productively rearranged kappa ig from myeloma m0p41. the conflicts noted in the sites table refer to the published differences between the germline and active genes. they are probably typographical errors since [1] says that no somatic mutation has occurred after recombination. j.g. seidman (personal communication) said that the published germline sequence is correct <musigkvc>. [2] finds that deletion of 1.3kb 5' to the constant region exon results in a lowered rate of transcription and an

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 30, 2003, 22:10:01 ; Search time 217.987 Seconds
(without alignments)
1795.608 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 740

Sequence: 1 MGAPQAIGLFLLLFPFTRC.....IKRADAAPVTSIFPPSSKLG 145

Scoring table:

BLOSUM62
Xgapop 10.0 ; Xgapext 0.5
Ygapop 10.0 ; Ygapext 0.5
Fgapop 6.0 ; Fgapext 7.0
Delop 6.0 ; Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DRV=xlh
-Q/crn2_1/USPTO.spool/US08836455/runat_29082003_132901_22271/app_query.fasta_1.654
-DB=N.Geneseq_19Jun03 -Qfmt=fastp -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08836455 @CGN_1_1_401 @runat_29082003_132901_22271 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG
-DRV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	740	100.0	435	18	AAT85149	Murine monoclonal
2	740	100.0	435	20	AAV83772	Antibody 11D10 11g
3	740	100.0	435	25	AA51273	Mouse 11D10 antibo
4	662	89.5	450	4	AA30165	Sequence encoding
5	633	85.5	407	21	AA249548	Mouse light chain
6	527	71.2	387	18	AAT77851	Murine anti-human
7	527	71.2	387	24	AA32138	Murine 44H104 mab
8	507	68.5	739	14	AA046084	Sequence encoding
9	507	68.5	739	17	AAT36880	520C9 anti-c-erbB-
10	507	68.5	739	19	AAV21798	520C9 anti-c-erbB-
11	507	68.5	739	20	AAV63399	520C9 sfv DNA sequ
12	505	68.4	324	21	AA249534	Mouse anti-IL-18 a
13	505	68.2	756	24	AA597136	P4-3 single chain
14	505	68.2	1497	24	AA597145	3B10xP4-3 bispecif
15	503	68.0	432	12	AAQ15114	IL-2 chimeric anti
16	503	68.0	438	22	AAH41157	Human coding sequ
17	502	67.8	711	21	AA249542	pESCFv#125-2H reco
18	502	67.8	729	21	AA249543	pESCFv#125-2H.Ht r
19	502	67.8	771	24	AA597142	P5-10 single chain
20	497	67.2	432	12	AAQ15113	IL-2 chimeric anti
21	495	66.9	1605	14	AA046086	Sequence encoding
22	492	66.5	321	21	AAA38908	520C9 hybridoma VL
23	492	66.5	439	18	AAT73443	Human immunoglobul
24	492	66.5	439	20	AA221995	Partial nucleotide
25	486	65.7	3819	18	AAT78825	Kappa light chain
26	486	65.7	3819	19	AAV39266	Plasmid pLC665 nuc
27	486	65.7	3819	20	AA228220	Nucleotide sequenc
28	484	65.5	737	24	AA231829	Human pancreatic t
29	483	65.3	449	15	AAQ78732	Murine anti-human
30	482	65.1	817	21	AAA27389	Human IGFAM-9 immu
31	481	65.0	714	21	AAA46899	DNA encoding the k
32	481	65.0	19035	19	AAV61794	Traget plasmid Man
33	479	64.7	456	22	AAQ66996	Filamentous phage
34	479	64.7	867	22	AAQ67002	Filamentous phage
35	479	64.7	1066	14	AAQ49943	Human anti-HBs lig
36	473	63.9	974	24	AA599473	Anti-human AILIM m
37	471	63.6	447	17	AAT34541	Monoclonal anti-id
38	471	63.6	447	17	AAT31540	3H1 light chain va
39	471	63.6	447	18	AAT99434	Anti-idiotypic anti
40	471	63.6	447	21	AA235842	Murine MAB against
41	471	63.6	447	22	AAQ09316	Mouse anti-idiotyp
42	471	63.6	447	24	ABL60799	Antibody 3H1 light
43	471	63.6	447	24	AAK98279	Mouse 3H1 antibody
44	468	63.2	321	16	AAQ97504	Light chain variab
45	468	63.2	321	16	AAQ97507	Light chain variab

ALIGNMENTS

RESULT 1

AAT85149
ID AAT85149 standard; cDNA; 435 BP.

AC AAT85149;

DT 25-MAR-2003 (updated)

DT 04-JAN-1998 (first entry)

DE Murine monoclonal anti-idiotypic antibody 11D10 VL cDNA.

KW Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;

KW human milk fat globule; HMFg; tumour; breast cancer; vaccine; ss.

XX Mus musculus.

XX Key Location/Qualifiers

FH

```

FT sig_peptide 1..60
FT /*tag= a
FT mat_peptide 61..435
FT /*tag= b
XX
XX WO922699-A2.
XX
XX 26-JUN-1997.
XX
XX 19-DEC-1996; 96WO-US20757.
XX
XX 20-DEC-1995; 95US-0575762.
XX
XX 26-JAN-1996; 96US-0591985.
XX
XX 13-DEC-1996; 96US-0766350.
XX
XX (KENT ) UNIV KENTUCKY.
XX
XX Chatterjee M, Chatterjee SK, Foon KA;
XX
XX WPI; 1997-341690/31.
XX
XX P-PSDB; AAW27119.
XX
XX Monoclonal anti-idiotype antibody 11D10 - elicits immune response
XX against human milk fat globule disease associated tumours,
XX especially breast cancer
XX
XX Claim 11; Page 94; 130pp; English.
XX
XX This cDNA sequence encodes the light chain variable region VL
XX (AAW85149) of monoclonal anti-idiotype antibody 11D10 produced by
XX hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
XX naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype
XX response. It elicits an immune response against a specific epitope
XX of a high mol.wt. mucin of human milk fat globule (HMFG). It
XX induces an immunological response to HMFG in mice, rabbits, monkeys
XX and patients with advanced HMFG-associated tumours. Pharmaceutical
XX compositions and vaccines comprising 11D10, 11D10 polypeptides
XX and/or 11D10 polynucleotides are claimed. Also claimed are
XX diagnostic kits and methods of using 11D10, 11D10 polypeptides
XX and/or 11D10 polynucleotides, including methods of treating HMFG-
XX associated tumours.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1.81e-61 Length: 435
XX Score: 740.00 Matches: 145
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 18 Gaps: 0
XX
XX US-08-836-455-2 (1-145) x AAT85149 (1-435)
XX
XX QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
XX
XX Db 1 ATGGGGGCCCTGCTCAGATTCTTGGGTCTTGTCTTGTTCAGGTACCATGATGT 60
XX
XX QY 21 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerLeuGlyGlnArgValSer 40
XX
XX Db 61 GACATCCAGATGACCCAGTCCATCTCTTATCTGCTCTCTGGACAAAGAGTCAGT 120
XX
XX QY 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnPro 60
XX
XX Db 121 CTCACCTGTTCGGCAGATCAGGACATGGTATTAACTTACATTGGCTTCAGCAGGAACCA 180
XX
XX QY 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
XX
XX Db 181 GATGGAACTATTAAACGCCCTGATCTAGCCACATCCAGTTTAGGTCTTGTGTCCCAAAA 240
XX
XX QY 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
XX
XX

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Db 241 AGTTTCAGTGGCAGTAGGCTCTGGGTACAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 300
QY 101 GluAspPheValAlaIaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
Db 301 GAAGATTTTCTAGCCTATTACTGCTACATATGCTAGTCTCCGTACACGTTCCGGAGG 360
QY 121 GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
Db 361 GGGACCAAGCTGGAATAAAACGGGTGATGCTGCACCAACTGATCATCTTCCCAACCA 420
QY 141 SerSerLysLeuGly 145
Db 421 TCCAGTAAGCTTGGG 435
XX
XX RESULT 2
XX ID AAV83772 standard; cDNA; 435 BP.
XX
XX AC AAV83772;
XX
XX 16-MAR-1999 (first entry)
XX
XX Antibody 11D10 light chain variable region coding sequence.
XX
XX Murine; mouse; antibody; light chain; variable region; anti-idiotype; ss;
XX human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..435
XX FT /*tag= a
XX FT /product= "antibody 11D10 light chain variable region"
XX FT /transl_except= (pos:163..165, aa:Thr)
XX FT /note= "no stop codon is given at the 3' end of the
XX FT sig_peptide 1..60
XX FT mat_peptide 61..435
XX FT /*tag= c
XX
XX WO9856419-A1.
XX
XX 17-DEC-1998.
XX
XX 12-JUN-1998; 98WO-US12250.
XX
XX 11-JUN-1998; 98US-0096244.
XX 13-JUN-1997; 97US-0049540.
XX
XX (KENT ) UNIV KENTUCKY RES FOUND.
XX
XX Chatterjee M, Foon KA;
XX
XX WPI; 1999-060029/05.
XX P-PSDB; AAW87593.
XX
XX Delaying development of, or treating, HMFG-associated tumours -
XX using anti-idiotype antibody 11D10 raised against antibodies to
XX human milk fat globule protein
XX
XX Disclosure; Fig 1; 54pp; English.
XX
XX This sequence represents the coding sequence for the murine antibody
XX 11D10 light chain variable region. This anti-idiotype antibody is used
XX to delay the development of, or treat, a human milk fat globule (HMFG)
XX associated tumour in an individual having low tumour burden.
XX The antibody 11D10 is used to prevent the recurrence of HMFG-associated
XX tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma,
XX especially for treating breast tumours.
XX
XX Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;
XX

```

Alignment Scores:

Pred. No.: 1.81e-61 Length: 435
 Score: 740.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-08-836-455-2 (1-145) x AAV83772 (1-435)

QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 DB 1 ATGGGGCCCCCTCTCAGATCTTGGGTCTTCTTGTTCAGGTACAGATGT 60
 QY 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 DB 61 GACATCCAGATGACCCAGTCTCATCTCTATCTGCCCTCTCTGGGACAAAGAGTCAGT 120
 QY 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGluPro 60
 DB 121 CTCACCTTGTGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGGCTTCAGCAGGAACCA 180
 QY 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 DB 181 GATGGAACTATTAAACGCCCTGATCTACGCCACATCCAGTTAGGTCTGTGGTGTCCCAAA 240
 QY 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 DB 241 AGGTTTCAGTGGCAGTAGGTCTGGTCTGAGATTTCTCTCACCATCAGCAGCCTTGAGTCT 300
 QY 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 DB 301 GAAGATTTGTAGCCCTATTACTCTACAAATATGCTAGTTCTCCGTACAGTTCGGAGGG 360
 QY 121 GlyThrLysLeuGluIleLysArgAlaAspAlaProThrValSerIlePheProPro 140
 DB 361 GGGACCAAGCTGGAATAAACGGGCTGATCTGCACCAACTGTATCCATCTTCCCAACCA 420
 QY 141 SerSerLysLeuGly 145
 DB 421 TCCAGTAAGCTTGGG 435

RESULT 3

AAL51273
 ID AAL51273 standard; cdna; 435 BP.

XX AC AAL51273;

XX DT 20-MAR-2003 (first entry)

XX DE Mouse 11D10 antibody light chain variable region coding sequence.

KW Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; HMFG;
 KW carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour;
 KW CEA-associated tumour; anti-idiotype antibody.

XX OS Mus musculus.

XX FH Key Location/Qualifiers
 XX CDS 1..435

FT /*tag= a

FT /product= "Mouse 11D10 anti-idiotype antibody light chain
 FT variable region"

FT /note= "No stop codon is given"

FT sig_peptide 1..60

FT /*tag= b

FT mat_peptide 61..435

FT /*tag= c

XX WO200292012-A2.

XX PN 21-NOV-2002.

PD

XX

PF 17-MAY-2002; 2002WO-US15840.

XX PR 17-MAY-2001; 2001US-0861294.

XX PA (KENT) UNIV KENTUCKY RES FOUND.

XX PI Chatterjee M, Foon KA;

XX WPI; 2003-129216/12.

DR P-PSDB; AAO16292.

XX Use of anti-idiotypic antibodies for human milk fat globules (HMFG) - or

PT carcinoembryonic antigen (CEA)-associated tumor for delaying the

PT development of, or treating a HMFG- or CEA-associated tumor (e.g.

PT breast tumor) in humans

XX Disclosure; Fig 1; 98pp; English.

XX The invention comprises a method for delaying the development of, or

CC treating a tumour that is associated with human milk fat globules (HMFG)

CC or carcinoembryonic antigen (CEA). The method of the invention involves

CC administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an

CC anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for

CC delaying the development, of or treating HMFG/CEA-associated tumours. The

CC present cDNA sequence encodes the light chain variable region of the

CC mouse 11D10 anti-idiotype antibody.

XX Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;

SQ

Alignment Scores:

Pred. No.: 1.81e-61 Length: 435
 Score: 740.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0

US-08-836-455-2 (1-145) x AAL51273 (1-435)

QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 DB 1 ATGGGGCCCCCTCTCAGATCTTGGGTCTTCTTGTTCAGGTACAGATGT 60
 QY 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCCCTCTCTGGGACAAAGAGTCAGT 120
 QY 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGluPro 60
 DB 121 CTCACCTTGTGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGGCTTCAGCAGGAACCA 180
 QY 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 DB 181 GATGGAACTATTAAACGCCCTGATCTACGCCACATCCAGTTAGGTCTGTGGTGTCCCAAA 240
 QY 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 DB 241 AGGTTTCAGTGGCAGTAGGTCTGGTCTGAGATTTCTCTCACCATCAGCAGCCTTGAGTCT 300
 QY 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 DB 301 GAAGATTTGTAGCCCTATTACTCTACAAATATGCTAGTTCTCCGTACAGTTCGGAGGG 360
 QY 121 GlyThrLysLeuGluIleLysArgAlaAspAlaProThrValSerIlePheProPro 140
 DB 361 GGGACCAAGCTGGAATAAACGGGCTGATCTGCACCAACTGTATCCATCTTCCCAACCA 420
 QY 141 SerSerLysLeuGly 145
 DB 421 TCCAGTAAGCTTGGG 435

RESULT 4

PS Example 1; Page 28-29; 32pp; English.

XX The present sequence encodes mouse light chain variable region. This
 CC recombinant DNA is derived from PCR A which amplifies antibody light
 CC chain variable region (VL). The transformant produced using the VL gene
 CC was used transform competent E. coli cells. The peptide produced by
 CC preventing neutralises interleukin-18. This is useful for treating and
 CC transforming immunopathies, inflammatory disorders and autoimmune diseases
 CC which are caused by excessive immunoreaction. The peptide has
 CC anti-allergic, anti-inflammatory, immunosuppressive, hematopoietic,
 CC leukocytopenic, antialgic, antipyretic and hepatic-function improving
 CC activities.

XX Sequence 407 BP; 96 A; 99 C; 96 G; 116 T; 0 other;

Alignment Scores:
 Pred. No.: 2.3e-51 Length: 407
 Score: 633.00 Matches: 125
 Percent Similarity: 94.07% Conservativity: 2
 Best Local Similarity: 92.59% Mismatches: 8
 Query Match: 85.54% Indels: 0
 DB: 21 Gaps: 0

US-08-836-455-2 (1-145) x AAZ49548 (1-407)

Qy 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 Db 1 ATGAGGGCCCTGCTCAGATTGTTGGCTTCTGTGCTCTGTTCAGGTACCAGATGT 60
 Qy 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 Db 61 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCCTCTCTGGGAGAAAGATCAGT 120
 Qy 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnPro 60
 Db 121 CTCACTTGTGGGCAAGTACGACATGGTAGTAATATACCTGCTTCAACAGGAACCA 180
 Qy 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 Db 181 GATGGAACCTTTAAACGCCCTGATCTACGCCACATCCAGTTAGATTCTGGTGTCCCAAG 240
 Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 Db 241 AGGTTACAGTGGCAGTAGGCTGGGTACAGATTATCTCTCACCATCAGCAGCCTTGAGTCT 300
 Qy 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 Db 301 GAGATTTTCTAGACTATTACTGTCTACAAATATGCTAGTTCTCCGTACACGTTCCGAGGG 360
 Qy 121 GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrVal 135
 Db 361 GGGACCAAGCTGGCAATAAACGGCTGATGCTGCACCAACTGTGA 405

RESULT 6

AAAT77851
 ID AAT77851 standard; CDNA; 387 BP.

XX AC AAT77851;

XX 03-NOV-1997 (first entry)

XX Murine anti-human class II monoclonal antibody 44H104 VL chain cDNA.

XX Antibody: light chain; variable region; hybridoma cell line 44H104;
 KW immune response; enhance; stimulate; vaccine; immunodiagnosis;
 KW antigen delivery; ss.

XX Mus musculus.

XX Key Location/Qualifiers

XX CDS 1..387

XX /*tag= a

XX /note= "Encodes 44H104 light chain variable region,

FT including secretion signal; termination
 FT codon not given"

PN WO9640941-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-CA00400.

XX 07-JUN-1995; 95US-0483576.

XX (CONN-) CONNAUGHT LAB LTD.

XX Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH;

XX WPI; 1997-077271/07.

XX P-PSDB; AAW22537.

XX Recombinant conjugate antibody mol., modified for delivering an
 PT antigen - elicits enhanced immune response without the use of
 PT adjuvant to generate antibodies which are useful in vaccines or
 PT immuno:diagnosis

XX Example 1; Fig 1A; 64pp; English.

XX Novel recombinant conjugate antibody molecules comprise a monoclonal
 CC antibody specific for a surface structure of antigen presenting
 CC cells (APC), genetically modified to contain at least one antigen
 CC exclusively at one or more preselected sites. The conjugate is capable
 CC of delivering the antigen to APC and eliciting an immune response to
 CC the antigen. The new conjugates are useful as vaccines and are able
 CC to elicit an enhanced immune response without the use of an adjuvant.
 CC In a specific example, a conjugate was constructed using the murine
 CC anti-human class II monoclonal antibody secreted by hybridoma
 CC 44H104. The peptide CLTB36 was chosen as antigen; it consists of
 CC a tandemly linked T and B cell epitope derived from HIV MN strain.
 CC The present sequence encodes the light chain variable region which
 CC was PCR amplified from 44H104 and used in the preparation of a
 CC conjugate with antigen CLTB36.

XX Sequence 387 BP; 90 A; 95 C; 90 G; 112 T; 0 other;

Alignment Scores:

Pred. No.: 2.39e-41 Length: 387
 Score: 527.00 Matches: 103
 Percent Similarity: 86.61% Conservativity: 7
 Best Local Similarity: 81.10% Mismatches: 17
 Query Match: 71.22% Indels: 0
 DB: 18 Gaps: 0

US-08-836-455-2 (1-145) x AAT77851 (1-387)

Qy 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 Db 7 ATGAGGGTCTCTGCTCAGTTTGTGCTTCTGTGCTGTTCAGGTACCAGATGT 66
 Qy 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 Db 67 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCCTCTCTGGGACAAAGATCAGT 126
 Qy 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnPro 60
 Db 127 CTCACCTTGTGGGCAAGTACAGAAATTAGTGGTTACTTAACCTGGCTTCAGCAGAAACCA 186
 Qy 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 Db 187 GATGGAACCTATTAAACGCCCTGCTACGCCGCTCAGTTAGATTCTGTGTGCCCAAAA 246
 Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 Db 247 AGGTTACAGTGGCAGTAGGCTGGGTACAGATTATCTCTCACCATCAGCAGCCTTGAGTCT 306
 Qy 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120

Db 307 GAGATTTCAGACTATTCTGTACAAATATACTAATTATCGCTCAGCTTCGGTGCT 366
 QY 121 GlyThrLysLeuGluLeuLys 127
 Db 367 GGGACCAAGCTGGAGCTGAAA 387

RESULT 7
 ID AAD32138 standard; DNA; 387 BP.
 AC AAD32138;
 XX 18-JUN-2002 (first entry)
 DT Murine 44H104 mab variable light chain (VL) DNA.
 DE Murine; mab; light chain; VL; conjugate antibody; antigen delivery;
 KW immune system; vaccine; detecting agent; antibacterial; gene; ds.
 XX Mus sp.
 OS
 XX Key Location/Qualifiers
 FT 1..387
 CDS /product= "Murine 44H104 mab VL"
 FT /transl_except= (pos:277..279, aa:Thr)
 FT /note= "This translation exception occurs while
 FT decoding for murine mab VL alternative version
 FT (AAE20204); CDS does not include stop codon"
 FT /partial

US2002025315-A1.

28-FEB-2002.

14-JAN-1998; 98US-0007093.

14-JAN-1998; 98US-0007093.

(ANAN/) ANAND N N.

(BARB/) BARBER B H.

(CATE/) CATES G A.

(CATE/) CATERINI J E.

(KLEI/) KLEIN M H.

Anand NN, Barber BH, Cates GA, Caterini JE, Klein MH;

WPI; 2002-267519/31.

P-PSDB; AAE20200, AAE20204.

Novel recombinant conjugate antibody, useful as a vaccine against pathogens having a specific antigen, comprises a monoclonal antibody specific for an antigen presenting cell surface structure -

Example 1; Fig 1A; 28pp; English.

The invention relates to a recombinant conjugate antibody, comprising a monoclonal antibody specific for a surface structure of antigen presenting cells genetically modified to contain an antigen moiety for the purpose of delivery of the antigen moiety to antigen-presenting cells of the immune system. The conjugate antibody is formulated as a vaccine to protect a host against a disease caused by a pathogen expressing the antigen. The antibody is useful as a detecting agent. The present sequence is murine 44H104 mab variable light chain (VL) DNA.

Sequence 387 BP; 90 A; 95 C; 90 G; 112 T; 0 other;

Alignment Scores:

Pred. No.: 2.39e-41 Length: 387

Score: 527.00 Matches: 103

Percent Similarity: 86.61% Conservative: 7

Best Local Similarity: 81.10% Mismatches: 17
 Query Match: 71.22% Indels: 0
 DB: 24 Gaps: 0
 US-08-836-455-2 (1-145) x AAD32138 (1-387)
 QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 Db 7 ATGAGGGTTCCTGCTCAGCTTTTGGCTTCTTGTTGCTCTGTTCCAGGTACCAGATGT 66
 QY 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 Db 67 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGACAAAGAGTCAGT 126
 QY 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnPro 60
 Db 127 CTCACITGTGGGCAAGTCAGGAATAGTGGTTACTTAACCTGGCTTCAGCACAACCA 186
 QY 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 Db 187 GATGGAACATATTAACGCTGGTCTAGCGCGCTCCACTTAGATTTCTGGTGTCCCAAA 246
 QY 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 Db 247 AGGTTCAGTGGCAGTAGTCTGGGTCTAGATTTCTCTCACCATCAGCAGCTTGAGTCT 306
 QY 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 Db 307 GAAGATTTTCAGACATATTACTGTCTACAATATATACTAATTATCGCTCAGTTCGGTGCT 366
 QY 121 GlyThrLysLeuGluLeuLys 127
 Db 367 GGGACCAAGCTGGAGCTGAAA 387

RESULT 8

AAQ46084

ID AAQ46084 standard; cDNA; 739 BP.

XX AC AAQ46084;

XX DT 25-MAR-2003 (updated)

XX DT 07-FEB-1994 (first entry)

XX DE Sequence encoding 520C9 sFv protein.

KW Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;
 XX biosynthetic single polypeptide chain binding site; ss.
 XX OS Synthetic.

XX FH Key Location/Qualifiers

XX CDS 1..739

XX FT /*tag= a

XX XX WO9316185-A2.

XX XX PD 19-AUG-1993.

XX XX PF 05-FEB-1993; 93WO-US01055.

XX XX PR 06-FEB-1992; 92US-0831967.

XX XX PA (CETU) CETUS ONCOLOGY CORP.

XX XX PA (CREA-) CREATIVE BIOMOLECULES INC.

XX XX PI Houston LL, Huston JS, Oppermann H, Ring DB;

XX XX DR WPI; 1993-272889/34.

XX XX DR P-PSDB; AAR39569.

XX PT New single chain Fv polypeptide binding to C-erbB-2 tumour
 XX PT antigen - for imaging or treating breast or ovarian cancer etc.
 XX

Db 700 GGGACCAACCTGGAAATAAAACGGGCTGAT 729

RESULT 10

AAV21798

ID AAV21798 standard; cDNA; 739 BP.

XX

AC AAV21798;

XX

DT 16-JUL-1998 (first entry)

XX

DE 520C9 anti-c-erbB-2 sfv' dimeric construct gene sequence.

XX

KW Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer;

KW c-erbB-2; tumour; diagnosis; ss.

XX

OS Synthetic.

OS Mus sp.

XX

FH Key Location/Qualifiers

FT CDS 1..732

FT /*tag= a

FT /product= "520C9 sfv' polypeptide"

XX

US5753204-A.

XX

PD 19-MAY-1998.

XX

XX

PF 05-JUN-1995; 95US-0461838.

XX

PR 07-OCT-1993; 93US-0133804.

PR 06-FEB-1992; 92US-0831967.

PR 05-JUN-1995; 95US-0461838.

XX

XX

PA (CHIR) CHIRON CORP.

PA (CREA-) CREATIVE BIOMOLECULES INC.

XX

PI Houston LL, Huston JS, Oppermann H, Ring DB;

XX

DR WPI; 1998-311318/27.

DR P-PSDB; AAW53170.

XX

Imaging of antigens in vivo - using dimers of single-chain antibody

Fv fragments

XX

XX

PS Example 1; Columns 33-36; 30pp; English.

XX

CC This is the nucleotide sequence of a 520C9 sfv' (single chain Fv)

CC construct. This was constructed by connecting the Vh and Vl genes with

CC a DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal

CC antibody useful in targeting c-erbB-2 antigen. This dimeric construct

CC can be used in the methods of invention of imaging a preselected antigen

CC expressed in a mammal. The methods are used in magnetic resonance imaging

CC of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic

CC constructs have enhanced properties as in vivo targeting agents in

CC comparison with intact monoclonal antibodies or their Fab fragments. The

CC dimeric constructs permit the in vivo targeting of an epitope on an

CC antigen with greater apparent avidity, including greater tumour

CC specificity, tumour localisation and tumour retention properties than

CC that of the Fab fragment having the same CDRS as the construct.

XX

SQ Sequence 739 BP; 188 A; 177 C; 181 G; 193 T; 0 other;

Alignment Scores:

Pred. No.:	3.95e-39	Length:	739
Score:	507.00	Matches:	101
Percent Similarity:	93.64%	Conservative:	2
Best Local Similarity:	91.82%	Mismatches:	7
Query Match:	68.51%	Indels:	0
DB:	19	Gaps:	0

US-08-836-455-2 (1-145) x AAV21798 (1-739)

Qy 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40

Db 400 GATATCCAGATGACCCAGTCTCCATCTCTCTATCTGCCTCTCTGGGAGAAAGAGTCAGT 459

Qy 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnPro 60

Db 460 CTCACITGTCGGGCAAGTCAGGACATGGTAATAGCTTAACCTGGCTTCAGCAGAACCA 519

Qy 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProlys 80

Db 520 GATGGAACTATTAAACGCCCTGATCTACGCCACATCCAGTTAGATTCTGGTGTCCCAAA 579

Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGlySer 100

Db 580 AGGTTCAGTGGCAGTGGTCTGGCTCAGATTATCTCTCACCATCAGTAGCCTTGATCT 639

Qy 101 GluAspPheValAlaTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120

Db 640 GAAGATTTTCTAGTCTATTACTGTCTACAATATGCTATTTTTCGCTACACGTTCCGAGGG 699

121 GlyThrLysLeuGluIleLysArgAlaAsp 130

700 GGGACCAACCTGGAAATAAAACGGGCTGAT 729

RESULT 11

AAV63399

ID AAV63399 standard; cDNA; 739 BP.

XX

AC AAV63399;

XX

DT 28-JAN-1999 (first entry)

XX

DE 520C9 sfv DNA sequence.

XX

KW 520C9 sfv; antigen; tumour cell; antibody 520C9;

KW targeted delivery; antigen-expressing cell; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 1..732

FT /*tag= a

FT /product= 520C9 sfv

XX

US5837846-A.

XX

PD 17-NOV-1998.

XX

PF 05-JUN-1995; 95US-0461386.

XX

PR 07-OCT-1993; 93US-0133804.

PR 06-FEB-1992; 92US-0831967.

PR 05-JUN-1995; 95US-0461386.

XX

PA (CHIR) CHIRON CORP.

PA (CREA-) CREATIVE BIOMOLECULES INC.

XX

PI Houston LL, Huston JS, Oppermann H, Ring DB;

XX

DR WPI; 1999-023541/02.

DR P-PSDB; AAW80424.

XX

Nucleic acid encoding single-chain Fv fragment specific for antigens

- and having C-terminal tail for crosslinking to form dimer with

improved pharmacokinetic properties, used to deliver drugs and

imaging agents, especially to tumours

Example 1; Columns 33-36; 29pp; English.

The present sequence encodes an antibody 520C9 sfv. Variable heavy

and light sequences of antibody 7520C9 are connected, together with a

serine linker, to produce the present single chain Fv gene. The present

sequence exemplifies the invention. Dimers of the single chain Fv are

used for targeted delivery of drugs or imaging agents (e.g. cytotoxins,

CC prodrugs or 99m-technetium) to antigen-expressing cells, particularly
 XX for treatment or diagnosis of tumours (especially of ovary or breast).
 SQ Sequence 739 BP; 188 A; 177 C; 181 G; 193 T; 0 other;

Alignment Scores:
 Pred. No.: 3.95e-39 Length: 739
 Score: 507.00 Matches: 101
 Percent Similarity: 93.64% Conservative: 2
 Best Local Similarity: 91.82% Mismatches: 7
 Query Match: 68.51% Indels: 0
 DB: 20 Gaps: 0

US-08-836-455-2 (1-145) x AAV63399 (1-739)

Qy 21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 Db 400 GATATCCAGATGACCCAGTCCTCTTATCTGCTCTCTGGGAGAAAGAGTCAGT 459
 Qy 41 LeuThrCysArgAlaSerGlnAspIleGlyLeuHisTrpLeuGlnGlnGluPro 60
 Db 460 CTCACCTTGTGGGCAAGTCAGGACATTTGTAATAGCTTAACCTGGCTTCAGCAGGAACCA 519
 Qy 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 Db 520 GATGGAACATATTAACCGCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAA 579
 Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 Db 580 AGGTTTCAGTGGCAGTCGGTGGTCAGATTATTTCTCACCATCAGTAGCCTTGAGTCT 639
 Qy 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 Db 640 GAAGATTTTGTAGTCTATTACTGTCTACAATATCTATTTTCCGTACACGTTTCGGAGGG 699
 Qy 121 GlyThrLysLeuGluIleLysArgAlaAsp 130
 Db 700 GGGACCAACCTGGAAATAAACGGGCTGAT 729

RESULT 12
 AAZ49534
 ID AAZ49534 standard; cDNA; 324 BP.
 AC AAZ49534;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE Mouse anti-IL-18 antibody VL encoding cDNA from hybridoma #125-2H.
 XX
 KW Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
 KW hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18;
 KW antiinflammatory; immunosuppressive; leucocytopenic; antialgic;
 KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
 KW immunopathy; inflammatory disorder; immunoreaction; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 1..324
 FT /*tag= a
 FT /label= Anti-IL-18_antibody_light_chain_variable_region
 XX
 EP974600-A2.
 XX
 PD 26-JAN-2000.
 XX
 XX 24-JUN-1999; 99EP-0304977.
 XX
 PR 24-JUN-1998; 98JP-0177580.
 PR 12-OCT-1998; 98JP-0289044.
 PR 22-DEC-1998; 98JP-0365023.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;
 XX WPI: 2000-118341/11.
 DR P-PSDB: AAY44587.
 XX
 PT New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 XX inflammatory disorders and autoimmune diseases -
 PS Claim 11; Page 21; 36pp; English.
 XX
 CC The present cDNA sequence derived from hybridoma #125-2H, encodes mouse
 CC anti-interleukin-18 antibody light chain variable region (VL). It can be
 CC used in the production of recombinant monoclonal antibody #125-2HmAb,
 CC which is capable of neutralising biological activities of interleukin-18.
 CC The antibody has antiinflammatory; immunosuppressive; leucocytopenic;
 CC antialgic; antipyretic; antiallergic and hepatotropic activity and can be
 CC used for prevention and treatment of autoimmune diseases, immunopathies
 CC and inflammatory disorders caused by excessive immunoreaction.
 XX
 SQ Sequence 324 BP; 83 A; 78 C; 76 G; 87 T; 0 other;

Alignment Scores:
 Pred. No.: 1.9e-39 Length: 324
 Score: 506.00 Matches: 100
 Percent Similarity: 94.44% Conservative: 2
 Best Local Similarity: 92.59% Mismatches: 6
 Query Match: 68.38% Indels: 0
 DB: 21 Gaps: 0

US-08-836-455-2 (1-145) x AAZ49534 (1-324)

Qy 21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 Db 1 GACATCCAGATGACCCAGTCCTCTTATCTGCTCTCTGGGAGAAAGAGTCAGT 60
 Qy 41 LeuThrCysArgAlaSerGlnAspIleGlyLeuHisTrpLeuGlnGlnGluPro 60
 Db 61 CTCACCTTGTGGGCAAGTCAGGACATTTGTAATAGCTTAATATCTGGCTTCACAGGAACCA 120
 Qy 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 Db 121 GATGGAACATTTTAACCGCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAG 180
 Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 Db 181 AGGTTTCAGTGGCAGTCAGTGGTGGTCAGATTATTTCTCACCATCAGCAGCCTTGAGTCT 240
 Qy 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 Db 241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCGGTACACGTTTCGGAGGG 300
 Qy 121 GlyThrLysLeuGluIleLysArg 128
 Db 301 GGGACCAAGCTGGCAATAAAACGG 324

RESULT 13
 AAS97136
 ID AAS97136 standard; DNA; 756 BP.
 XX
 AC AAS97136;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE P4-3 single chain Fv DNA.
 XX
 KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
 KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
 KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
 KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
 KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; ds;
 KW helminth; cytostatic; antimicrobial; immunomodulatory; P4-2; P4-3; P4-14;

```
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
OS Homo sapiens.
PN WO200171005-A2.
XX 27-SEP-2001.
XX 26-MAR-2001; 2001WO-EP03414.
XX 24-MAR-2000; 2000EP-0106467.
XX (KUFE/) KUFER P.
XX Kufer P, Riethmueller G, Lutterbues R, Borschert K, Kischel R;
PI Mayer M, Hofmeister R;
XX WPI; 2002-055119/07.
DR P-PSDB; AAU72862.
XX Multifunctional polypeptides comprising binding sites that specifically
PT recognise extracellular groups of the NKG2D receptor complex and
PT domains which function as receptors or ligands, useful for treating
PT cancers and infectious diseases -
XX Example 7; Fig 16; 114pp; English.
CC The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NKG2D receptor complex and a second domain which functions
CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. The sequences represent DNA encoding the
CC polypeptides of the invention.
XX SQ Sequence 756 BP; 184 A; 180 C; 204 G; 188 T; 0 other;

Alignment Scores:
Pred. No.: 6.27e-39 Length: 756
Score: 505.00 Matches: 100
Percent Similarity: 92.24% Conservative: 7
Best Local Similarity: 86.21% Mismatches: 9
Query Match: 68.24% Indels: 0
DB: 24 Gaps: 0

US-08-836-455-2 (1-145) x AAS97136 (1-756)
QY 17 GlyThrArgCysAspIleGlnMetThrGlnSerProSerLeuSerAlaSerLeuGly 36
DB 388 GGTGGTGGTTCGTAGCTCGTCATGACCCAGTCTCAUCCCTCTATCTGCTCTCTGGGA 447
QY 37 GlnArgValSerLeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeu 56
DB 448 GAAAGAGTCAGTCTCACTTCGCGCAAGTCAGGACATTTGGTAGTCTTAAGCTGGCTT 507
QY 57 GlnGlnGluProAspGlyThrIleIysArgLeuIleTyrAlaThrSerSerLeuGlySer 76
DB 508 CAGCAGGAACAGATGGAACTATTAAACGCTGTACTACGCCACATCCAGTTTAGATTC 567
QY 77 GlyValProLysArgPheSerGlySerArgSerGlySerGlySerLeuThrIleSer 96
DB 568 GGTGTCCCAAAAGGTTTCAGTGGCAGTAGGTCGTGGTCAGATATTCTCTCACCATCAGC 627

QY 97 SerLeuGluSerGluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyr 116
DB 628 AGCCTTGAGTCTGAAGATTTTGTAGACTATTACTCTCTACAATATGCTAGTCTCCGTAC 687
QY 117 ThrPheGlyGlyGlyThrIysLeuGluIleLysArgAlaAspAlaAla 132
DB 688 ACGTTCGAGGGGGGACCAAGCTTGAGATCAACGCTACGACTAGTTTC 735

RESULT 14
AAS97145
ID AAS97145 standard; DNA; 1497 BP.
XX AC AAS97145;
XX 26-FEB-2002 (first entry)
XX 3B10xP4-3 bispecific single chain Fv DNA.
XX Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; ds;
KW helminth; cytostatic; antimicrobial; immunomodulatory; P4-2; P4-3; P4-14;
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
XX OS Homo sapiens.
XX WO200171005-A2.
XX 27-SEP-2001.
XX 26-MAR-2001; 2001WO-EP03414.
XX 24-MAR-2000; 2000EP-0106467.
XX (KUFE/) KUFER P.
XX Kufer P, Riethmueller G, Lutterbues R, Borschert K, Kischel R;
PI Mayer M, Hofmeister R;
XX WPI; 2002-055119/07.
DR P-PSDB; AAU72871.
XX Multifunctional polypeptides comprising binding sites that specifically
PT recognise extracellular groups of the NKG2D receptor complex and
PT domains which function as receptors or ligands, useful for treating
PT cancers and infectious diseases -
XX Example 5; Fig 16; 114pp; English.
CC The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NKG2D receptor complex and a second domain which functions
CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. The sequences represent DNA encoding the
CC polypeptides of the invention.
XX SQ Sequence 1497 BP; 364 A; 358 C; 407 G; 368 T; 0 other;
```

Alignment Scores:

Pred. No.: 1.38e-38 Length: 1497
 Score: 505.00 Matches: 100
 Percent Similarity: 92.24% Conservative: 7
 Best Local Similarity: 86.21% Mismatches: 9
 Query Match: 68.24% Indels: 0
 DB: 24 Gaps: 0

US-08-836-455-2 (1-145) x AAS97145 (1-1497)

QY 17 GlyThrArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGly 36
 DB 1129 GGTGGGGTCTGAGCTCGTCAGCCAGCTCCATCTCTATCTGCTCTCTGGGA 1188
 QY 37 GlnArgValSerLeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeu 56
 DB 1189 GAAAGACTCAGTCTCACTTCTCGGGCAAGTCAGGACATTTGCTAGCTTAACCTGGCTT 1248
 QY 57 GlnGlnGluProaspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySer 76
 DB 1249 CAGCAGGACACAGATGGAACTATTAAACGCTGATCTACGCCACATCCAGTTAGATTCT 1308
 QY 77 GlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSer 96
 DB 1309 GGTGTCCCAAAAGGTTCACTGGCAGTAGGTCTGGGTCAGATTATTCTCACCATCAGC 1368
 QY 97 SerLeuGluSerGluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyr 116
 DB 1369 AGCCTTGAGTCTGAAGATTTGTAGACTATTACTGTCTACATATGCTAGTTCTCCGTAC 1428
 QY 117 ThrPheGlyGlyThrLysLeuGluIleLysArgAlaAspAlaLa 132
 DB 1429 ACGTTCGGAGGGGGACCAAGCTTGAGATCAACAGTACGACTAGTTCC 1476

RESULT 15

AAQ15114
 ID AAQ15114 standard; DNA; 432 BP.

AC AAQ15114;

DT 25-MAR-2003 (updated)

DT 16-MAR-1992 (first entry)

DE IL-2 chimeric antibody light chain clone 447.

XX Interleukin-2; immunosuppressant.

XX Chimeric Homo sapiens.

OS Chimeric Mus musculus.

XX Key Location/Qualifiers

FT CDS 1..432

FT /*tag= a

FT sig_peptide 1..60

FT /*tag= b

FT mat_peptide 61..432

FT /*tag= c

XX EP460674-A.

XX PN

XX PD

XX 11-DEC-1991.

XX 06-JUN-1991; 91EP-0109303.

XX 08-JUN-1990; 90DE-4018442.

XX (BOEF) BOEHRINGER MANNHEIM GMBH.

XX Weidlu U, Kaluza B, Knapp W;

XX WPI; 1991-363168/50.

XX P-PSDB; AAR15322.

XX

PT New recombinant DNA encoding chimeric antibody - with human
 PT constant and non-human variable regions, esp. directed against
 PT interleukin 2 receptor

XX Disclosure; Page 11; 24pp; German.

XX The sequence encodes the interleukin-2 (IL-2) chimeric antibody light
 CC chain clone 447. Antibodies against IL-2 receptors are useful as
 CC immunosuppressants, and are much less immunogenic than mouse or
 CC rat antibodies. The DNA sequence provides much higher yields of
 CC chimeric antibodies than known methods. See also AAQ15114-015118.
 CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 432 BP; 106 A; 102 C; 104 G; 120 T; 0 other;

Alignment Scores:

Pred. No.: 5.1e-39 Length: 432
 Score: 503.00 Matches: 100
 Percent Similarity: 79.86% Conservative: 11
 Best Local Similarity: 71.94% Mismatches: 28
 Query Match: 67.97% Indels: 0
 DB: 12 Gaps: 0

US-08-836-455-2 (1-145) x AAQ15114 (1-432)

QY 5 AlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCysAspIleGlnMet 24
 DB 13 GCTCAGTTCTTGCATCTTGTGTTGTTCCAGTGCAAGATCTGACATCTCTGATG 72
 QY 25 ThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSerLeuThrCysArg 44
 DB 73 ACCCAATCTCCATCTCCATCTCTGTTCTCTGGGAGACACAGTCACATCTGTCAT 132
 QY 45 AlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnProAspGlyThrIle 64
 DB 133 GCAGTCAGGGCATTAGAACTATATATAGTGTGTTGCAGCAGAAACACGGGAATCATTT 192
 QY 65 LysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLysArgPheSerGly 84
 DB 193 AAGGGCTGATCTATCATGATGGAACCACTTGGAAAGATGGAGTTCATCAGGTTCCAGTGGC 252
 QY 85 SerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSerGluAspPheVal 104
 DB 253 AGTGGATCTGGAGCAGATTATTCTCACCAGTACGAGCCTGGGAATCTGAAGATTTTGA 312
 QY 105 AlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGlyThrLysLeu 124
 DB 313 GACTATTACTGTGTACAGTATGCTCAGTTTCTCGGAGCTTCGTTGGTGGGAGGACCAAGCTG 372
 QY 125 GluIleLysArgAlaAspAlaAlaProThrValSerIlePheProProSerSerLys 143
 DB 373 GAAATCAAGGGGCTGATGCTGCACCAACTGTATCTCATCTTCCACCATCCAGTGA 429

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Job time : 218.987 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 30, 2003, 22:11:56 ; Search time 192.198 seconds
(without alignments)
1730.853 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 740

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Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1533700 seqs, 1147125425 residues

Total number of hits satisfying chosen parameters: 3067400

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	740	100.0	435	9	US-09-861-294-1 Sequence 1, Appli

2	740	100.0	435	12	US-10-367-506-1	Sequence 1, Appli
3	633	85.5	407	10	US-09-924-099-27	Sequence 27, Appli
4	616	83.2	402	8	US-08-779-784-5	Sequence 5, Appli
5	541	73.1	390	12	US-10-268-883-10	Sequence 10, Appli
6	532	71.9	351	8	US-08-779-784-16	Sequence 16, Appli
7	532	71.9	351	8	US-08-779-784-17	Sequence 17, Appli
8	527	71.2	387	9	US-09-007-093-1	Sequence 1, Appli
9	507	68.5	739	10	US-09-887-853-5	Sequence 5, Appli
10	506	68.4	324	10	US-09-924-099-11	Sequence 11, Appli
11	502	67.8	711	10	US-09-924-099-19	Sequence 19, Appli
12	502	67.8	729	10	US-09-924-099-20	Sequence 20, Appli
13	484.5	65.5	737	10	US-09-919-344-7	Sequence 7, Appli
14	481	65.0	714	14	US-10-153-382-18	Sequence 18, Appli
15	473	63.9	974	10	US-09-859-053-29	Sequence 29, Appli
16	471	63.6	447	9	US-09-797-481-1	Sequence 1, Appli
17	471	63.6	447	9	US-09-844-736-3	Sequence 3, Appli
18	471	63.6	447	14	US-10-162-396-3	Sequence 3, Appli
19	469	63.4	490	11	US-09-918-995-37859	Sequence 37859, A
20	467	63.1	447	9	US-09-861-294-19	Sequence 19, Appli
21	467	63.1	447	12	US-10-367-506-19	Sequence 19, Appli
22	464	62.7	728	14	US-10-158-646-55	Sequence 55, Appli
23	464	62.7	728	10	US-09-844-684-15	Sequence 15, Appli
24	464	62.7	728	14	US-10-040-244-15	Sequence 15, Appli
25	462	62.4	716	10	US-09-844-684-13	Sequence 13, Appli
26	462	62.4	716	14	US-10-040-244-13	Sequence 13, Appli
27	462	62.4	729	14	US-10-216-484-125	Sequence 125, App
28	461	62.3	393	8	US-08-779-784-20	Sequence 20, Appli
29	455.5	61.6	928	14	US-10-221-945-5	Sequence 5, Appli
30	447	60.4	514	14	US-10-066-543-2025	Sequence 2025, Ap
31	447	60.4	537	14	US-10-066-543-186	Sequence 186, App
32	445	60.1	705	9	US-09-740-002-16	Sequence 16, Appli
33	444	60.0	840	9	US-09-766-543-11	Sequence 11, Appli
34	442	59.7	520	13	US-09-878-178-1210	Sequence 1210, Ap
35	442	59.7	520	13	US-10-046-935-1210	Sequence 1210, Ap
36	442	59.7	520	14	US-10-146-502-1210	Sequence 1210, Ap
37	439	59.3	381	12	US-10-268-883-4	Sequence 4, Appli
38	439	59.3	819	14	US-10-158-646-65	Sequence 65, Appli
39	438	59.2	698	10	US-09-844-684-11	Sequence 11, Appli
40	438	59.2	698	14	US-10-040-244-11	Sequence 11, Appli
41	438	59.2	711	14	US-10-006-593-70	Sequence 70, Appli
42	436.5	59.0	494	10	US-09-878-178-1811	Sequence 1811, Ap
43	436.5	59.0	494	13	US-10-046-935-1811	Sequence 1811, Ap
44	436.5	59.0	494	14	US-10-146-502-1811	Sequence 1811, Ap
45	436	58.9	408	9	US-09-764-304-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-861-294-1
; Sequence 1, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(435)

; NAME/KEY: sig_peptide
; LOCATION: (1)...(60)
; NAME/KEY: mat_peptide
; LOCATION: (61)...(435)
US-09-861-294-1

Alignment Scores:

Pred. No.: 1,48e-84 Length: 435
Score: 740.00 Matches: 145
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-08-836-455-2 (1-145) x US-09-861-294-1 (1-435)

QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCys 20
DB 1 ATGGGGCCCTGCTCAGATTCTTGGGTCTTGTGTCTTGTTCAGGTACAGATGT 60
QY 21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGATCAGT 120
QY 41 LeuThrCysArgAlaSerGlnAspileGlyIleasnLeuHisTrpLeuGlnGlnPro 60
DB 121 CTCACCTTGTGGGCAAGTCAGGACATGTGTTAACTTACATTGCTTTCAGCAGGAACA 180
QY 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
DB 181 GATGGAACATATAACGGCTGATCTACGCCATCCAGTTAGGTCTGTGGTCCCCAAA 240
QY 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
DB 241 AGGTTACGTGCGAGTAGTCTGGGTACAGATTATCTCTCACCATCAGCAGCCTTGAGTCT 300
QY 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
DB 301 GAAGATTTGTAGGCTATTACTGTCTACAAATATGCTAGTCTCCGATACACGCTTCGAGGG 360
QY 121 GlyThrLysLeuGluIleLysArgAlaAspAlaProThrValSerIlePheProPro 140
DB 361 GGGACCAAGCTGGAATAAAGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA 420
QY 141 SerSerLysLeuGly 145
DB 421 TCCAGTAAGCTTGGG 435

RESULT 2

US-10-367-506-1

; Sequence 1, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMEG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (1)...(435)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(60)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (61)...(435)
US-10-367-506-1

Alignment Scores:

Pred. No.: 1,48e-84 Length: 435
Score: 740.00 Matches: 145
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-2 (1-145) x US-10-367-506-1 (1-435)

QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCys 20
DB 1 ATGGGGCCCTGCTCAGATTCTTGGGTCTTGTGTCTTGTTCAGGTACAGATGT 60
QY 21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGATCAGT 120
QY 41 LeuThrCysArgAlaSerGlnAspileGlyIleasnLeuHisTrpLeuGlnGlnPro 60
DB 121 CTCACCTTGTGGGCAAGTCAGGACATGTGTTAACTTACATTGCTTTCAGCAGGAACA 180
QY 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
DB 181 GATGGAACATATAACGGCTGATCTACGCCATCCAGTTAGGTCTGTGGTCCCCAAA 240
QY 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
DB 241 AGGTTACGTGCGAGTAGTCTGGGTACAGATTATCTCTCACCATCAGCAGCCTTGAGTCT 300
QY 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
DB 301 GAAGATTTGTAGGCTATTACTGTCTACAAATATGCTAGTCTCCGATACACGCTTCGAGGG 360
QY 121 GlyThrLysLeuGluIleLysArgAlaAspAlaProThrValSerIlePheProPro 140
DB 361 GGGACCAAGCTGGAATAAAGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA 420
QY 141 SerSerLysLeuGly 145
DB 421 TCCAGTAAGCTTGGG 435

RESULT 3

US-09-924-099-27

; Sequence 27, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 27

; LENGTH: 407
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(407)
 ; NAME/KEY: sig peptide
 ; LOCATION: (1)...(60)
 US-09-924-099-27

Alignment Scores:
 Pred. No.: 4,79e-71 Length: 407
 Score: 633.00 Matches: 125
 Percent Similarity: 94.07% Conservative: 2
 Best Local Similarity: 92.59% Mismatches: 8
 Query Match: 85.54% Indels: 0
 DB: 10 Gaps: 0

US-08-836-455-2 (1-145) x US-09-924-099-27 (1-407)

Qy 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 Db 1 ATGAGGCCCTGCTCAGATTTTGGCTTCTTGTGCTCTGTTCAGGTACCAGATGT 60
 Qy 21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 Db 61 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 120
 Qy 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGluPro 60
 Db 121 CTCACTTGTGGCAAGTACAGACATTTGGTAGTAATAATATATCTTCAACAGGAACCA 180
 Qy 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 Db 181 GATGGAACCTTTAAACGCCCTGATCTAGCCACATCCAGTTTAGATTCTGGTGTCCCAAG 240
 Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 Db 241 AGGTTAGTGGCAGTAGGTCTGGGTGAGATTTCTCTCACCATCAGCAGCCTTGAGTCT 300
 Qy 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 Db 301 GAAGATTTCTAGACTATTACTGCTACATATGCTAGTTCTCCGTACACGTTCCGAGGG 360
 Qy 121 GlyThrLysLeuGluIleLysArgAlaAspAlaProThrVal 135
 Db 361 GGGACCAAGTGGCAATAAAACGGCTGATGCTGCACCAACTGTA 405

RESULT 4

US-08-779-784-5
 ; Sequence 5, Application US/08779784
 ; Publication No. US20020164325A1

GENERAL INFORMATION:

; APPLICANT: Rodriguez, Moses
 ; APPLICANT: Miller, David J.
 ; APPLICANT: Asakura, Kunihiko
 ; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
 ; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
 ; NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/779,784
 ; FILING DATE: 07-JAN-1997
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/692,084
 ; FILING DATE: 08-AUG-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/236,520
 ; FILING DATE: 29-APR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 402 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Mus musculus
 ; US-08-779-784-5

Alignment Scores:

Pred. No.: 6,69e-69 Length: 402
 Score: 616.00 Matches: 122
 Percent Similarity: 95.45% Conservative: 4
 Best Local Similarity: 92.42% Mismatches: 6
 Query Match: 83.24% Indels: 0
 DB: 8 Gaps: 0

US-08-836-455-2 (1-145) x US-08-779-784-5 (1-402)

Qy 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 Db 7 ATGAGGCCCTGCTCAGATTTTGGCTTCTTGTGCTCTGTTCAGGTACCAGATGT 66
 Qy 21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 Db 67 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 126
 Qy 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGluPro 60
 Db 127 CTCACTTGTGGCAAGTACAGACATTTGGTAGTAATAACTGGCTTCAACAGGAACCA 186
 Qy 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 Db 187 GATGGAACCTTTAAACGCCCTGATCTAGCCACATCCAGTTTAGATTCTGTGTGCCCAAA 246
 Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 Db 247 AGGTTAGTGGCAGTAGGTCTGGGTGAGATTTCTCTCACCATCAGCAGCCTTGAGTCT 306
 Qy 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 Db 307 GAAGATTTCTAGACTATTACTGCTACATATGCTAGTTCTCCGTACACGTTCCGAGGG 366
 Qy 121 GlyThrLysLeuGluIleLysArgAlaAspAla 132
 Db 367 GGGACCAAGTGGAAATAAAACGGCTGATGCTTCA 402

RESULT 5

US-10-268-883-10
 ; Sequence 10, Application US/10268883
 ; Publication No. US20030138862A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tso, J. Yun
 ; APPLICANT: Green, Jennifer Macphate

Db 61 CTCACCTGTGGGCAAGTCAGGACATTTGGTAGTAAATATTAATCTGCTTCAACAGGAACCA 120
QY 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
Db 121 GATGGAACTTTTAAAGCGCTGATCTACGCCACATCCAGTTAGATTCTGGTGTCCCAAG 180
QY 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
Db 181 AGCTTCAGTGGCAGTAGGTCTGGTGCAGATTATCTCTCACCACATCAGCAGCCCTTGAGTCT 240
QY 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
Db 241 GAAGATTCTTGACGACTATTACTGCTACAAATATGCTAGTTCTCCGTACACGTTCCGGAGGG 300
QY 121 GlyThrLysLeuGluIleLysArg 128
Db 301 GGCACCAAGTCGCAATAAAACGG 324
RESULT 11
US-09-924-099-19
; Sequence 19, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 19
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of
; OTHER INFORMATION: SEQ
; OTHER INFORMATION: ID NO:9
US-09-924-099-19
Alignment Scores:
Pred. No.: 3.89e-54 Length: 711
Score: 502.00 Matches: 100
Percent Similarity: 91.89% Conservative: 2
Best Local Similarity: 90.09% Mismatches: 9
Query Match: 67.84% Indels: 0
DB: 10 Gaps: 0
US-08-836-455-2 (1-145) x US-09-924-099-19 (1-711)
QY 17 GlyThrArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGly 36
Db 379 GGTGGCGGATCGGACATCCAGATGACCCAGTCTCCATCTCTATCTGCTCTCTGGGA 438
QY 37 GlnArgValSerLeuThrCysArgAlaSerGlnAspIleGlyLeuAsnLeuHisTripleu 56
Db 439 GAAGAGTCACTCTCACTTCTCGGGCAAGTCAGGACATTTAGTAAATATTAATCTGCTT 498
QY 57 GlnGlnGluProAspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySer 76
Db 499 CAACAGCAACAGATGGAACCTTTTAAACGCTGATCTACGCCACATCCAGTTAGATTCT 558
QY 77 GlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSer 96
Db 559 GGTGTCCCAAGAGGTTTCAGTGGCAGTAGGTCTGGTGGTACAGATTATCTCTCACCATCAGC 618
QY 97 SerLeuGluSerGluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyr 116
Db 619 AGCTTCAGTCTGAAGATTTTGTAGACTATTACTGTCTACAAATATGCTAGTTCTCCGTAC 678
QY 117 ThrPheGlyGlyThrLysLeuGluIleLys 127
Db 679 ACGTTCCGAGGGGGGCAACAGCTGGCAATAAAA 711

QY 97 SerLeuGluSerGluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyr 116
Db 619 AGCTTCAGTCTGAAGATTTTGTAGACTATTACTGTCTACAAATATGCTAGTTCTCCGTAC 678
QY 117 ThrPheGlyGlyThrLysLeuGluIleLys 127
Db 679 ACGTTCCGAGGGGGGCAACAGCTGGCAATAAAA 711
RESULT 12
US-09-924-099-20
; Sequence 20, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 20
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of
; OTHER INFORMATION: SEQ
; OTHER INFORMATION: ID NO:10
US-09-924-099-20
Alignment Scores:
Pred. No.: 4.02e-54 Length: 729
Score: 502.00 Matches: 100
Percent Similarity: 91.89% Conservative: 2
Best Local Similarity: 90.09% Mismatches: 9
Query Match: 67.84% Indels: 0
DB: 10 Gaps: 0
US-08-836-455-2 (1-145) x US-09-924-099-20 (1-729)
QY 17 GlyThrArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGly 36
Db 379 GGTGGCGGATCGGACATCCAGATGACCCAGTCTCCATCTCTATCTGCTCTCTGGGA 438
QY 37 GlnArgValSerLeuThrCysArgAlaSerGlnAspIleGlyLeuAsnLeuHisTripleu 56
Db 439 GAAAGAGTCACTCTCACTTCTCGGGCAAGTCAGGACATTTAGTAAATATTAATCTGCTT 498
QY 57 GlnGlnGluProAspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySer 76
Db 499 CAACAGCAACAGATGGAACCTTTTAAACGCTGATCTACGCCACATCCAGTTAGATTCT 558
QY 77 GlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSer 96
Db 559 GGTGTCCCAAGAGGTTTCAGTGGCAGTAGGTCTGGTGGTACAGATTATCTCTCACCATCAGC 618
QY 97 SerLeuGluSerGluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyr 116
Db 619 AGCTTCAGTCTGAAGATTTTGTAGACTATTACTGTCTACAAATATGCTAGTTCTCCGTAC 678
QY 117 ThrPheGlyGlyThrLysLeuGluIleLys 127
Db 679 ACGTTCCGAGGGGGGCAACAGCTGGCAATAAAA 711


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; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; NAME/KEY: sig_peptide
; LOCATION: (39)...(104)
US-09-859-053-29

Alignment Scores:
Pred. No.:      2,78e-50      Length:      974
Score:          473.00      Matches:      95
Percent Similarity: 76.92%      Conservative: 15
Best Local Similarity: 66.43%      Mismatches: 33
Query Match:      63.92%      Indels:      0
DB:              10      Gaps:      0

US-08-836-455-2 (1-145) x US-09-859-053-29 (1-974)

QY      1  MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
Db      45  ATGAGGGTCCCGCTCAGCTCCTGGGGCTCTGCTGCTGCTGCTGCCAGGTTCCAGATGC 104

QY      21  AsnIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
Db      105 GACATCCAGATGACCCAGTCTCCATCTCCGTGCTGTCATCTGTAGGAGACAGAGTCACC 164

QY      41  LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnPro 60
Db      165 ATCACTGTGGCGGAGTCAGGTAATTAGCAGGTTGTTAGCCCTGGTATCAGCAGAAACCA 224

QY      61  AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
Db      225 GGGAAAGCCCCAAACTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 284

QY      81  ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
Db      285 AGGTTTCAGCGGAGTGGATCTGGCAGAGATTTCACTCTCACCATCAGCAGCCTGACGCT 344

QY      101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
Db      345 GAAGATTTTGCACCTTACTATTGTCAACAGGCTACAGGTTCCCGTGGAGCGTTGGGCCAA 404

QY      121 GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
Db      405 GGGACCAAGTGGAAATCAACAGCAACTGTGGCTGGCACCATCTCTTCTTCATCTTCCGCCCA 464

QY      141 SerSerLys 143
Db      465 TCTGATGAG 473
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Search completed: August 31, 2003, 01:08:46
Job time : 194.198 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 30, 2003, 22:11:21 ; Search time 1744.87 Seconds
(without alignments)
2019.725 Million cell updates/sec

Title: US-08-836-455-2
Perfect score: 740
Sequence: 1 MGAPQILGFLLLFPPTRC.....IKRADAAPTIVSIFPPSKLG 145

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2_1/USPTO.spool/US08836455/runat_29082003_132902_22290/app_query.fasta_1.654
-DB=EST -QPMF=fastap -SUFFIX=p2n.est -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR_SCORE=pcpt -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08836455.ecgn_1.1.3596.erunat_29082003_132902_22290 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	630	85.1	630	10	BF138788	BF138788 601780387
2	618	83.5	926	12	BG962572	BG962572 602829953
3	546	73.0	714	12	BG963548	BG963548 602831226
4	526	71.1	374	13	BY083003	BY083003 BY083003
5	516	69.7	874	10	BG518527	BG518527 602578261
6	509	68.8	827	12	BI152061	BI152061 602916512
7	506	68.4	669	10	BF123422	BF123422 601760623
8	504	68.1	762	10	BF144806	BF144806 601791486
9	500	67.6	886	10	BG756818	BG756818 602710291
10	498.5	67.4	891	10	BF579422	BF579422 602093833
11	497	67.2	1459	13	BQ918407	BQ918407 AGENCOURT
12	491	66.4	772	10	BF581992	BF581992 602099448
13	490	66.2	695	10	BE284224	BE284224 601099161
14	489	66.1	708	12	BI103114	BI103114 602889345
15	489	66.1	901	13	BQ943305	BQ943305 AGENCOURT
16	489	66.1	961	10	BG341988	BG341988 602463136
17	486	65.7	725	10	BF580940	BF580940 602100636
18	484	65.4	788	14	CB957342	CB957342 AGENCOURT
19	483	65.3	912	10	BF129120	BF129120 601811580
20	483	65.3	1100	10	BF663472	BF663472 602144635
21	482	65.1	464	2	HS070437	Bx480430 Homo sapi
22	482	65.1	685	10	BG518543	BG518543 602578277
23	481	65.0	767	14	CB985164	CB985164 AGENCOURT
24	481	65.0	813	10	BG431143	BG431143 602498773
25	480	64.9	943	10	BF976230	BF976230 602245105
26	479	64.7	1038	10	BG757218	BG757218 602710591
27	478	64.6	992	10	BF976253	BF976253 602245130
28	477	64.5	651	14	CA946490	CA946490 n107b12.x
29	477	64.5	796	14	CB986053	CB986053 AGENCOURT
30	477	64.5	830	12	BI455041	BI455041 603173343
31	477	64.5	977	14	CB984937	CB984937 AGENCOURT
32	476	64.3	626	10	BF582283	BF582283 602101109
33	476	64.3	764	14	CB956251	CB956251 AGENCOURT
34	476	64.3	807	14	CB957785	CB957785 AGENCOURT
35	474	64.1	639	12	BM819912	BM819912 K-EST0088
36	474	64.1	724	12	BI837410	BI837410 603086702
37	473.5	64.0	903	13	BQ706785	BQ706785 AGENCOURT
38	473	63.9	736	14	CB986552	CB986552 AGENCOURT
39	473	63.9	745	14	CB958128	CB958128 AGENCOURT
40	473	63.9	891	13	BX336281	BX336281 BX336281
41	472.5	63.9	767	14	CB958542	CB958542 AGENCOURT
42	472	63.8	837	14	CB984807	CB984807 AGENCOURT
43	471	63.6	740	14	CB956527	CB956527 AGENCOURT
44	471	63.6	785	14	CB986236	CB986236 AGENCOURT
45	471	63.6	797	14	CB987347	CB987347 AGENCOURT

ALIGNMENTS

RESULT 1
BF138788
LOCUS
DEFINITION 601780387F1 NCI_CGAP_Lu30 Mus musculus cdna clone IMAGE:4008404 5',
630 bp mRNA linear EST 24-OCT-2000
mRNA sequence.
ACCESSION BF138788
VERSION BF138788.1 GI:10977828
KEYWORDS EST.
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 630)

AUTHORS NTH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rc@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1AM9242 row: n column: 21
 High quality sequence stop: 628.
 Location/Qualifiers

source
 1. 630
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CZECH I"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:408404"
 /tissue_type="tumor, metastatic to mammary"
 /lab_host="DH10B"
 /clone_lib="NCI-CGAP_Lu30"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies.
 Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 162 a 158 c 150 g 160 t
 ORIGIN

Alignment Scores:
 Pred. No.: 4.83e-61 Length: 630
 Score: 630.00 Matches: 122
 Percent Similarity: 92.20% Conservative: 8
 Best Local Similarity: 86.52% Mismatches: 11
 Query Match: 85.14% Indels: 0
 DB: 10 Gaps: 0

US-08-836-455-2 (1-145) x BF138788 (1-630)

QY 3 AlaProAlaGlnLeuLeuGlyPheLeuLeuLeuPheProGlyThrArgCysAspIle 22
 Db 3 GCCTCGCGCAGGTTTGGCTTCTGTGCTGTGTTCCAGGTGCCAGATGGACATC 62
 QY 23 GlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSerLeuThr 42
 Db 63 CAGATGACCAGTCTCCATCTCTATCTGCTCTCTGGGAGAAAGATCAGTCTCACT 122
 QY 43 CysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGluProAspGly 62
 Db 123 TGGCGGCAAGTCAGGACATTTGGTGTAGCTTAACTTAACTTCAAGCAAGAACAGATGGA 182
 QY 63 ThrIleLysArgLeuIleTyAlaThrSerSerLeuGlySerGlyValProLysArgPhe 82
 Db 183 ACTATTAAACCCCTGATCTAGGCACATCCAGTTTAGATTCTGTGTGCCCAAAAGGTC 242
 QY 83 SerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSerGluAsp 102
 Db 243 AGTGGCAGTAGTCTGGGTGAGATATTCTCTCACCATCAGCAGCCCTTGAGTCTGAAGAC 302
 QY 103 PheValAlaTyTyCysLeuGlnTyAlaSerSerProTyrThrPheGlyGlyGlyThr 122
 Db 303 TTTTTCAGACATTACTCTTTTACATATGCTAGTTATCTCTCTCAGTTCGGTGTGGACC 362
 QY 123 LysLeuGlnIleLysArgAlaAspAlaAlaProThrValSerIlePheProProSer 142
 Db 363 AAGCTGAGGCTGAACGGGTGATGCTGCACCAACTGTATCCATCTTCCACCATTCAGT 422
 QY 143 Lys 143
 Db 423 GAG 425

RESULT 2
 BG962572
 LOCUS
 DEFINITION
 602829953F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4984788 5', mRNA sequence.
 ACCSSION
 BG962572
 VERSION
 BG962572.1 GI:14350209
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rc@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1AM10991 row: i column: 13
 High quality sequence stop: 685.
 Location/Qualifiers

source
 1. 926
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:4984788"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Co24"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 230 a 259 c 205 g 232 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.79e-59 Length: 926
 Score: 618.00 Matches: 117
 Percent Similarity: 91.61% Conservative: 14
 Best Local Similarity: 81.82% Mismatches: 12
 Query Match: 83.51% Indels: 0
 DB: 12 Gaps: 0

US-08-836-455-2 (1-145) x BG962572 (1-926)

QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 Db 15 ATGAGGTTCTCTGCTCAGCTTTTGGCTTCTGTGCTCTGCTGTTCCAGTACCAGATGT 74
 QY 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 Db 75 GACATCAGATGACCCAGTCTCCATCTCTCTCTCTCTGAGAAAGAGTCACT 134
 QY 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGluPro 60
 Db 135 CTCACCTTGTGGGCAAGTCAGGAAAGTGGTGTCTTAAAGTTGGCTTCAGCAAAACCA 194
 QY 61 AspGlyThrIleLysArgLeuIleTyAlaThrSerSerLeuGlySerGlyValProLys 80
 Db 195 GATGGAACTTTTAAAGCCGCTGATCTACCCCAACCACTTAGATTCTGGTGTCCCAAAA 254
 QY 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 Db 255 AGGTTTCAGTGGCAGTCTGGGTGAGATATTCTCTCACCCTCAGTACGCTTGAGTCT 314

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QY 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 315 GAGATTTCACACTATTAATCTCTACATATGCTAAATATTCCTGGAGCTTCGGTGA 374

QY 121 GlyThrLysLeuGlnLeuLysArgAlaAspAlaProThrValSerIlePheProPro 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 375 GGCACACGGCTGGAAATCAACGGCTGATGCTGCACCACTGTATCCATCTTCCACCA 434

QY 141 SerSerLys 143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 435 TCCAGTGAG 443

RESULT 3
BG963548
LOCUS 714 bp mRNA linear EST 12-JUN-2001
DEFINITION 60283126F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4985791 5',
    mRNA sequence.
ACCESSION BG963548
VERSION BG963548.1 GI:14351185
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 714)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL NTH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished
    Contact: Robert Strausberg, Ph.D.
    Email: cygaps-re@mail.nih.gov
    Tissue Procurement: Jeffrey E. Green, M.D.
    cDNA Library Preparation: Life Technologies, Inc.
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: L1AM10994 row: c column: 08
    High quality sequence stop: 712.
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            /strain="FVB/N"
            /db_xref="taxon:10090"
            /clone="IMAGE:4985791"
            /lab_host="DH10B (T1 phage-resistant)"
            /clone_lib="NCI_CGAP_Co24"
            /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
            Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.6 kb. Constructed by Life
            Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 189 a 178 c 167 g 180 t
ORIGIN
Alignment Scores:
Pred. No.: 8.55e-51 Length: 714
Score: 540.00 Matches: 108
Percent Similarity: 82.98% Conservative: 9
Best Local Similarity: 76.60% Mismatches: 24
Query Match: 12.97% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-2 (1-145) x BG963548 (1-714)

QY 3 AlaProAlaGlnIleLeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCysAspIle 22
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 22 GCTCCTGCTCAGTTCTTCTGGCATCTTGTGCTGTTCCAGGTGCAGATGTGACCTC 81

QY 23 GlnMetThrGlnSerProSerSerLeuGlnAlaSerLeuGlnArgValSerLeuThr 42
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 82 CAGATGATTCAGTCTCCATGCTCCATGTTTGCCTCTCTGGGAGACAGTGTGCTCTCT 141

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QY 43 CysArgAlaSerGlnAspIleGlyIleAsnLeuHistrPleuGlnGlnProAspGly 62
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 142 TGTCCGACTAGTCAGGCATTCAGAGTAATTTAGACTGGTATCAGCAGAACCCAGGTGA 201

QY 63 ThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLysArgPhe 82
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 202 ACTATTAAAGTCTGTACTCTACTCCACATCAATTTAAATTTCTGTGTCTCCATCAAGGTT 261

QY 83 SerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSerGluAsp 102
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 262 AGTGGCAGTGGTCTGGTCTCAGATTATCTCTCACCATCAGCAGCTAGAGTCTGAAGAT 321

QY 103 PheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGlyThr 122
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 322 TTTCACACTATTAATCTCTACACGTCGTCATCCGTCGTCGTCGTCGTCGTCGTCGTC 381

QY 123 LysLeuGlnIleLysArgAlaAspAlaAlaProThrValSerIlePheProProSer 142
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 382 AAGCTGGAATCAACACGGCTGATGCTGCACCACTGTATCCATCTTCCACCATCCAGT 441

QY 143 Lys 143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 442 GAG 444

RESULT 4
BG963003
LOCUS 374 bp mRNA linear EST 07-DEC-2002
DEFINITION BY083003 RIKEN full-length enriched, pooled tissues, adult spleen,
    etc. Mus musculus cDNA clone K630040M06 5', mRNA sequence.
ACCESSION BY083003
VERSION BY083003.1 GI:26193211
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 374)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
    Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H.,
    Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,
    Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A.,
    Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S.,
    Beisel, K. W., Blake, J. A., Brad, D., Brusic, V., Chotha, C., Corbani,
    L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest,
    A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,
    Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J.,
    Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M.,
    King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons,
    P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki,
    H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perle, G.,
    Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D.,
    Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring,
    B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sample, C. A., Setou,
    M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale,
    R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,
    Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa,
    M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,
    Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura,
    M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
    Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,
    Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., D., Shibata,
    K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander,
    E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
    Analysis of the mouse transcriptome based on functional annotation
    of 60,770 full-length cDNAs
    Nature 420, 563-573 (2002)
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
    Laboratory for Genome Exploration Research Group, RIKEN Genomic
    Sciences Center (GSC), Yokohama Institute
    The Institute of Physical and Chemical Research (RIKEN)

```

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@esc.riken.go.jp,
URL: http://genome.esc.riken.go.jp/

Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source Location/Qualifiers

1..374
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_lib="R630040M06"
/clone_lib="RIKEN full-length enriched, pooled tissues, adult spleen, etc."
/note="(dev_stage=adult,tissue_type=spleen,sex=male), (dev_stage=adult,tissue_type=kidney,sex=male), (dev_stage=adult,tissue_type=testis,sex=male), (dev_stage=adult,tissue_type=thymus,sex=male), (dev_stage=adult,tissue_type=heart,sex=male), (dev_stage=adult,tissue_type=colon,sex=male), (dev_stage=adult,tissue_type=stomach,sex=male), (dev_stage=adult,tissue_type=liver,sex=male), (dev_stage=13 days embryo,tissue_type=whole body,sex=mix), (dev_stage=14 days embryo,tissue_type=whole body,sex=mix), (dev_stage=16 days embryo,tissue_type=whole body,sex=mix), (dev_stage=17 days embryo,tissue_type=whole body,sex=mix), (dev_stage=15 days pregnant, adult,tissue_type=amniion,sex=female), (dev_stage=10 days neonate,tissue_type=brain,sex=mix), (dev_stage=10 days neonate,tissue_type=thymus,sex=mix), (dev_stage=10 days neonate,tissue_type=heart,sex=mix)"

BASE COUNT 88 a 89 c 85 g 111 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 1.44e-49 Length: 374
Score: 526.00 Matches: 105
Percent Similarity: 94.74% Conservative: 3
Best Local Similarity: 92.11% Mismatches: 6
Query Match: 71.08% Indels: 0
DB: 13 Gaps: 0

US-08-836-455-2 (1-145) x BY083003 (1-374)

Qy 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
Db 33 ATGAGGGCTCTGCACAGATTTTGGCTCTCTGTGCTCTCTGTTCCAGGTACCAGATGT 92
Qy 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlnArgValSer 40

Db 93 GACATCCAGATGACCCAGTCTCCATCTCTCTATCTGCTCTCTGGGAGAAAGAGTCAGT 152
Qy 41 LeuThrCysArgAlaSerGlnAsnIleGlyLeuHisTrpLeuGlnGlnGluPro 60
Db 153 CTCACCTTGTGGGCAAGTCAGGACATTTGGTAGTAGCTTAACCTGGCTTCAGCAGACCA 212
Qy 61 AspGlyThrIleLysArgLeuIleTyAlaThrSerSerLeuGlySerGlyValProLys 80
Db 213 GATGGAACCTATTAAACGCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTNCCCAA 272
Qy 81 ArgPheSerGlySerArgSerGlySerAspTySerLeuThrIleSerSerLeuGluSer 100
Db 273 AGGTTTCAGTGGCAGTAGTCTGGTCAGATTTCTTCACCATCAGCAGCCTTGAGTCT 332
Qy 101 GluAspPheValAlaTyTrCysLeuGlnTyAlaSerSer 114
Db 333 GAACATTTGTAGACTATTACTGTCTACAAATATGCTAGTTCT 374

RESULT 5

BG518527 874 bp mRNA linear EST 02-APR-2001
LOCUS 602578261F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491798 5',
DEFINITION mRNA sequence.
ACCESSION BG518527
VERSION BG518527.1 GI:13513491
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LIAW8536 row: i column: 15

High quality sequence stop: 843.

FEATURES

source

1..874
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C2ECH II"
/db_xref="taxon:10090"
/clone_image="IMAGE:3491798"
/tissue_type="spontaneous tumor, metastatic to mammary. Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 234 a 232 c 205 g 203 t

ORIGIN

Alignment Scores:

Pred. No.: 5.73e-48 Length: 874
Score: 516.00 Matches: 102
Percent Similarity: 79.72% Conservative: 12
Best Local Similarity: 71.33% Mismatches: 29
Query Match: 69.73% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-2 (1-145) x BG518527 (1-874)

QY 1 MetGlyAlaProLagInIleLeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCys 20
 DB 35 ATGAGGCCCCCTGCTAGTCTTTTGGGATCTTGTGCTCTGTTTCCAGGTATCAGATGT 94
 QY 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 DB 95 GACATCAAGATGACCCAGTCTCCATCTCCATGATGATCGCTGGGAGAGAGTCACT 154
 QY 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGluPro 60
 DB 155 ATCATTGCAAGCGGAGTCAAGACATTAAGCTATTAAGCTGGTACACAGACAAACCA 214
 QY 61 AspGlyThrIleLysArgLeuIleTyAlaThrSerSerLeuGlySerGlyValProLys 80
 DB 215 TGGAAATCTCTTAAGACCCCTGATCTATTATGCAACAGCTTGGCAGATGGGCTCCCATCA 274
 QY 81 ArgPheSerGlySerArgSerGlySerAspTySerLeuThrIleSerSerLeuGluSer 100
 DB 275 AGATTGAGTGGCAGTGGATCTGGCAGAGATTATCTTAACCATCAGCAGCCTGGAGTCT 334
 QY 101 GluAspPheValAlaTyTrpCysLeuGlnTyAlaSerSerProTyTrpPheGlyGly 120
 DB 335 GAGCATACAGCAACTTATTACTGCTACAGCATGGTGAGAGCCGTTACGTTCCGATCG 394
 QY 121 GlyThrIleGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
 DB 395 GGGACCAAGCTGGAATAAAACGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA 454
 QY 141 SerSerLys 143
 DB 455 TCCAGTGAG 463

RESULT 6
 BIL52061 602916512F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5066931 5',
 LOCUS mRNA sequence.
 DEFINITION BIL52061
 VERSION BIL52061.1 GI:14612062
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 827)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM1180 row: h column: 04
 High quality sequence stop: 827.
 Location/Qualifiers
 FEATURES
 source
 1. 827
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="Czech II"
 /db_xref="taxon:10090"
 /clone="IMAGE:5066931"
 /tissue_type="spontaneous tumor, metastatic to mammary."
 Stem cell origin.
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Lu29"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Salt;
 Site_2: NotI; Cloned unidirectionally. Primer: oligo dr.
 Library constructed by Life Technologies. Investigator

BASE COUNT 235 a 219 c 180 g 193 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.3e-47 Length: 827
 Score: 509.00 Matches: 100
 Percent Similarity: 82.35% Conservative: 12
 Best Local Similarity: 73.53% Mismatches: 24
 Query Match: 68.78% Indels: 0
 DB: 12 Gaps: 0
 US-08-836-455-2 (1-145) x BIL52061 (1-827)
 QY 8 LeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCysAspIleGlnMetThrGlnSer 27
 DB 35 TTGGGTCTCTGTTGCTCTGTTTCAAGGTACCATGATGTATCCAGATGACACACT 94
 QY 28 ProSerSerLeuSerAlaSerLeuGlyGlnArgValSerLeuThrCysArgAlaSerGln 47
 DB 95 ACATCTCTCCCTGCTCTCTCTGGGAGACAGAGTACCATCAGTTCAGGGCAAGTCAG 154
 QY 48 AspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluProAspGlyThrIleLysArgLeu 67
 DB 155 GACATTAGCAATATTATTTAAACTGGTATCAGCAGAAACCATGGAAGTGTAAACTACTG 214
 QY 68 IleTyAlaThrSerSerLeuGlySerGlyValProLysArgPheSerGlySerArgSer 87
 DB 215 ATCTACTACATCAAGATTACACTCAGGAGTCCCATCAGGTTCAGTTCGCGGTCT 274
 QY 88 GlySerAspTyTrpSerLeuThrIleSerSerLeuGluSerGluAspPheValAlaTyTrp 107
 DB 275 GGGACAGATTATTCTCTCACTATTAGCAACTGGCAACAAGATATTGCCACTTACTTT 334
 QY 108 CysLeuGlnTyAlaSerSerProTyTrpPheGlyGlyThrIleLysLeuGluIleLys 127
 DB 335 TGCCACAGGATGATAGCATCCGATACGTTCGGATCGGGGACCAAGCTGGAATAAAAA 394
 QY 128 ArgAlaAspAlaAlaProThrValSerIlePheProSerSerLys 143
 DB 395 CGGCTGATGCTGCACCAACTGTATCCATCTTCCACCATCCAGTGAG 442
 RESULT 7
 BIL23422 601760623F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4023749 5',
 LOCUS mRNA sequence.
 DEFINITION BIL23422
 VERSION BIL23422.1 GI:10962462
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 669)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM9282 row: n column: 06
 High quality sequence stop: 649.
 Location/Qualifiers
 FEATURES
 source
 1. 669
 /organism="Mus musculus"
 /mol_type="mRNA"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1692 row: e column: 23
High quality sequence stop: 864.

FEATURES
source
1..886
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4850686"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH-MGC_48"
Note: "Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
BASE COUNT 211 a 238 c 219 g 197 t 1 others

Alignment Scores:
Pred. No.: 3,76e-46 Length: 886
Score: 500.00 Matches: 100
Percent Similarity: 79.72% Conservative: 14
Best Local Similarity: 69.93% Mismatches: 29
Query Match: 67.57% Indels: 0
DB: 10 Gaps: 0
US-08-836-455-2 (1-145) x BG756818 (1-886)

QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
DB 16 ATGAGGTCCTCCGCTCAGCTCGTGGGCTCCTGCTGCTGGTTCCAGGTGCAGGTGT 75
QY 21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlnArgValSer 40
DB 76 GACATCAGATGACCCAGTCTCCATCTCCCTGCTGCAATCTGTAGGACAGAGTCAAC 135
QY 41 LeuThrCysArgAlaSerGlnAspIleGlyLeuAsnLeuHisTrpLeuGlnGluPro 60
DB 136 ATCACTTCGGCGCAAGTCAGGCAATGAGAATGATTAGCTGGTATCAGCAACCA 195
QY 61 AspGlyThrIleLysArgLeuIleTyAlaThrSerSerLeuGlySerGlyValProLys 80
DB 196 GGGAAAGCCCTAAGCGCTGATCTATGCTGCATCCAGTTGCAAAAGTGGGTCCCATCA 255
QY 81 ArgPheSerGlySerArgSerGlySerAspTySerLeuThrIleSerSerLeuGluSer 100
DB 256 AGTTTCAGCGGAGTGGATCTGGACAGAAATCACTCTCAATCAGCAGCCGTGCAGCCT 315
QY 101 GluAspPheValAlaTyTrCysLeuGlnTyAlaSerSerProTyTrThrPheGlyGly 120
DB 316 GAAGATTTCGAACCTATTACTCTACACGATTAATAGTTACCGGTACACATTTGGCGTG 375
QY 121 GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140

Db 376 GGGACCAAGCTGGAGATCAACGAACGTGGTGCACCACTGTCTTTCATCTTCCCGCCA 435
QY 141 SerSerLys 143
Db 436 TCTGATCAG 444
RESULT 10
BF579422 891 bp mRNA linear EST 12-DEC-2000
LOCUS 602093833F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208144 5'
DEFINITION mRNA sequence.
ACCESSION BF579422
VERSION BF579422.1 GI:11653134
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9772 row: a column: 09
High quality sequence stop: 711.
FEATURES
source
1..891
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4208144"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 246 a 226 c 204 g 215 t
ORIGIN
Alignment Scores:
Pred. No.: 5,6e-46 Length: 891
Score: 498.50 Matches: 101
Percent Similarity: 79.72% Conservative: 13
Best Local Similarity: 70.63% Mismatches: 29
Query Match: 67.36% Indels: 1
DB: 10 Gaps: 0
US-08-836-455-2 (1-145) x BF579422 (1-891)
QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
DB 13 ATGAGGACCCCTGCTCAGTTCTTGGAAATCTTGTGCTCTGGTTCCAGGTATCAATGT 72
QY 21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlnArgValSer 40
DB 73 GACATCAAGATGACCCAGTCTCCATCTCCATCTCTCATCTCTAGGAGAGAGTCACT 132
QY 41 LeuThrCysArgAlaSerGlnAspIleGlyLeuAsnLeuHisTrpLeuGlnGluPro 60
DB 133 ATCACTTGCAGCGGAGTCCAGACATTAATAGCTATTATTAAGCTGGTTCAGCAACCA 192
QY 61 AspGlyThrIleLysArgLeuIleTyAlaThrSerSerLeuGlySerGlyValProLys 80

Db 193 GGAATCTCCT -AAGACCCCTGATCTATCGTACAAACAGAAATGATAGCTGGGTCCTCCGCTCA 251
 Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 Db 252 AGGTTCAAGTGGCAGTGGGACAGATATTCTCTCACCATCAGCAGTCTGGATAT 311
 Qy 101 GluAspPheValAlaTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 Db 312 GAAGATATGGAAATTTATTATTTGCTACAGTATGATGATGTTCCGTACAGCTCGGAGGG 371
 Qy 121 GlyThrLysLeuGluLysArgAlaAspAlaProThrValSerIlePheProPro 140
 Db 372 GGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTCCCA 431
 Qy 141 SerSerLys 143
 Db 432 TCCAGTGAG 440

RESULT 11
 BQ918407
 LOCUS
 DEFINITION AGENCOURT 8895602 NCI_CGAP_Co24 Mus musculus CDNA clone
 IMAGE:6397382 5', mRNA sequence.
 ACCESSION BQ918407
 VERSION BQ918407.1 GI:22333105
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1459)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1459 row: c column: 15
 High quality sequence start: 165
 High quality sequence stop: 634.

FEATURES

source
 1..1459
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:6397382"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Co24"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 393 a 441 c 306 g 315 t 4 others
 ORIGIN

Alignment Scores:

Pred. No.: 1.55e-45 Length: 1459
 Score: 497.00 Matches: 99
 Percent Similarity: 80.42% Conservative: 16
 Best Local Similarity: 69.23% Mismatches: 28
 Query Match: 67.16% Indels: 0
 DB: 13 Gaps: 0

US-08-836-455-2 (1-145) x BQ918407 (1-1459)

Qy 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 Db 190 ATGATGCTCTCTCAGTTCCCTGGTCTCTCTGCTGCTCTTTCTTAGGTTCCAGATGT 249
 Qy 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 Db 250 GAAATCCAGATGACACAGACTACATCTCTCTGCTGCTCTCTCTGGAGACAGAGTCA 309
 Qy 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnPro 60
 Db 310 ATCACTTGCAGTCAAGTCAGGACATAGTAATATTATTAACCTGGTATCAGCAGAACCA 369
 Qy 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 Db 370 GATGGAACATTTAAACTCCTGATCTACTACACATCAAAATATACACTCAGAAGTCCCATCA 429
 Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 Db 430 AGGTTCAAGTGGCAGTGGGCTGGAAACAGATATTCTCTCACCATTACCACTCGAGCAA 489
 Qy 101 GluAspPheValAlaTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 Db 490 GAGGATATTGCCACTTACTTTTGCACAGGGTAATACACTTCCTGGAGCTTCGGTGA 549
 Qy 121 GlyThrLysLeuGluLysArgAlaAspAlaProThrValSerIlePheProPro 140
 Db 550 GGCACCAAACTAGAAAGTCAATCGGGCTGATGCTGCACCAACTGTATCCATCTCCCA 609
 Qy 141 SerSerLys 143
 Db 610 TCCAGTGAG 618

RESULT 12

BQ918407
 LOCUS
 DEFINITION 602099448F1 NCI_CGAP_Co24 Mus musculus CDNA clone EST 12-DEC-2000
 mRNA sequence.
 ACCESSION BQ918407
 VERSION BQ918407.1 GI:11655613
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 772)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1459 row: o column: 11
 High quality sequence stop: 715.

FEATURES

source
 1..772
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4219618"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Co24"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 216 a 204 c 175 g 176 t 1 others

Search completed: August 31, 2003, 01:02:01
Job time : 1748.87 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 31, 2003, 00:02:06 ; Search time 2967.15 seconds
(without alignments)
1999.191 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 145

Sequence: 1 MGAQAQILGFLILLFPGR.....IKRADAAPTVSIFPPSSKILG 145

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5773148

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-O/cgn2_1/USPTO.spool/US08836455/runat.29082003_132953_23045/app_query.fasta_1.654
-DB=GenEmbl -QFW=fastap -SUFFIX=p2noli.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
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1: gb_ba:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
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17: em_hum:*
18: em_in:*
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20: em_on:*
21: em_or:*
22: em_ov:*
23: em_pat:*
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27: em_sts:*
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32: em_htg_other:*
33: em_htg_mus:*
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35: em_htg_rod:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_hgtgo_hum:*
40: em_hgtgo_mus:*
41: em_hgtgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	145	100.0	435	6	AR164505	AR164505 Sequence
2	145	100.0	435	6	BD085737	BD085737 Methods o
3	125	86.2	381	10	AF124721	AF124721 Mus muscu
4	33	22.8	387	6	AR169918	AR169918 Sequence
5	31	21.4	535	6	BD021878	BD021878 Humanized
6	30	20.7	438	6	E09035	E09035 cDNA encodi
7	30	20.7	438	6	I32991	I32991 Sequence 45
8	30	20.7	452	10	AB050077	AB050077 Mus muscu
9	30	20.7	453	10	AB050084	AB050084 Mus muscu
10	30	20.7	456	10	MUSIGKCNK	M19914 Mouse Ig re
11	29	20.0	218	10	MMVJIG	X54757 Mouse reart
12	29	20.0	269	10	MMVJIG7	X54760 Mouse reart
13	29	20.0	273	10	MMU21066	U21066 Mus musculus
14	29	20.0	276	6	AR026090	AR026090 Sequence
15	29	20.0	276	6	AR026094	AR026094 Sequence
16	29	20.0	276	10	MMVJIG12	X54765 Mouse reart
17	29	20.0	279	10	MMVKMRB11	X63811 M.musculus
18	29	20.0	283	10	AF144956	AF144956 Mus muscu
19	29	20.0	285	10	MMU29617	U29617 Mus musculus
20	29	20.0	300	10	AF137626	AF137626 Mus muscu
21	29	20.0	302	10	MMU55588	U55588 Mus musculus
22	29	20.0	303	10	MUSIGLAFA	M36246 Mouse Ig ka
23	29	20.0	306	10	MUSIGKAPT	M64168 Mus musculus
24	29	20.0	321	10	AF163749	AF163749 Mus muscu
25	29	20.0	321	10	MUSIGKAA3	M5920 Mouse Ig ge
26	29	20.0	323	10	AY229938	AY229938 Mus muscu
27	29	20.0	324	6	AX722008	AX722008 Sequence
28	29	20.0	324	6	E54967	E54967 Peptide. 1/
29	29	20.0	324	6	I03643	I03643 Sequence 4
30	29	20.0	324	6	I07835	I07835 Sequence 4
31	29	20.0	324	10	MUSX	L48667 Mus musculus
32	29	20.0	326	10	MMVJIG3	X54756 Mouse reart
33	29	20.0	348	10	MMVJIG	X54755 Mouse reart
34	29	20.0	354	10	AB089681	AB089681 Mus muscu
35	29	20.0	381	10	AF045495	AF045495 Mus muscu
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38	29	20.0	384	10	AB017434	AB017434 Mus muscu
39	29	20.0	390	10	MUSIKCC	L41880 Mus musculus
40	29	20.0	407	6	E54981	E54981 Peptide. 1/
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42	29	20.0	447	6	AR03800	AR03800 Sequence
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45	29	20.0	455	10	AB050082	AB050082 Mus muscu

ALIGNMENTS

RESULT 1

AR164505
LOCUS AR164505 435 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6274143.
ACCESSION AR164505
VERSION AR164505.1 GI:162237555
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 435)
AUTHORS Chatterjee, M. and Foon, K.A.
TITLE Methods of delaying development of HMFG-associated tumors using anti-idiotypic antibody 11D10
JOURNAL Patent: US 6274143-A 1 14-AUG-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 100 a 111 c 102 g 122 t
ORIGIN
Alignment Scores:
Pred. No.: 4.91e-142 Length: 435
Score: 145.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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US-08-836-455-2 (1-145) x AR164505 (1-435)
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Qy 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
Db 61 GACATCCAGATGACCCAGTCTCCATCTCTATCTGCTCTGGGACAAAGATGATGAT 120
Qy 41 LeuThrCysArgAlaSerGlnAspIleGlyLeuLeuLeuHisTrpLeuGlnGluPro 60
Db 121 CTCATTGTCTGGGCAAGTCAGGACATGGTATTAACTTACATTTGGCTTCAGCAGGAACCA 180
Qy 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
Db 181 GATGGAACTATTAAACGCCCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCAAA 240
Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
Db 241 AGGTTCAAGTGGCAGTAGGTCCTGGGTACAGATTATTCTCTCACCATCAGCAGCTTGAGTCT 300
Qy 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaThrSerSerProTyrThrPheGlyGly 120
Db 301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCGATGCTACAGTTTCGGAGGG 360
Qy 121 GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
Db 361 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCAACCA 420
Qy 141 SerSerLysLeuGly 145
Db 421 TCCAGTAAGCTTGGG 435
RESULT 2
BD085737
LOCUS BD085737 435 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods of delaying development of HMFG-associated tumors using anti-idiotypic antibody 11D10.
ACCESSION BD085737
VERSION BD085737.1 GI:22631347
KEYWORDS JP 2001523269-A/1.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 435)
AUTHORS Chatterjee, M. and Foon, K.A.
TITLE Methods of delaying development of HMFG-associated tumors using anti-idiotypic antibody 11D10
JOURNAL Patent: JP 2001523269-A 1 20-NOV-2001;
COMMENT THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
OS Unidentified
PN JP 2001523269-A/1
PD 20-NOV-2001
PF 12-JUN-1998 JP 1999503252
PR 13-JUN-1997 US 60/049540, 11-JUN-1998 US 09/096244 PI
PC A61K39/395, A61K39/39//C07K16/42
CC Strandedness: Single;
CC Topology: Linear;
CC Methods of delaying development of HMFG-associated tumors CC
using
CC anti-idiotypic antibody 11D10
FH Key Location/Qualifiers
FT CDS 1..435
FT mat peptide 61.
FEATURES
source Location/Qualifiers
BASE COUNT 100 a 111 c 102 g 122 t
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Alignment Scores:
Pred. No.: 4.91e-142 Length: 435
Score: 145.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
Db 61 GACATCCAGATGACCCAGTCTCCATCTCTATCTGCTCTGGGACAAAGATGATGAT 120
Qy 41 LeuThrCysArgAlaSerGlnAspIleGlyLeuLeuLeuHisTrpLeuGlnGluPro 60
Db 121 CTCATTGTCTGGGCAAGTCAGGACATGGTATTAACTTACATTTGGCTTCAGCAGGAACCA 180
Qy 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
Db 181 GATGGAACTATTAAACGCCCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCAAA 240
Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
Db 241 AGGTTCAAGTGGCAGTAGGTCCTGGGTACAGATTATTCTCTCACCATCAGCAGCTTGAGTCT 300
Qy 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaThrSerProTyrThrPheGlyGly 120
Db 301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCGATGCTACAGTTTCGGAGGG 360
Qy 121 GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
Db 361 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCAACCA 420
Qy 141 SerSerLysLeuGly 145
Db 421 TCCAGTAAGCTTGGG 435
RESULT 3
AF124721


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C12N15/00,
PC C12N5/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.38% Indels: 0
DB: 6 Gaps: 0
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QY 115 ProTyrThrPheGlyGlyThrLysLeuGlulileLysArgAlaAspAlaProThr 134
Db 373 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAACGGGCTGATGCTGCACCAACT 432
QY 135 ValSerIlePheProSerSerLysLeuGly 145
Db 433 GTATCCATCTCCCAACCATCCAGTAAGCTTGGG 465
RESULT 6
E09035
LOCUS E09035.1 GI:22025661
DEFINITION E09035 438 bp RNA linear PAT 29-SEP-1997
CDNA encoding light chain variable region of mouse antiidiotype
antibody named Idiol7 against CLN-IgG idiotype.
ACCESSION E09035
VERSION E09035.1 GI:22025661
KEYWORDS JP 1995101999-A/7.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
    1 (bases 1 to 438)
Hagiwara.H. and Aozuka.Y.
AMINO ACID SEQUENCE OF ANTI-IDIOTYPE ANTIBODY TO ANTI-CANCER HUMAN
MONOCLONAL ANTIBODY AND DNA BASE SEQUENCE CODING FOR THE SAME
Patent: JP 1995101999-A 7 18-APR-1995;
HAGIWARA YOSHIHIDE
OS Mus musculus (mouse)
PN JP 1995101999-A/7
PD 18-APR-1995
PF 06-OCT-1993 JP 1993272950
PI HAGIWARA HIDEAKI, AOZUKA YASUYUKI
PC C07K16/42,C12N5/10,C12N15/02,C12N15/09,C12P21/08,(C12P21/08,
CC C12R1:91);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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        /clone="17Kb1"
    1..39
FT sig_peptide
    40..438
FT mat_peptide
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    antibody named Idiol7 against CLN-IgG FT
    idiotype"
    1..438
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BASE COUNT 104 a 120 c 112 g 102 t
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Alignment Scores:
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Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.69% Indels: 0
DB: 6 Gaps: 0
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QY 116 TyrThrPheGlyGlyThrLysLeuGlulileLysArgAlaAspAlaProThrVal 135
Db 334 TACACGTTCCGAGGGGGACCAAGCTGGAATAAACGGGCTGATGCTGCACCAACTGTA 393
QY 136 SerIlePheProSerSerLysLeuGly 145
Db 394 TCCATCTCCCAACCATCCAGTAAGCTTGGG 423
RESULT 7
I32991
LOCUS I32991
DEFINITION I32991 Sequence 45 from patent US 5589573.
ACCESSION I32991
VERSION I32991.1 GI:1823782
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 438)
AUTHORS Hagiwara,H. and Aotsuka,Y.
TITLE Amino acid sequences of anti-idiotypic antibodies against
anti-cancer human monoclonal antibody, and DNA base sequences
encoding those sequences
Patent: US 5589573-A 45 31-DEC-1996;
JOURNAL
FEATURES
    source
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            Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 9.31e-22 Length: 438
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0

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US-00-03

US-08-030-433-Z (1-143) X AB030084 (1-433)

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Db      363  TACAGTTCGAGGGGACCAACAGCTGGAATAAACAAGGGCTGATGCTGCACCAACTGTA 422
Qy      136  SerIlePheProSerSerLysLeuGly 145
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Db      423  TCCATCTTCCACCATCCAGTAAGCTGGG 452

RESULT 10
MUSIGKCNK
LOCUS
DEFINITION Mouse Ig rearranged kappa-chain mRNA, clone AN12K.
ACCESSION M19914 J03832
VERSION M19914.1 GI:197035
KEYWORDS C-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 56)
AUTHORS Rule,G.S.
JOURNAL Unpublished (1988)
REFERENCE 2 (bases 1 to 456)
AUTHORS Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.
TITLE Sequences of 12 monoclonal anti-dinitrophenyl spin-label antibodies for NMR studies
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3661-3665 (1988)
MEDLINE 88234486
PUBMED 3375235
COMMENT Original source text: Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
Draft entry and computer-readable sequence [2] kindly submitted by G.Rule, 20-JUL-1988.
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mat_peptide 91..>456
BASE COUNT 118 a 114 c 108 g 116 t
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Alignment Scores:
Pred. No.: 9.66e-22 Length: 456
Score: 30.00 Matches: 30
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.69% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-2 (1-145) x MUSIGKCNK (1-456)

Qy      113  SerSerProThrPheGlyGlyThrLysLeuGluIleLysArgAlaAspAlaAla 132
          |||||
Db      367  AGTCTCCGTACAGTTCGAGGGGGACCAAGCTGGAATAAACAAGGGCTGATGCTGCA 426

Qy      133  ProThrValSerIlePheProProSer 142
          |||||
Db      427  CCAACTGTATCATCTCTCCACCATCCAGT 456

RESULT 11
MUSIGKCNK
LOCUS
DEFINITION Mouse rearranged kappa immunoglobulin light chain (V,J).
ACCESSION X54757
VERSION X54757.1 GI:21998639
KEYWORDS Ig light chain; immunoglobulin.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 218)
AUTHORS Harada,K. and Yamagishi,H.
TITLE Lack of feedback inhibition of V kappa gene rearrangement by productively rearranged alleles
JOURNAL J. Exp. Med. 173 (2), 409-415 (1991)
MEDLINE 91108338
PUBMED 1988542
REFERENCE 2 (bases 1 to 218)
AUTHORS Yamagishi,H.
TITLE Direct Submission
JOURNAL Submitted (02-OCT-1990) Yamagishi H., Dept of Biophysics Faculty of Science Kyoto University, Sakyo-ku Kyoto 606, Japan
FEATURES
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    1..218
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            /clone="MSI-N102"
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misc_feature 179..216
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Pred. No.: 5.46e-21 Length: 218
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
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US-08-836-455-2 (1-145) x MMVJIG4 (1-218)

Qy      76  SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
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Db      60  TCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGTGCAGATTATTCTCTCACCATC 119

Qy      96  SerSerLeuGluSerGluAspPheVal 104
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Db      120  AGCAGCCTTGCAGTCTGAAGATTGTGA 146

RESULT 12
MMVJIG7
LOCUS
DEFINITION Mouse rearranged kappa immunoglobulin light chain (V,J).

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JOURNAL
FEATURES
Technology
Patent: US 5855885-A 44 05-JAN-1999;
Location/Qualifiers

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source 1..276
BASE COUNT 68 a 65 c 80 t
ORIGIN
Alignment Scores:
Pred. No.: 6.77e-21 Length: 276
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 6 Gaps: 0

US-08-836-455-2 (1-145) x AR026090 (1-276)
QY 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
Db 142 TCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGGCTGGGTCTGAGATTATCTCTCACCATC 201
QY 96 SerSerLeuGluSerGluAspPheVal 104
Db 202 AGCAGCCTTGAGTCTGAAGATTGTA 228

RESULT 15
AR026094 LOCUS 276 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 52 from patent US 5855885.
ACCESSION AR026094
VERSION AR026094.1 GI:5936934
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 276)
AUTHORS Smith,R., McCafferty,J., Chiswell,D., Darsley,M.J., Fitzgerald,K.,
Kenten,J.H., Martin,M.T., Titmas,R.C. and Williams,R.O.
TITLE Isolation and production of catalytic antibodies using phage
technology
JOURNAL Patent: US 5855885-A 52 05-JAN-1999;
FEATURES
Location/Qualifiers
source 1..276
BASE COUNT 67 a 65 c 64 g 80 t
ORIGIN
Alignment Scores:
Pred. No.: 6.77e-21 Length: 276
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 6 Gaps: 0

US-08-836-455-2 (1-145) x AR026094 (1-276)
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QY 96 SerSerLeuGluSerGluAspPheVal 104
Db 202 AGCAGCCTTGAGTCTGAAGATTGTA 228

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GenCore version 5.1.6
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Title: US-08-836-455-2

Perfect score: 145

Sequence: 1 MGAQAQILGFLLLFPGR.....IKRAAPATVTSIFPPSSKLG 145

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Searched: 2552756 seqs, 1349719017 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5103490

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_19Jun03:.*
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:.*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:.*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:.*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:.*
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:.*
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:.*
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:.*
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:.*
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:.*
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:.*
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:.*
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:.*
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:.*
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:.*
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:.*
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:.*
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:.*
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:.*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:.*
25: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	145	100.0	435	18	AAT85149	Murine monoclonal
2	145	100.0	435	20	AAV83772	Antibody 11D10 lig
3	145	100.0	435	25	AAV51273	Murine 11D10 antibo
4	33	22.8	387	18	AAT77851	Murine anti-human
5	33	22.8	387	24	AAV32138	Murine 44H104 mab
6	31	21.4	535	19	AAV20086	Consensus DNA sequ
7	30	20.7	438	16	AAQ90431	DNA encoding anti-
8	29	20.0	276	20	AAQ00879	Mouse derived RT3
9	29	20.0	276	20	AAQ00875	Mouse derived RT3
10	29	20.0	321	21	AAA38908	520C9 hybridoma VL
11	29	20.0	324	21	AA249534	Mouse anti-IL-18 a
12	29	20.0	390	25	AAV52607	Escherichia coli 1
13	29	20.0	407	21	AA249548	Mouse light chain
14	29	20.0	447	17	AAT31332	Anti-idiotypic mono
15	29	20.0	447	20	AAT31365	MAB 1A7 light chai
16	29	20.0	447	20	AA289552	Light chain variab
17	29	20.0	450	4	AA30165	Sequence encoding
18	29	20.0	711	21	AA249542	pESCFV#125-2H reco
19	29	20.0	729	21	AA249543	pESCFV#125-2H.HT r
20	29	20.0	739	14	AA046084	Sequence encoding
21	29	20.0	739	17	AAT36880	520C9 anti-c-erbB-
22	29	20.0	739	19	AAV21798	520C9 anti-c-erbB-
23	29	20.0	739	20	AAV63399	520C9 sfv DNA sequ
24	29	20.0	756	24	AA597136	P4-3 single chain
25	29	20.0	771	24	AA597142	P5-10 single chain
26	29	20.0	1497	24	AA597145	3B10xP4-3 bispecif
27	29	20.0	1605	14	AA046086	Sequence encoding
28	28	19.3	321	21	AA338909	650E2 hybridoma VL
29	28	19.3	456	22	AA66996	Filamentous phage
30	28	19.3	639	10	AA91657	Chimeric antibody
31	28	19.3	642	18	AA91657	Mouse monoclonal a
32	28	19.3	651	21	AAA44346	Human secreted exp
33	28	19.3	652	17	AAT87818	Antibody 3c2 light
34	28	19.3	654	25	ACC44908	TSH receptor antib
35	28	19.3	654	25	ACC44909	TSH receptor antib
36	28	19.3	678	21	AA27849	WOW-1 Fab light ch
37	28	19.3	698	25	ABX16574	Mouse DNA encoding
38	28	19.3	723	16	AAQ92503	Mouse antibody F4-
39	28	19.3	738	21	AA261037	Nucleotide sequenc
40	28	19.3	867	22	AA667002	Filamentous phage
41	28	19.3	979	24	ABS2791	Murine m166 antibo
42	27	18.6	366	13	AAQ27140	ICAM-1 inhibiting
43	27	18.6	429	18	AAT70811	Mouse anti-idiotyp
44	27	18.6	465	16	AAQ85387	MAB 4197X light ch
45	27	18.6	882	14	AAQ48038	Monoclonal antiod

ALIGNMENTS

RESULT 1

AAT85149
ID AAT85149 standard; cDNA; 435 BP.

AC AAT85149;

DT 25-MAR-2003 (updated)

DT 04-JAN-1998 (first entry)

XX Murine monoclonal anti-idiotypic antibody 11D10 VL cDNA.

XX Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;

KW human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss.

KX Mus musculus.

OS Mus musculus.

XX Key Location/Qualifiers

FH Key Location/Qualifiers

FT sig_peptide 1..60
 FT /*tag= a
 FT mat_peptide 61..435
 FT /*tag= b
 XX
 PN WO9272699-A2.
 XX
 PD 26-JUN-1997.
 XX
 XX 19-DEC-1996; 96WO-US20757.
 XX
 XX 20-DEC-1995; 95US-0575762.
 PR 26-JAN-1996; 96US-0591965.
 PR 13-DEC-1996; 96US-0766350.
 XX
 XX (KENT) UNIV KENTUCKY.
 PA
 XX Chatterjee M, Chatterjee SK, Foon KA;
 PI
 XX
 DR WPI; 1997-341690/31.
 DR P-PSDB; AAW27119.
 XX
 XX Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
 PT against human milk fat globule disease associated tumours,
 PT especially breast cancer
 XX
 PS Claim 11; Page 94; 130pp; English.
 XX
 XX This cDNA sequence encodes the light chain variable region VL
 CC (AAW85149) of monoclonal anti-idiotypic antibody 11D10 produced by
 CC hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
 CC naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotypic
 CC response. It elicits an immune response against a specific epitope
 CC of a high mol.wt. mucin of human milk fat globule (HMFG). It
 CC induces an immunological response to HMFG in mice, rabbits, monkeys
 CC and patients with advanced HMFG-associated tumours. Pharmaceutical
 CC compositions and vaccines comprising 11D10, 11D10 polypeptides
 CC and/or 11D10 polynucleotides are claimed. Also claimed are
 CC diagnostic kits and methods of using 11D10, 11D10 polypeptides
 CC and/or 11D10 polynucleotides, including methods of treating HMFG-
 CC associated tumours.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;

Alignment Scores:
 Pred. NO.: 1.09e-124 Length: 435
 Score: 145.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 18 Gaps: 0

US-08-836-455-2 (1-145) x AAT85149 (1-435)

Qy 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 Db 1 ATGGGGGCCCTGCTCAGATTCTTGGGTCTTGTGCTCTGTTCAGGTACCATGATG 60
 Qy 21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlnArgValSer 40
 Db 61 GACATCCAGATGACCCAGTCCATCTCTTATCTGCTCTCTGGGACAAAGAGTCACT 120
 Qy 41 LeuThrCysArgAlaSerGlnAspileGlyIleAsnLeuHisTrpLeuGlnGluPro 60
 Db 121 CTCACCTGTTCGGGCAAGTCAGGACATGGTATTAACTTACATTCGCTTCAGCAGAACCA 180
 Qy 61 AspGlyThrIleLysArgLeuIleTyAlaThrSerSerLeuGlySerGlyValProLys 80
 Db 181 GATGGAATATTAAACCCCTGATCTACGCCATCCAGTTAGGTTCTGGTGTCCCAAA 240
 Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100

Db 241 AGTTTCAGTGGCAGTAGGTCTGGGTCTGAGATTATTTCTCTCACCATCAGCAGCCTTGAGTCT 300
 Qy 101 GluAspPheValAlaIleTyrCysLeuGlnIleTyrAlaSerProTyrThrPheGlyGly 120
 Db 301 GAAGATTTTGTAGCTTATTACTGCTACATATGCTAGTATTCGCTACAGTTCGGAGG 360
 Qy 121 GlyThrLysLeuGlnIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
 Db 361 GGGACCAAGCTGGAATAAAACGGCTGATGTCACCAACTGTATTCATCTTCCCAACA 420
 Qy 141 SerSerLysLeuGly 145
 Db 421 TCCAGTAAGCTTGGG 435
 RESULT 2
 AAV83772
 ID AAV83772 standard; cDNA; 435 BP.
 XX
 AC AAV83772;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Antibody 11D10 light chain variable region coding sequence.
 XX
 KW Murine; mouse; antibody; light chain; variable region; anti-idiotypic; ss;
 KW human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..435
 FT /*tag= a
 FT /product= "antibody 11D10 light chain variable region"
 FT /transl_except= (pos:163..165, aa:Thr)
 FT /note= "no stop codon is given at the 3' end of the
 FT sequence"
 FT sig_peptide 1..60
 FT /*tag= b
 FT mat_peptide 61..435
 FT /*tag= c
 XX
 PN WO9856419-A1.
 XX
 PD 17-DEC-1998.
 XX
 PF 12-JUN-1998; 98WO-US12250.
 XX
 PR 11-JUN-1998; 98US-0096244.
 PR 13-JUN-1997; 97US-0049540.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 XX Chatterjee M, Foon KA;
 XX
 XX WPI; 1999-060029/05.
 DR P-PSDB; AAW87593.
 XX
 PT Delaying development of, or treating, HMFG-associated tumours -
 PT using anti-idiotypic antibody 11D10 raised against antibodies to
 PT human milk fat globule protein
 XX
 PS Disclosure; Fig 1; 54pp; English.
 XX
 CC This sequence represents the coding sequence for the murine antibody
 CC 11D10 light chain variable region. This anti-idiotypic antibody is used
 CC to delay the development of, or treat, a human milk fat globule (HMFG)
 CC associated tumour in an individual having low tumour burden.
 CC The antibody 11D10 is used to prevent the recurrence of HMFG-associated
 CC tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma,
 CC especially for treating breast tumours.
 XX
 SQ Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;

Alignment Scores:

Pred. No.: 1.09e-124 Length: 435
 Score: 145.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-08-836-455-2 (1-145) x AAV83772 (1-435)

QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 DB 1 ATGGGGCCCTCCTCAGATCTTGGGTTCTTGTCTCTGTTCCAGGTACAGATGT 60
 QY 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCCTCTCTGGACAAAGAGTCAGT 120
 QY 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGluPro 60
 DB 121 CTCACCTGTGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGGCTTCAGCAGGAACCA 180
 QY 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 DB 181 GATGGAACTATTAAACGCCCTGATCTAGCCACATCCAGTTAGTCTGTGTGCCCAAA 240
 QY 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 DB 241 AGGTTTCAGTGGCAGTAGGTCGGTCAGATTTATCTCACCATCAGCAGCCTTGAGTCT 300
 QY 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 DB 301 GAAGATTTGTAGCCCTATTACTCTACAAATATGCTAGTTCCTCGTACACGTTCCGAGGG 360
 QY 121 GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
 DB 361 GGGACCAAGCTGGAATAAAACGGCTGATGCTGCACCACTGTATCCATCTTCCCAACA 420
 QY 141 SerSerLysLeuGly 145
 DB 421 TCCAGTAAGCTTGGG 435

RESULT 3

AAL51273

ID AAL51273 standard; cDNA; 435 BP.

XX AC AAL51273;

XX DT 20-MAR-2003 (first entry)

XX DE Mouse 11D10 antibody light chain variable region coding sequence.

XX KW Mouse; murine; gens; ss; vaccine; tumour; human milk fat globules; HMFG;

XX KW carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour;

XX KW CEA-associated tumour; anti-idiotype antibody.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT CDS 1..435

FT /tag= a

FT /partial

FT /product= "Mouse 11D10 anti-idiotype antibody light chain

FT variable region"

FT /note= "No stop codon is given"

FT sig_peptide 1..60

FT /tag= b

FT mat_peptide 61..435

FT /tag= c

XX WO200292012-A2.

XX PN 21-NOV-2002.

XX PD

XX

XX 17-MAY-2002; 2002WO-US15840.

XX 17-MAY-2001; 2001US-0861294.

XX (KENT) UNIV KENTUCKY RES FOUND.

XX Chatterjee M, Foon KA;

XX WPI: 2003-129216/12.

XX P-PSDB; AAO16292.

XX Use of anti-idiotypic antibodies for human milk fat globules (HMFG)- or

XX carcinoembryonic antigen (CEA)-associated tumor for delaying the

XX development of, or treating a HMFG- or CEA-associated tumor (e.g.

XX breast tumor) in humans

XX Disclosure; Fig 1; 98pp; English.

XX The invention comprises a method for delaying the development of, or

XX treating a tumour that is associated with human milk fat globules (HMFG)

XX or carcinoembryonic antigen (CEA). The method of the invention involves

XX administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an

XX anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for

XX delaying the development, of or treating HMFG/CEA-associated tumours. The

XX present cDNA sequence encodes the light chain variable region of the

XX mouse 11D10 anti-idiotype antibody.

XX SQ Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;

Alignment Scores:

Pred. No.: 1.09e-124 Length: 435
 Score: 145.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0

US-08-836-455-2 (1-145) x AAL51273 (1-435)

QY 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
 DB 1 ATGGGGCCCTCCTCAGATCTTGGGTTCTTGTCTCTGTTCCAGGTACAGATGT 60
 QY 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
 DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCCTCTCTGGACAAAGAGTCAGT 120
 QY 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGluPro 60
 DB 121 CTCACCTGTGGGCAAGTCAGGACATTTGGTATTAACTTACATTTGGCTTCAGCAGGAACCA 180
 QY 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
 DB 181 GATGGAACTATTAAACGCCCTGATCTAGCCACATCCAGTTAGTCTGTGTGCCCAAA 240
 QY 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
 DB 241 AGGTTTCAGTGGCAGTAGGTCGGTCAGATTTATCTCACCATCAGCAGCCTTGAGTCT 300
 QY 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
 DB 301 GAAGATTTGTAGCCCTATTACTCTACAAATATGCTAGTTCCTCGTACACGTTCCGAGGG 360
 QY 121 GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
 DB 361 GGGACCAAGCTGGAATAAAACGGCTGATGCTGCACCACTGTATCCATCTTCCCAACA 420
 QY 141 SerSerLysLeuGly 145
 DB 421 TCCAGTAAGCTTGGG 435

RESULT 4

AAAT77851
ID AAAT77851 standard; cDNA; 387 BP.

XX
AC AAAT77851;

XX
DT 03-NOV-1997 (first entry)

XX
DE Murine anti-human class II monoclonal antibody 44H104 VL chain cDNA.

XX
KW Antibody; light chain; variable region; hybridoma cell line 44H104;
KW immune response; enhance; stimulate; vaccine; immunodiagnosis;
KW antigen delivery; ss.

XX
OS Mus musculus.

XX
FH Key Location/Qualifiers

FT CDS 1..387

FT /*tag= a

FT /note= "Encodes 44H104 light chain variable region,
including secretion signal; termination
codon not given"

XX
PN W09640941-AL.

XX
PD 19-DEC-1996.

XX
PF 07-JUN-1996; 96WO-CA00400.

XX
PR 07-JUN-1995; 95US-0483576.

XX
PA (CONN-) CONNAUGHT LAB LTD.

XX
PI Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH;

XX
WPI; 1997-077271/07.

XX
P-PSDB; AAW22537.

XX
PT Recombinant conjugate antibody mol., modified for delivering an
PT antigen - elicits enhanced immune response without the use of
PT adjuvant to generate antibodies which are useful in vaccines or
PT immuno:diagnosis

XX
PS Example 1; Fig 1A; 64pp; English.

XX
CC Novel recombinant conjugate antibody molecules comprise a monoclonal
CC antibody specific for a surface structure of antigen presenting
CC cells (APC), genetically modified to contain at least one antigen
CC exclusively at one or more preselected sites. The conjugate is capable
CC of delivering the antigen to APC and eliciting an immune response to
CC the antigen. The new conjugates are useful as vaccines and are able
CC to elicit an enhanced immune response without the use of an adjuvant.
CC In a specific example, a conjugate was constructed using the murine
CC anti-human class II monoclonal antibody secreted by hybridoma
CC 44H104. The peptide CLPB36 was chosen as antigen; it consists of
CC a tandemly linked T and B cell epitope derived from HIV MN strain.
CC The present sequence encodes the light chain variable region which
CC was PCR amplified from 44H104 and used in the preparation of a
CC conjugate with antigen CLPB36.

XX
SQ Sequence 387 BP; 90 A; 95 C; 90 G; 112 T; 0 other;

Alignment Scores:

Pred. No.: 2.25e-21 Length: 387
Score: 33.00 Matches: 33
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.76% Indels: 0
DB: 18 Gaps: 0

US-08-836-455-2 (1-145) x AAAT77851 (1-387)

QY 15 PheProGlyThrArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSer 34
|||||

Db 49 TTTCAGGTACCATGATGTGACATCCAGATGACATCCAGATGACATCCATCTTATCTGCTCT 108

QY 35 LeuGlyGlnArgValSerLeuThrCysArgAlaSerGln 47
|||||

Db 109 CTGGACAAAGAGTCAGTCTCCTGTCGGGCAAGTCAG 147

RESULT 5

AAAD32138

ID AAD32138 standard; DNA; 387 BP.

XX
AC AAD32138;

XX
DT 18-JUN-2002 (first entry)

XX
DE Murine 44H104 mab variable light chain (VL) DNA.

XX
KW Murine; mab; light chain; VL; conjugate antibody; antigen delivery;
KW immune system; vaccine; detecting agent; antibacterial; gene; ds.

XX
OS Mus sp.

XX
FH Key Location/Qualifiers

FT CDS 1..387

FT /*tag= a

FT /product= "Murine 44H104 mab VL"

FT /transl_except= (pos:277..279, aa:Thr)

FT /note= "This translation exception occurs while

decoding for murine mab VL alternative version

(AAE20204); CDS does not include stop codon"

FT /partial

XX
PN US2002025315-A1.

XX
PD 28-FEB-2002.

XX
PF 14-JAN-1998; 98US-0007093.

XX
PR 14-JAN-1998; 98US-0007093.

XX
PA (ANAN/) ANAND N N.

XX
PA (BARB/) BARBER B H.

XX
PA (CATE/) CATES G A.

XX
PA (CATE/) CATERINI J E.

XX
PA (KLEI/) KLEIN M H.

XX
PI Anand NN, Barber BH, Cates GA, Caterini JE, Klein MH;

XX
WPI; 2002-267519/31.

XX
P-PSDB; AAE20200, AAE20204.

XX
PT Novel recombinant conjugate antibody, useful as a vaccine against
PT pathogens having a specific antigen, comprises a monoclonal antibody
PT specific for an antigen presenting cell surface structure -

XX
PS Example 1; Fig 1A; 28pp; English.

XX
CC The invention relates to a recombinant conjugate antibody, comprising
CC a monoclonal antibody specific for a surface structure of antigen
CC presenting cells genetically modified to contain an antigen moiety
CC for the purpose of delivery of the antigen moiety to antigen-
CC presenting cells of the immune system. The conjugate antibody is
CC formulated as a vaccine to protect a host against a disease caused
CC by a pathogen expressing the antigen. The antibody is useful as a
CC detecting agent. The present sequence is murine 44H104 mab variable
CC light chain (VL) DNA.

XX
SQ Sequence 387 BP; 90 A; 95 C; 90 G; 112 T; 0 other;

Alignment Scores:

Pred. No.: 2.25e-21 Length: 387
Score: 33.00 Matches: 33
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 22.76% Indels: 0
DB: 24 Gaps: 0

US-08-836-455-2 (1-145) x AAD32138 (1-387)

QY 15 PheProGlyThrArgCysAspIleGlnMetThrGlnSerProSerLeuSerAlaSer 34
|||||
DB 49 TTTCCAGGTACCATGTGACATCCAGATGACCATCTCCATCTCTTATCTGCTCT 108

QY 35 LeuGlyGlnArgValSerLeuThrCysArgAlaSerGln 47
|||||
DB 109 CTGGGACAAAGATGATCTACTTGTGGGCAAGTCAG 147

RESULT 6
AAV20086
ID AAV20086 standard; DNA: 535 BP.
XX
AC AAV20086;
XX
DT 14-JUL-1998 (first entry)
XX
DE Consensus DNA sequence of the murine variable light chain region.
XX
KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
KW humanised antibody; murine antigen binding region; inhibition;
KW leukocyte infiltration of tissue; treatment; inflammatory disease;
KW inflammatory bowel disease; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 16..435
FT FT /*tag= a
FT FT /note= "no stop codon given"
FT FT
FT sig_peptide 16..75
FT FT /*tag= b
FT mat_peptide 76..435
FT FT /*tag= c
XX
XX WO9806248-A2.
XX
XX
XX PD 19-FEB-1998.
XX
XX PF 06-AUG-1997; 97WO-US13884.
XX
XX PR 15-AUG-1996; 96US-0700737.
XX
XX PA (LEUK-) LEUKOSITE INC.
XX
XX PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
XX PI Saldanha J;
XX
XX DR WPI; 1998-159172/14.
XX DR P-PSDB; AAV53817.
XX
XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
XX used for treating inflammatory disease, pancreatitis, diabetes,
XX asthma, graft versus host disease and sarcoidosis
XX
XX PS Example 1; Fig 3; 145pp; English.
XX
XX
XX The present sequence represents the consensus nucleotide sequence
XX comprising the variable region of murine Act-1 antibody determined from
XX several independent mouse light chain variable region clones. Act-1 is
XX active against human alpha4-beta7 integrin. Muscosal adressin cell
XX adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
XX The Act-1 antibody interferes with alpha4-beta7 integrin binding to
XX MadCAM-1, which is present of high endothelial venules in mucosal
XX lymph nodes. Variable regions were amplified from DNA encoding Act-1
XX using degenerate PCR primers AAV20083-84. The degeneracy of the PCR
XX primers produced several different sequences, of which the present
XX sequence is a consensus sequence. The present sequence was used to

CC construct chimeric, humanised Act-1 antibodies, which contain murine
CC antigen binding regions. The humanised immunoglobulin can be used to
CC inhibit the interaction of cells bearing alpha4-beta7 with cells bearing
CC a ligand for alpha4-beta7. It can be used for inhibiting leukocyte
CC infiltration of tissues, e.g. for treating inflammatory diseases such
CC as inflammatory bowel disease. The immunoglobulin can also be used for
CC detection, isolation and diagnosis.
XX
SQ Sequence 535 BP; 126 A; 128 C; 132 G; 149 T; 0 other;

Alignment Scores:
Pred. No.: 2.14e-19 Length: 535
Score: 31.00 Matches: 31
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.38% Indels: 0
DB: 19 Gaps: 0

US-08-836-455-2 (1-145) x AAV20086 (1-535)

QY 115 ProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAspAlaProThr 134
|||||
DB 373 CCGTACACGTCGGAGGGGGACCAAGCTGGAAATAAACGGGCTGATGTCACCAACT 432

QY 135 ValSerIlePheProProSerSerLysLeuGly 145
|||||
DB 433 GTATCCATCTCCACCATCCAGTAAGCTTGGG 465

RESULT 7

AAQ90431
ID AAQ90431 standard; DNA: 438 BP.
XX
AC AAQ90431;

DT 02-FEB-1996 (first entry)
XX
DE DNA encoding anti-idiotypic antibody Idiol7 clone 17KB1.
XX
KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW complementarity determining region, ds.
XX
OS Mus sp.

FH Key Location/Qualifiers
FT CDS 1..438
FT FT /*tag= a
FT FT /product= anti-idiotypic_antibody_Idiol7
FT FT 1..39
FT sig_peptide /*tag= b

JP07101999-A.
XX
XX PN 18-APR-1995.
XX
XX PD 06-OCT-1993; 93JP-0272950.
XX
XX PF 06-OCT-1993; 93JP-0272950.
XX
XX PR (HAGI/) HAGIWARA Y.
XX
XX PA WPI; 1995-182987/24.
XX
XX DR P-PSDB; AAR74966.
XX
XX

Novel anti-idiotypic antibody against an human anticancer monoclonal
PT antibody - and DNA sequences encoding the antibody, useful in
PT pharmacology, medicine and biochemical fields.
XX
XX Example 5; Page 19; 28pp; Japanese.

AAQ90425-Q90434 are DNA molecules encoding anti-idiotypic antibodies
CC Idiol3, Idiol7, Idiol20, Idiol27 and Idiol33 against a human anticancer
CC monoclonal antibody. These antibodies and DNA encoding them are useful
CC in pharmacological, medical and biochemical fields of research.

```

XX SQ Sequence 438 BP; 104 A; 120 C; 112 G; 102 T; 0 other;
Alignment Scores:
Pred. No.: 1.48e-18 Length: 438
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.69% Indels: 0
DB: 16 Gaps: 0

US-08-836-455-2 (1-145) x AAQ90431 (1-438)
Qy 116 TyrThrPheGlyGlyThrLysLeuGluLeuLysArgAlaAspAlaProThrVal 135
Db 334 TACACGTTCCGAGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAACTGTA 393
Qy 136 SerTlePheProSerSerLysLeuGly 145
Db 394 TCCATCTCCACCACCATCCAGTAAGCTTGGG 423

RESULT 8
AAX00879
ID AAX00879 standard; DNA; 276 BP.
XX
AC AAX00879;
XX
DT 29-MAR-1999 (first entry)
XX
DE Mouse derived RT3 phase antibody light chain pattern C genetic sequence.
XX
KW Catalytic; antibody; phase display; immunising; phase expression vector;
KW prodrug; scFv; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..276
FT /*tag= a
FT /note= "the start and stop codons are not indicated"
XX
PN US5855885-A.
XX
PD 05-JAN-1999.
XX
PF 14-JUL-1994; 94US-0273146.
XX
PR 22-JAN-1993; 93US-0007684.
PR 14-JUL-1994; 94US-0273146.
XX
PA (CHIS/) CHISWELL D.
PA (DARS/) DARSLEY M J.
PA (FITZ/) FITZGERALD K.
PA (KENT/) KENTEN J H.
PA (MART/) MARTIN M T.
PA (MCCA/) MCCAFFERTY J.
PA (SMIT/) SMITH R.
PA (TITM/) TITMAS R C.
PA (WILL/) WILLIAMS R O.
XX
XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;
XX
XX WPI; 1999-105036/09.
DR P-FSDB; AAW95480.
XX
XX Production of catalytic antibodies displayed on bacteriophages -
PT comprises generating a gene library of antibody-derived domains
PT inserting coding into a phase expression vector and isolating the
PT catalytic antibodies
XX
XX Example 4; Fig 11; 117pp; English.
XX

```

The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene library of antibody-derived domains; (b) inserting coding for the domains into a phase expression vector; and (c) isolating the catalytic antibodies. The phase expression vector incorporates a histidine peptide in tandem with a myc peptide. The catalytic antibodies can be isolated by preparing an antigen; optionally immunising an animal with the antigen; generating a library of VH and VL domains from the immunised animal; cloning the VH and VL domains into a phase expression vector to generate phage display antibodies; selecting phage display antibodies which bind specifically to the antigen; screening the selected phage display antibodies for catalytic activity to substrate; and isolating the catalytic antibodies, where the phase expression vector incorporates a histidine peptide in tandem with a myc peptide. The processes are used to produce catalytic antibodies, which can be used for in vivo activation of a prodrug. The present sequence represents a genetic sequence of light chain PCR pattern C from mouse derived RT3 phase antibodies.

Sequence 276 BP; 67 A; 65 C; 64 G; 80 T; 0 other;

Alignment Scores:

Pred. No.:	8.01e-18	Length:	276
Score:	29.00	Matches:	29
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	20.00%	Indels:	0
DB:	20	Gaps:	0

US-08-836-455-2 (1-145) x AAX00879 (1-276)

Qy 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
 Db 142 TCTGTGTCCTCCCAAGAGTTTCAGTGGCAGTAGTCTGGTCTCAGATTATCTCTCACCATC 201
 Qy 96 SerSerLeuGluSerGluAspPheVal 104
 Db 202 AGCAGCCTTCAGTCTGAGATTTCGTA 228

RESULT 9
 AAX00875
 ID AAX00875 standard; DNA; 276 BP.
 XX
 AC AAX00875;
 XX
 DT 29-MAR-1999 (first entry)
 XX
 DE Mouse derived RT3 phase antibody light chain pattern A genetic sequence.
 XX
 KW Catalytic; antibody; phase display; immunising; phase expression vector;
 KW prodrug; scFv; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..276
 FT /*tag= a
 FT /note= "the start and stop codons are not indicated"
 XX
 PN US5855885-A.
 XX
 PD 05-JAN-1999.
 XX
 PF 14-JUL-1994; 94US-0273146.
 XX
 PR 22-JAN-1993; 93US-0007684.
 PR 14-JUL-1994; 94US-0273146.
 XX
 PA (CHIS/) CHISWELL D.
 PA (DARS/) DARSLEY M J.
 PA (FITZ/) FITZGERALD K.
 PA (KENT/) KENTEN J H.
 PA (MART/) MARTIN M T.
 PA (MCCA/) MCCAFFERTY J.
 PA (SMIT/) SMITH R.
 PA (TITM/) TITMAS R C.
 PA (WILL/) WILLIAMS R O.
 XX
 XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
 PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;
 XX
 XX WPI; 1999-105036/09.
 DR P-FSDB; AAW95480.
 XX
 XX Production of catalytic antibodies displayed on bacteriophages -
 PT comprises generating a gene library of antibody-derived domains
 PT inserting coding into a phase expression vector and isolating the
 PT catalytic antibodies
 XX
 XX Example 4; Fig 11; 117pp; English.
 XX

PA (SMIT/) SMITH R.
 PA (TITM/) TITMAS R C.
 PA (WILL/) WILLIAMS R O.
 XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
 PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;
 XX WPI; 1999-105036/09.
 DR P-PSDB; AAW95476.
 XX Production of catalytic antibodies displayed on bacteriophages -
 PT comprises generating a gene library of antibody-derived domains
 PT inserting coding into a phage expression vector and isolating the
 PT catalytic antibodies
 XX Example 4; Fig 9A-F; 117pp; English.
 XX The invention relates to methods for producing catalytic antibodies
 CC displayed on a phage. The method comprises: (a) generating a gene library
 CC of antibody-derived domains; (b) inserting coding for the domains into a
 CC phage expression vector; and (c) isolating the catalytic antibodies. The
 CC phage expression vector incorporates a histidine peptide in tandem with a
 CC myc peptide. The catalytic antibodies can be isolated by preparing an
 CC antigen; optionally immunising an animal with the antigen; generating a
 CC library of VH and VL domains from the immunised animal; cloning the VH
 CC and VL domains into a phage expression vector to generate phage display
 CC antibodies; selecting phage display antibodies which bind specifically
 CC to the antigen; screening the selected phage display antibodies for
 CC catalytic activity to substrate; and isolating the catalytic antibodies
 CC where the phage expression vector incorporates a histidine peptide in
 CC tandem with a myc peptide. The processes are used to produce catalytic
 CC antibodies, which can be used for in vivo activation of a prodrug. The
 CC present sequence represents a genetic sequence of light chain pattern A
 CC from mouse derived RT3 phage antibodies.
 XX SQ Sequence 276 BP; 68 A; 65 C; 53 G; 80 T; 0 other;
 Alignment Scores:
 Pred. No.: 8,01e-18 Length: 276
 Score: 29.00 Matches: 29
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 20.00% Indels: 0
 DB: 20 Gaps: 0
 US-08-836-455-2 (1-145) x AAX00875 (1-276)
 QY 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
 Db 142 TCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGTGCAGATTATTCTCACCATC 201
 QY 96 SerSerLeuGluSerGluAspPheVal 104
 Db 202 AGCAGCCTTCAGTCTGAAGATTGTGA 228
 RESULT 10
 AAA38908
 ID AAA38908 standard; DNA; 321 BP.
 XX AC AAA38908;
 XX AC AAA38908;
 XX DT 29-AUG-2000 (first entry)
 XX DE 520C9 hybridoma VL domain encoding DNA SEQ ID NO:25.
 XX Antigen binding site; immunoglobulin; cancer antigen; immunological;
 KW antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;
 KW specific binding assay; affinity purification; drug targeting;
 KW toxin targeting; imaging; genetic; therapeutic; ss.
 XX OS Homo sapiens.
 XX OS US6054561-A.
 PN

XX 25-APR-2000.
 PD 07-JUN-1995; 95US-0483749.
 PF 21-MAR-1986; 86US-0842476.
 PR 08-MAY-1988; 88US-0190778.
 PR 08-FEB-1984; 84US-0577976.
 PR 11-JAN-1985; 85US-0690750.
 PR 11-AUG-1994; 94US-0288981.
 XX (CHIR) CHIRON CORP.
 PA Ring DB;
 XX WPI; 2000-338508/29.
 DR P-PSDB; AAY90824.
 XX Monoclonal antibody capable of binding to human breast cancer antigen
 PT useful for affinity purification, drug or toxin targeting, imaging, and
 PT treating cancer
 XX Disclosure; Fig 13; 57pp; English.
 XX The present invention describes a monoclonal antibody (MAB) (I) that
 CC binds to a human breast cancer antigen that is also bound by MAB 454C11
 CC and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also
 CC described is a hybridoma that produces (I). (I) is useful in specific
 CC binding assays, affinity purification, drug or toxin targeting, imaging,
 CC and genetic or immunological therapeutics for various cancers. The
 CC present sequence encodes a VL domain derived from a 520C9 hybridoma,
 CC which is used in the exemplification of the present invention.
 XX SQ Sequence 321 BP; 82 A; 78 C; 72 G; 89 T; 0 other;
 Alignment Scores:
 Pred. No.: 9,24e-18 Length: 321
 Score: 29.00 Matches: 29
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 20.00% Indels: 0
 DB: 21 Gaps: 0
 US-08-836-455-2 (1-145) x AAA38908 (1-321)
 QY 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
 Db 166 TCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGTGCAGATTATTCTCACCATC 225
 QY 96 SerSerLeuGluSerGluAspPheVal 104
 Db 226 AGTAGCCTTCAGTCTGAAGATTGTGA 252
 RESULT 11
 AAZ49534
 ID AAZ49534 standard; cDNA; 324 BP.
 XX AC AAZ49534;
 XX AC AAZ49534;
 XX DT 04-APR-2000 (first entry)
 XX DE Mouse anti-IL-18 antibody VL encoding cDNA from hybridoma #125-2H.
 XX Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
 KW hybridoma #125-2H; mouse; monoclonal antibody #125-2Hmab; interleukin-18;
 KW antiinflammatory; immunosuppressive; leucocytopenic; antialgic;
 KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
 KW immunopathy; inflammatory disorder; immunoreaction; ss.
 XX OS Mus musculus.
 XX OS
 XX PH Key Location/Qualifiers
 FT mat_peptide 1..324

```
FT      /*tag= a
XX      /label= Anti-IL-18_antibody_light_chain_variable_region
PN      EP974600-A2.
XX
XX
PD      26-JAN-2000.
XX
XX
PF      24-JUN-1999; 99EP-0304977.
XX
XX
PR      24-JUN-1998; 98JP-0177580.
XX
PR      12-OCT-1998; 98JP-0289044.
XX
PR      22-DEC-1998; 98JP-0365023.
XX
PA      (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX
PI      Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX
XX
DR      WPI; 2000-118341/11.
XX
DR      P-FSDB; AAY44587.
XX
XX
PT      New artificially produced peptide for neutralizing biological activity
PT      of interleukin-18, useful for treating and preventing immunopathies,
PT      inflammatory disorders and autoimmune diseases.
XX
XX
PS      Claim 11; Page 21; 36pp; English.
XX
XX
CC      The present cDNA sequence derived from hybridoma #125-2H, encodes mouse
CC      anti-interleukin-18 antibody light chain variable region (VL). It can be
CC      used in the production of recombinant monoclonal antibodies #125-2HmAb,
CC      which is capable of neutralising biological activities of interleukin-18.
CC      The antibody has antiinflammatory, immunosuppressive, leucocytopenetic,
CC      antiangiogenic, antipyretic, antiallergic and hepatotropic activity and can
CC      be used for prevention and treatment of autoimmune diseases, immunopathies
CC      and inflammatory disorders caused by excessive immunoreaction.
XX
XX
SQ      Sequence 324 BP; 83 A; 78 C; 76 G; 87 T; 0 other;

Alignment Scores:
Pred. No.:      9.32e-18      Length:      324
Score:      29.00      Matches:      29
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      20.00%      Indels:      0
DB:      21      Gaps:      0

US-08-836-455-2 (1-145) x AAZ49534 (1-324)

Oy      76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
      |||||
Db      166 TCTGGTGTCCCAAGAGGTTTCAGTGGCAGTAGGTCGTGGTCAGATTATCTCTCACCATC 225
      |||||

Oy      96 SerSerLeuGluSerGluAspPheVal 104
      |||||
Db      226 AGCAGCCTTGAGTCTGAAGATTGTGA 252
      |||||

RESULT 12
AAD52607
ID      AAD52607 standard; cDNA; 390 BP.
XX
XX
AC      AAD52607;
XX
XX
DT      14-MAY-2003 (first entry)
XX
XX
DE      Escherichia coli light chain variable region cDNA.
XX
XX
KW      S-surface antigen; Hepatitis B virus; HBV; therapy; infection; virucide;
KW      hepatotropic; gene; ss.
XX
OS      Escherichia coli.
XX
XX
FH      Key      Location/Qualifiers
FT      CDS      1..390
      /*tag= a
```

```
FT      /product= "Escherichia coli light chain variable region"
FT      /note= "CDS does not include start and stop codon"
FT      /partial
XX
XX
PN      WO200292819-A1.
XX
XX
PD      21-NOV-2002.
XX
XX
PF      15-MAY-2002; 2002WO-KR00905.
XX
XX
PR      16-MAY-2001; 2001KR-0026634.
XX
XX
PA      (YUHA-) YUHAN CORP.
XX
XX
PI      Lee JW, Ko IY, Kang HK, Song MY, Song TH, Kim CS;
XX
XX
DR      WPI; 2003-140281/13.
XX
DR      P-FSDB; AAE34366.
XX
XX
PT      New light and heavy chain variable regions of a monoclonal antibody
PT      against the S-surface antigen of the hepatitis B virus (HBV), useful
PT      for neutralizing or removing HBV, or for preventing or treating HBV
PT      infection.
XX
XX
PS      Claim 3; Page 15; 20pp; English.
XX
XX
CC      The invention relates to light and heavy chain variable regions of a
CC      monoclonal antibody against S-surface antigen of the hepatitis B virus
CC      (HBV). The variable regions of the antibodies are useful against HBV
CC      S-surface antigens, e.g. adr, adw, ayr or ayw, particularly for
CC      neutralising or removing HBV. They may also be employed to treat or
CC      prevent HBV infection. The present sequence is Escherichia coli light
CC      chain variable region cDNA.
XX
XX
SQ      Sequence 390 BP; 99 A; 96 C; 98 G; 97 T; 0 other;

Alignment Scores:
Pred. No.:      1.11e-17      Length:      390
Score:      29.00      Matches:      29
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      20.00%      Indels:      0
DB:      25      Gaps:      0

US-08-836-455-2 (1-145) x AAD52607 (1-390)

Oy      117 ThrPheGlyGlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSer 136
      |||||
Db      304 ACGTTCGGTGGAGGACCACCACTGGAATCAACAGGGCTGATGCTGCACCACTGTATCC 363
      |||||

Oy      137 IlePheProProSerSerLysLeuGly 145
      |||||
Db      364 ATCTTCCCAACCATCCAGTAAGCTTGGG 390
      |||||

RESULT 13
AAZ49548
ID      AAZ49548 standard; cDNA; 407 BP.
XX
XX
AC      AAZ49548;
XX
XX
DT      04-APR-2000 (first entry)
XX
XX
DE      Mouse light chain variable region DNA.
XX
XX
KW      Mouse light chain variable region; VL; variable region light chain;
KW      interleukin-18; immunopathies; inflammatory disorder; autoimmune disease;
KW      mouse; anti-allergic; anti-inflammatory; immunosuppressive;
KW      hematopoietic; leukocytopenetic; antiangiogenic; antipyretic; ds.
XX
OS      Mus musculus.
XX
OS      Synthetic.
XX
XX
FH      Key      Location/Qualifiers
FT
```

```

FT mat_peptide 1..407
FT /*tag= a
FT /product= "Mouse light chain variable region"
FT sig_peptide 1..60
FT /*tag= b
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PE 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX WPI; 2000-118341/11.
DR P-PSDB; AAY44599.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
XX Example 1; Page 28-29; 32pp; English.
XX
CC The present sequence encodes mouse light chain variable region. This
CC recombinant DNA is derived from PCR A which amplifies antibody light
CC chain variable region (VL). The transformant produced using the VL gene
CC was used to transform competent E. coli cells. The peptide produced by
CC transformants neutralizes interleukin-18. This is useful for treating and
CC preventing immunopathies, inflammatory disorders and autoimmune diseases
CC which are caused by excessive immunoreaction. The peptide has
CC anti-allergic, anti-inflammatory, immunosuppressive, hematopoietic,
CC leukocytopenic, antialgic, antipyretic and hepatic-function improving
CC activities.
XX
SQ Sequence 407 BP; 96 A; 99 C; 96 G; 116 T; 0 other;

Alignment Scores:
Pred. No.: 1.16e-17 Length: 407
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 21 Gaps: 0

US-08-836-455-2 (1-145) x AA249548 (1-407)

QY 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
Db 226 TCTGGTGTCCCAAGAGGTTCACTGGCAGTAGTCTGGGTCAGATTATCTCTCCCATC 285
QY 96 SerSerLeuGluSerGluAspPheVal 104
Db 286 AGCAGCGCTTGAGTCTCAAGATTGTGA 312

RESULT 14
AAT31332
ID AAT31332 standard; cDNA; 447 BP.
XX
AC AAT31332;
XX
XX 25-MAR-2003 (updated)
DT 26-FEB-1997 (first entry)
XX
XX Anti-idiotype monoclonal antibody 1A7 variable light chain, cDNA.
DE
XX Murine; mouse; anti-idiotype; monoclonal antibody; MAb; 1A7;
KW variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma;

```

```

KW glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;
KW malignant melanoma; soft tissue sarcoma; small cell carcinoma;
KW vaccine; treatment; palliate; detection; diagnosis;
KW recombinant production; purification; probe; primer; assay;
KW amplification; gene therapy; ss.
XX
OS Mus musculus.
XX
XX Key Location/Qualifiers
XX mat_peptide 1..446
XX /*tag= a
XX
XX WO9622373-A2.
XX
XX 25-JUL-1996.
XX
XX 17-JAN-1996; 96WO-US00882.
XX
XX 17-JAN-1995; 95US-0372676.
XX 16-JAN-1996; 96US-0591196.
XX 17-JAN-1995; 95US-0372676.
XX 16-JAN-1996; 96US-0591196.
XX
XX (KENT ) UNIV KENTUCKY.
XX
XX Chatterjee M, Chatterjee SK, Foon KA;
XX
XX WPI; 1996-354530/35.
XX P-PSDB; AAW03199.
XX
XX Monoclonal antibody 1A7 and related polynucleotide(s) and
XX polypeptide(s) - useful to treat or palliate a GD2-associated
XX disease, e.g. melanoma and glioma
XX
XX Claim 10; Fig 1; 14pp; English.
XX
XX The present sequence encodes the murine anti-idiotype monoclonal
XX antibody (MAb) 1A7 variable light chain. MAb 1A7 was raised against
XX the anti-ganglioside 2 (GD2) MAb 14G2a, which binds an unique
XX epitope of GD2. As the glycosphingolipid GD2 is expressed at high
XX density by human neuroectodermal tumours, e.g. malignant melanoma,
XX neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma
XX of the lung, MAb 1A7, or its cDNA can be used in a vaccine to treat
XX or palliate such diseases. They can also be used to reduce the
XX risk of recurrence of a clinically detectable tumour, and detect an
XX anti-GD2 Ab bound to a tumour cell.
XX
XX MAb 1A7 overcomes immune tolerance and induces an immune response
XX against GD2, which comprises anti-GD2 Ab (humoral response) and
XX GD2-specific cells (cellular response). It can be used to purify
XX anti-1A7 (Ab3), anti-GD2 (Ab1') or 14G2a (Ab1), detect anti-1A7 or
XX anti-GD2 in a sample or measure the level of cellular anti-1A7 or
XX anti-GD2 activity.
XX
XX The cDNA can be used in expression systems for 1A7 prodn., and in
XX the prepn. of probes and primers to respectively assay for 1A7
XX cDNA, and amplify desired polynucleotides for use in gene therapy.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 447 BP; 106 A; 110 C; 108 G; 123 T; 0 other;

Alignment Scores:
Pred. No.: 1.27e-17 Length: 447
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 17 Gaps: 0

US-08-836-455-2 (1-145) x AAT31332 (1-447)

QY 117 ThrPheGlyGlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSer 136
Db 361 ACCTTCGGTGGAGGCACCAAGCTGGGAATCAACGGGCTGTCTGCACCACTGTATCC 420

```

Search completed: August 31, 2003, 01:16:24
Job time : 218.987 secs

```
Qy 137 IlePheProProSerSerLysLeuGly 145
Db 421 ATCTTCCACCATCCAGTAAGCTTGGG 447

RESULT 15
AAZ31365
ID AAZ31365 standard; cDNA; 447 BP.
XX
AC AAZ31365;
XX
DT 07-FEB-2000 (first entry)
XX
DE MAB 1A7 light chain variable region encoding cDNA.
XX
KW Monoclonal antibody; MAB; 1A7; GD2; immune response; melanoma;
KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
KW tumor-associated antigen; ss.
XX
OS Synthetic.
OS Mus sp.
XX
FN US5977316-A.
XX
PD 02-NOV-1999.
XX
PF 16-JAN-1996; 96US-0591196.
XX
PR 17-JAN-1995; 95US-0372676.
XX
PA (KENT ) UNIV KENTUCKY.
XX
PI Foon KA, Chatterjee SK, Chatterjee M;
XX
DR WPI; 1999-619711/53.
DR P-PSDB; AAY49209.
XX
PT Monoclonal antibody 1A7 which elicits an anti-GD2 immunological
PT response, useful for the development of products for the detection and
PT treatment of cancers -
XX
PS Disclosure; Fig 1; 74pp; English.
XX
CC The invention provides a monoclonal antibody (MAB) designated 1A7, which
CC elicits an anti-GD2 (tumor-associated antigen) immunological response in
CC humans. MAB 1A7 has defined light and heavy chain variable region
CC sequences. The MAB 1A7 and polypeptides can be used for eliciting an
CC anti-GD2 immune response. The polypeptides can also be used for detecting
CC or purifying anti-GD2 antibody. The products can be used for treating GD2
CC -associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue
CC carcinoma, and small cell carcinoma. They can be used for palliating the
CC disease or for reducing the risk of recurrence. The present sequence
CC represents the cDNA encoding the light chain variable region of MAB 1A7.
XX
SQ Sequence 447 BP; 106 A; 111 C; 107 G; 123 T; 0 other;

Alignment Scores:
Pred. NO.: 1.27e-17 Length: 447
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 20 Gaps: 0

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Db 361 ACGTTCGGTGAGCCACCAAGCTGGAATCAACGGGCTGTGCTGCCAACCTGTATCC 420

Qy 137 IlePheProProSerSerLysLeuGly 145
Db 421 ATCTTCCACCATCCAGTAAGCTTGGG 447
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 31, 2003, 01:02:06 ; Search time 192.198 Seconds
(without alignments)
1730.853 Million cell updates/sec

Title: US-08-836-455-2
Perfect score: 145
Sequence: 1 MGAQAIGLFLLLPGTRC.....IKRAAPTVSIFPPSSKIG 145

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1533700 segs, 1147125425 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3063161

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=PublishedApplications.NA -QFMT=fastap -SUFFIX=p2noli.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNIQS-bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DALIGN=200 -THR SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pcr -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US08836455.ecgn_1.1_271_runat_29082003_132954_23062
-NCPU=6 -ICPU=3 -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : PublishedApplications.NA:

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- 2: /cgn2.6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2.6/ptodata/2/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2.6/ptodata/2/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2.6/ptodata/2/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2.6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
- 7: /cgn2.6/ptodata/2/pubpna/US08_NEW_PUB.seq:
- 8: /cgn2.6/ptodata/2/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2.6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
- 10: /cgn2.6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
- 11: /cgn2.6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
- 12: /cgn2.6/ptodata/2/pubpna/US09_NEW_PUB.seq:
- 13: /cgn2.6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
- 14: /cgn2.6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
- 15: /cgn2.6/ptodata/2/pubpna/US10_NEW_PUB.seq:
- 16: /cgn2.6/ptodata/2/pubpna/US60_NEW_PUB.seq:
- 17: /cgn2.6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	145	100.0	435	9 US-09-861-294-1 Sequence 1, Appli

2	145	100.0	435	12 US-10-367-506-1
3	33	22.8	387	9 US-09-007-093-1
4	29	20.0	324	10 US-09-924-099-11
5	29	20.0	351	8 US-08-779-784-16
6	29	20.0	351	8 US-08-779-784-17
7	29	20.0	390	13 US-10-146-305-5
8	29	20.0	402	8 US-08-779-784-5
9	29	20.0	407	10 US-09-924-099-27
10	29	20.0	447	10 US-09-990-205-1
11	29	20.0	447	14 US-10-153-401-1
12	29	20.0	711	10 US-09-924-099-19
13	29	20.0	729	10 US-09-924-099-20
14	29	20.0	739	10 US-09-887-853-5
15	28	19.3	390	12 US-10-268-883-10
16	28	19.3	698	13 US-10-006-773-18
17	26	17.9	426	10 US-09-840-459-95
18	26	17.9	426	10 US-09-840-459-101
19	26	17.9	705	12 US-10-281-479A-22
20	26	17.9	714	14 US-10-216-484-10
21	26	17.9	729	13 US-10-006-773-10
22	26	17.9	831	10 US-09-903-327A-3
23	26	17.9	5711	10 US-09-897-006-8
24	26	17.9	5711	11 US-09-897-511A-8
25	26	17.9	6255	11 US-09-897-006-13
26	26	17.9	6255	11 US-09-897-511A-13
27	25	17.2	447	9 US-09-797-481-1
28	25	17.2	447	9 US-09-844-736-3
29	25	17.2	447	9 US-09-861-294-19
30	25	17.2	447	12 US-10-367-506-19
31	25	17.2	447	14 US-10-162-396-3
32	25	17.2	504	13 US-10-006-773-14
33	21	14.5	351	11 US-09-469-485-3
34	21	14.5	363	11 US-09-929-665-9
35	21	14.5	363	11 US-09-929-665-10
36	21	14.5	363	11 US-09-929-546-9
37	21	14.5	363	11 US-09-929-546-10
38	21	14.5	443	11 US-09-967-719C-3
39	20	13.8	809	13 US-10-027-770-1
40	19	13.1	384	9 US-09-905-243-20
41	19	13.1	737	10 US-09-919-344-7
42	18	12.4	387	9 US-09-905-243-27
43	17	11.7	368	11 US-09-940-727B-103
44	17	11.7	490	11 US-09-918-995-37859
45	17	11.7	514	14 US-10-066-543-2025

ALIGNMENTS

RESULT 1
US-09-861-294-1
; Sequence 1, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE OF INVENTION: TUMORS BEARING HMFg AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ IDS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(435)

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; NAME/KEY: sig_peptide
; LOCATION: (1)...(60)
; NAME/KEY: mat_peptide
; LOCATION: (61)...(435)
US-09-861-294-1

Alignment Scores:
Pred. No.: 2,36e-131 Length: 435
Score: 145.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-08-836-455-2 (1-145) x US-09-861-294-1 (1-435)

Qy 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
Db 1 ATGGGGGCCCTGCTCAGATTCTTGGGTTCTTGTGCTCTTGTTCAGGTACCAGATGT 60
Qy 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
Db 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGAGTCACT 120
Qy 41 LeuThrCysArgAlaSerGlnAspIleGlyLeuAsnLeuHisTrpLeuGlnGluPro 60
Db 121 CTCACCTTGTTCGGGCAAGTCAGGACATGGTATTAACTTACATTTGGCTTCAGCAGAACCA 180
Qy 61 AspGlyThrIleLysArgLeuLeuTyrAlaThrSerSerLeuGlySerGlyValProLys 80
Db 181 GATGGAACTATTAAACCCCTGATCTAGGACATTTGGTATTAACTTACATTTGGCTTCAGCAGAACCA 240
Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
Db 241 AGGTTCAAGTGGCAGTAGTCTGGGTCAGATTATTTCTCTCACCATCAGCAGCTTGGTCT 300
Qy 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
Db 301 GAAGATTTTGTAGCTTATTACTGTCTACAATATGCTGCTACAGTTTCGGTACAGCTTCGGAGGG 360
Qy 121 GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
Db 361 GGGACCAAGCTGGAAATAAAACGGCGTGCTGACCAACTGTATCCACTTCTCCACCA 420
Qy 141 SerSerLysLeuGly 145
Db 421 TCCAGTAAGCTTGGG 435

RESULT 2
US-10-367-506-1
; Sequence 1, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE OF INVENTION: TUMORS BEARING HMGF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (1)...(435)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(60)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (61)...(435)
US-10-367-506-1

Alignment Scores:
Pred. No.: 2,36e-131 Length: 435
Score: 145.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-2 (1-145) x US-10-367-506-1 (1-435)

Qy 1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20
Db 1 ATGGGGGCCCTGCTCAGATTCTTGGGTTCTTGTGCTCTTGTTCAGGTACCAGATGT 60
Qy 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
Db 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGAGTCACT 120
Qy 41 LeuThrCysArgAlaSerGlnAspIleGlyLeuAsnLeuHisTrpLeuGlnGluPro 60
Db 121 CTCACCTTGTTCGGGCAAGTCAGGACATGGTATTAACTTACATTTGGCTTCAGCAGAACCA 180
Qy 61 AspGlyThrIleLysArgLeuLeuTyrAlaThrSerSerLeuGlySerGlyValProLys 80
Db 181 GATGGAACTATTAAACCCCTGATCTAGGACATTTGGTATTAACTTACATTTGGCTTCAGCAGAACCA 240
Qy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
Db 241 AGGTTCAAGTGGCAGTAGTCTGGGTCAGATTATTTCTCTCACCATCAGCAGCTTGGTCT 300
Qy 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
Db 301 GAAGATTTTGTAGCTTATTACTGTCTACAATATGCTGCTACAGTTTCGGTACAGCTTCGGAGGG 360
Qy 121 GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
Db 361 GGGACCAAGCTGGAAATAAAACGGCGTGCTGACCAACTGTATCCACTTCTCCACCA 420
Qy 141 SerSerLysLeuGly 145
Db 421 TCCAGTAAGCTTGGG 435

RESULT 3
US-09-007-093-1
; Sequence 1, Application US/09007093
; Patent No. US20020025315A1
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,093
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,576
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-765
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-09-007-093-1
;
Alignment Scores:
Pred. No.: 5,28e-23 Length: 387
Score: 33.00 Matches: 33
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.76% Indels: 0
DB: 9 Gaps: 0

US-08-836-455-2 (1-145) x US-09-007-093-1 (1-387)

QY 15 PheProGlyThrArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSer 34
Db 49 TTTCCAGGTACCAAGATGTGACATGCCAGTCCATCCCTCCCTTATCTGCCTCT 108
QY 35 LeuGlyGlnArgValSerLeuThrCysArgAlaSerGln 47
Db 109 CTGGGACAAGAGTCACTCTCACTTCTGGGCAAGTCAG 147

RESULT 4
US-09-924-099-11
; Sequence 11, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 11
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Mus musculus
;
US-09-924-099-11
Alignment Scores:
Pred. No.: 3,35e-19 Length: 324
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 8 Gaps: 0

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,093
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,576
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-765
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-09-007-093-1
;
Alignment Scores:
Pred. No.: 5,28e-23 Length: 387
Score: 33.00 Matches: 33
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.76% Indels: 0
DB: 9 Gaps: 0

US-08-836-455-2 (1-145) x US-09-007-093-1 (1-387)

QY 15 PheProGlyThrArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSer 34
Db 49 TTTCCAGGTACCAAGATGTGACATGCCAGTCCATCCCTCCCTTATCTGCCTCT 108
QY 35 LeuGlyGlnArgValSerLeuThrCysArgAlaSerGln 47
Db 109 CTGGGACAAGAGTCACTCTCACTTCTGGGCAAGTCAG 147

RESULT 4
US-09-924-099-11
; Sequence 11, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 11
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Mus musculus
;
US-09-924-099-11
Alignment Scores:
Pred. No.: 3,35e-19 Length: 324
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 8 Gaps: 0

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-2 (1-145) x US-09-924-099-11 (1-324)

QY 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
Db 166 TCTGGTGTCCCAAGAGGTTCACTGGCAGTAGCTCTGGGTCACATTATTTCTTCACCATC 225
QY 96 SerSerLeuGluSerGluAspPheVal 104
Db 226 AGCAGCCTTGAGTCTGAAGATTGTGA 252

RESULT 5
US-08-779-784-16
; Sequence 16, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA: US 08/236,520
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
;
US-08-779-784-16
Alignment Scores:
Pred. No.: 3,6e-19 Length: 351
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 8 Gaps: 0
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US-08-836-455-2 (1-145) x US-08-779-784-16 (1-351)
QY 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerLeuThrIle 95
Db 232 TCTGGTGTGCCAAAGGTTTCAGTGGCAGTAGGTCTGGTCTCAGATTATTCTCTCACCATC 291
QY 96 SerSerLeuGluSerGluAspPheVal 104
Db 292 AGCAGCCTTGAGTCTGAAGATTTGTGA 318
RESULT 6
US-08-779-784-17
; Sequence 17, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYLINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1694
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
US-08-779-784-17
Alignment Scores:
Pred. No.: 3.6e-19 Length: 351
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 8 Gaps: 0
US-08-836-455-2 (1-145) x US-08-779-784-17 (1-351)
QY 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerLeuThrIle 95
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Db 232 TCTGGTGTGCCAAAGGTTTCAGTGGCAGTAGGTCTGGTCTCAGATTATTCTCTCACCATC 291
QY 96 SerSerLeuGluSerGluAspPheVal 104
Db 292 AGCAGCCTTGAGTCTGAAGATTTGTGA 318
RESULT 7
US-10-146-305-5
; Sequence 5, Application US/10146305
; Publication No. US20020173035A1
; GENERAL INFORMATION:
; APPLICANT: YUHAN CORPORATION
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
; TITLE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: OVI17440
; CURRENT APPLICATION NUMBER: US/10/146,305
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 5
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-146-305-5
Alignment Scores:
Pred. No.: 3.96e-19 Length: 390
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 13 Gaps: 0
US-08-836-455-2 (1-145) x US-10-146-305-5 (1-390)
QY 117 ThrPheGlyGlyThrLysLeuGluIleLysArgAlaAspAlaProThrValSer 136
Db 304 ACGTTCGGTGGAGGCACCAAGCTGGAATCAACGGGCTGATGCTGCACCAACTGTATCC 363
QY 137 IlePheProSerSerLysLeuGly 145
Db 364 ATCTTCCACCACCTCCAGTAAGCTGGG 390
RESULT 8
US-08-779-784-5
; Sequence 5, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYLINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-08-779-784-5

Alignment Scores:
Pred. No.: 4,07e-19 Length: 402
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
Gaps: 8

US-08-836-455-2 (1-145) x US-08-779-784-5 (1-402)
QY 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrile 95
Db 232 TCTGGTGTGCCAAAGAGTTTCAGTGGCAGTAGGTCTGGTGCAGATTATTCTCTCACCATC 291
QY 96 SerSerLeuGluSerGluAspPheVal 104
Db 292 AGCAGCCTTGAGTCTGAAGATTGTGA 318

RESULT 9
US-09-924-099-27
; Sequence 27, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 27
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(407)
; NAME/KEY: sig peptide
; LOCATION: (1)...(60)

US-08-836-455-2 (1-145) x US-09-924-099-27 (1-407)
QY 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrile 95
Db 226 TCTGGTGTGCCAAAGAGTTTCAGTGGCAGTAGGTCTGGTGCAGATTATTCTCTCACCATC 285
QY 96 SerSerLeuGluSerGluAspPheVal 104
Db 286 AGCAGCCTTGAGTCTGAAGATTGTGA 312

RESULT 10
US-09-990-205-1
; Sequence 1, Application US/09990205
; Patent No. US20020150572A1
; GENERAL INFORMATION:
; APPLICANT: FOON, Kenneth A.
; APPLICANT: CHATTERJEE, Malaya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000501
; CURRENT APPLICATION NUMBER: US/09/990,205
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: U.S. 09/192,838
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/065,774
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Mus Musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(447)
; NAME/KEY: mat peptide
; LOCATION: (58)...(447)
; US-09-990-205-1

Alignment Scores:
Pred. No.: 4,47e-19 Length: 447
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
Gaps: 10

US-08-836-455-2 (1-145) x US-09-990-205-1 (1-447)
QY 117 ThrPheGlyGlyThrLysLeuGluLeLysArgAlaAspAlaProThrValSer 136
Db 361 ACCTTCGGTGGAGGCCAACAGCTGGAAATCAACAGGCTGTGCTGCACCACTGTATCC 420
QY 137 IlePheProProSerSerLysLeuGly 145
Db 421 ATCTCCACCATCCAGTAGCTTGGG 447

RESULT 11
US-10-153-401-1
; Sequence 1, Application US/10153401
; Publication No. US20030114398A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
```

```
; Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,401
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/293,533
; FILING DATE: 1999-04-15
; APPLICATION NUMBER: US 08/372,676
; FILING DATE: 1995-01-17
; APPLICATION NUMBER: US 08/591,196
; FILING DATE: 1996-01-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine M. Polizzi
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 304142000202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..447
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-153-401-1
Alignment Scores:
Pred. No.: 4,47e-19 Length: 447
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 14 Gaps: 0
US-08-836-455-2 (1-145) x US-10-153-401-1 (1-447)
Qy 117 ThrPheGlyGlyThrLysLeuGluIleLysArgAlaAspAlaProThrValSer 136
Db 361 ACGTTCGGTGAGGACCAAGCTGGAATCAACGGGCTGTGCTGCACCAACTGTATCC 420
Qy 137 IlePheProSerLysLeuGly 145
Db 421 ATCTTCCCAACCATCCAGTAGCTGGG 447
RESULT 12
US-09-924-099-19
; Sequence 19, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-06-23
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 20
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of
; OTHER INFORMATION: SEQ
; OTHER INFORMATION: ID NO:10
US-09-924-099-20
; Sequence 20, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-06-23
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 20
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of
; OTHER INFORMATION: SEQ
; OTHER INFORMATION: ID NO:10
US-09-924-099-19 (1-711)
Qy 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
Db 556 TCTGGTGTCCCAAGAGGTTTCAGTGGCAGTAGGTCTGGGTGCAGATTATTCTCACCATC 615
Qy 96 SerSerLeuGluSerGluAspPheVal 104
Db 616 AGCAGCCTTGAGTCTGAAGATTTTGTGA 642
RESULT 13
US-09-924-099-20
; Sequence 20, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-06-23
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 20
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of
; OTHER INFORMATION: SEQ
; OTHER INFORMATION: ID NO:10
US-09-924-099-19 (1-711)
Alignment Scores:
Pred. No.: 6,77e-19 Length: 711
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 10 Gaps: 0
US-08-836-455-2 (1-145) x US-09-924-099-19 (1-711)
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Alignment Scores:
Pred. No.: 6,92e-19 Length: 729
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-2 (1-145) x US-09-924-099-20 (1-729)

Qy 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
|||||
Db 556 TCTGGTGTCCCAAGAGTTTCAGTGGCAGTAGGTCTGGGTCTGAGATTATCTCTCACCATC 615
Qy 96 SerSerLeuGluSerGluAspPheVal 104
|||||
Db 616 AGCAGCCTTGAGTCTGAAGATTGTGA 642

RESULT 14

US-09-887-853-5

; Sequence 5, Application US/09887853

; Patent No. US20020168375A1

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; Oppermann, Hermann

; Houston, L. L.

; Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; Imaging

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/887,853

; FILING DATE: 21-Jun-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/133,804

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Kelley, Robin D.

; REGISTRATION NUMBER: 34,637

; REFERENCE/DOCKET NUMBER: 2054/22

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-248-7477

; TELEFAX: 617-248-7100

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 739 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..729

; OTHER INFORMATION: /product= "520C9 sfv polypeptide

; sequence"

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-887-853-5

Alignment Scores:

Pred. No.: 7,01e-19 Length: 739
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.00% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-2 (1-145) x US-09-887-853-5 (1-739)

Qy 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
|||||
Db 565 TCTGGTGTCCCAAGAGTTTCAGTGGCAGTAGGTCTGGGTCTGAGATTATCTCTCACCATC 624
Qy 96 SerSerLeuGluSerGluAspPheVal 104
|||||
Db 625 AGTAGCCTTGAGTCTGAAGATTGTGA 651

RESULT 15

US-10-268-883-10

; Sequence 10, Application US/10268883

; Publication No. US20030138862A1

; GENERAL INFORMATION:

; APPLICANT: Tso, J. Yun

; APPLICANT: Green, Jennifer Macphate

; TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof

; FILE REFERENCE: 05882,0062.NPUS01

; CURRENT APPLICATION NUMBER: US/10/268,883

; CURRENT FILING DATE: 2003-03-26

; PRIOR APPLICATION NUMBER: USSN 60/329,178

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: USSN 60/331,965

; PRIOR FILING DATE: 2001-11-21

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 390

; TYPE: DNA

; ORGANISM: Mouse

US-10-268-883-10

Alignment Scores:

Pred. No.: 3,67e-18 Length: 390
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-2 (1-145) x US-10-268-883-10 (1-390)

Qy 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
|||||
Db 232 TCTGGTGTCCCAAGAGTTTCAGTGGCAGTAGGTCTGGGTCTGAGATTATCTCTCACCATC 291
Qy 96 SerSerLeuGluSerGluAspPhe 103
|||||
Db 292 AGCAGCCTTGAGTCTGAAGATTGT 315

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Title: US-08-836-455-2

Perfect score: 145

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-NORM-ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
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25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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9	28	19.3	805	12	BI454240
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11	28	19.3	854	13	BQ947692
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13	28	19.3	891	10	BF579422
14	28	19.3	906	10	BF785914
15	28	19.3	908	13	BQ524124
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25	26	17.9	540	12	BG964740
26	26	17.9	553	10	BE309991
27	26	17.9	569	12	BG964957
28	26	17.9	573	12	BM245196
29	26	17.9	574	13	BQ305476
30	26	17.9	594	13	BQ175706
31	26	17.9	601	13	BQ610021
32	26	17.9	611	13	BQ175762
33	26	17.9	620	10	BE368918
34	26	17.9	641	10	BF134573
35	26	17.9	643	10	BF579280
36	26	17.9	659	10	BF137298
37	26	17.9	671	12	BM194931
38	26	17.9	693	12	BG964281
39	26	17.9	698	12	BII109045
40	26	17.9	706	12	BG965094
41	26	17.9	709	12	BG962745
42	26	17.9	711	10	BF142976
43	26	17.9	712	12	BII100311
44	26	17.9	714	12	BG963548
45	26	17.9	716	12	BG964192

ALIGNMENTS

RESULT 1

BE309592

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

BE309592 601094848F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489635 5', mRNA linear EST 26-OCT-2000
mRNA sequence.

BE309592 GI:9168025

EST

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 594)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-r@mail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM8530 row: 0 column: 12
 High quality sequence stop: 591.

FEATURES
 source
 1. 594
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:3489635"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Mam5"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

BASE COUNT 158 a 149 c 143 g 144 t
 ORIGIN

Alignment Scores:
 Pred. No.: 5,51e-17 Length: 594
 Score: 30.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 20.69% Indels: 0
 DB: 10 Gaps: 0

US-08-836-455-2 (1-145) x BE309592 (1-594)

Qy 113 SerSerProThrPheGlyGlyThrLysLeuGlutLeLysArgAlaAspAlaAla 132
 |||||||
 Db 323 AGCTCTCCGTACACGTTTCGGAGGGGGACCAAGCTGGAATAAAACGGCTGCTGCA 382

Qy 133 ProThrValSerIlePheProProSerSer 142
 |||||||
 Db 383 CCAACTGTATCCATCTTCCACCACCATCCAGT 412

RESULT 2
 BQ956722
 LOCUS BQ956722 871 bp mRNA linear EST 21-AUG-2002
 DEFINITION AGENCOURT 8880951 NCI_CGAP_Co24 Mus musculus cDNA clone
 IMAGE:6396481 5', mRNA sequence.

ACCESSION BQ956722.1 GI:22372200
 VERSION BQ956722.1
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 871)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-r@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13892 row: n column: 02
 High quality sequence stop: 630.

FEATURES
 source
 Location/Qualifiers
 1. 871
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:6396481"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Co24"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: Sali; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP library."

BASE COUNT 218 a 268 c 182 g 193 t 10 others
 ORIGIN

Alignment Scores:
 Pred. No.: 6,53e-16 Length: 871
 Score: 29.00 Matches: 29
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 20.00% Indels: 0
 DB: 13 Gaps: 0

US-08-836-455-2 (1-145) x BQ956722 (1-871)

Qy 114 SerProThrPheGlyGlyThrLysLeuGlutLeLysArgAlaAspAlaAlaPro 133
 |||||||
 Db 187 TCCCGTACACGTTTCGGAGGGGGACCAAGCTGGAATAAAACGGCTGCTGCA 246

Qy 134 ThrValSerIlePheProProSerSer 142
 |||||||
 Db 247 ACTGTATCCATCTTCCACCACCATCCAGT 273

RESULT 3
 BQ83003

LOCUS BQ83003 374 bp mRNA linear EST 07-DEC-2002
 DEFINITION BQ83003 RIKEN full-length enriched, pooled tissues, adult spleen,
 ecc. Mus musculus cDNA clone K630040M6 5', mRNA sequence.

ACCESSION BQ83003
 VERSION BQ83003.1 GI:26193211

KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 374)
 AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaiki, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,
 Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,
 Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A.,
 Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S.,
 Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani,
 L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest,
 A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,
 Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J.,
 Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M.,
 King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lennhard, B., Lyons,
 P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki,
 H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perle, G.,
 Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D.,
 Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring,
 B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C.A., Setou,
 M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale,
 R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,
 Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa,
 M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,
 Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura

M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Shinoyoshi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

TITLE

JOURNAL
MEDLINE
PUBMED

COMMENT

Contact: Yoshihide Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers
1. .374
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_lib="RIKEN full-length enriched, pooled tissues, adult spleen, etc."
/note="(dev_stage=adult,tissue_type=spleen,sex=male), (dev_stage=adult,tissue_type=kidney,sex=male), (dev_stage=adult,tissue_type=testis,sex=male), (dev_stage=adult,tissue_type=thymus,sex=male), (dev_stage=adult,tissue_type=heart,sex=male), (dev_stage=adult,tissue_type=colon,sex=male), (dev_stage=adult,tissue_type=stomach,sex=male), (dev_stage=adult,tissue_type=liver,sex=male), (dev_stage=13 days embryo,tissue_type=whole body,sex=mix), (dev_stage=14 days embryo,tissue_type=whole body,sex=mix), (dev_stage=16 days embryo,tissue_type=whole body,sex=mix), (dev_stage=17 days embryo,tissue_type=whole body,sex=mix), (dev_stage=15 days pregnant, adult,tissue_type=amion,sex=female), (dev_stage=10 days neonate,tissue_type=brain,sex=mix), (dev_stage=10 days neonate,tissue_type=thymus,sex=mix), (dev_stage=10 days neonate,tissue_type=heart,sex=mix)"

BASE COUNT
ORIGIN

88 a 89 c 85 g 111 t 1 others

Alignment Scores:

Pred. No.: 2.21e-15 Length: 374

Score:

Percent Similarity: 28.00 Matches: 28
Best Local Similarity: 100.00% Conservatives: 0
Query Match: 19.31% Mismatches: 0
DB: 13 Indels: 0
Caps: 0

US-08-836-455-2 (1-145) x BY083003 (1-374)

QY

9 GlyPheLeuLeuLeuLeuPheProGlyThrArgCysAspIleGlnMetThrGlnSerPro 28
|||||
|||||

Db

57 GGCTCTTCTGTCCTCTGTTCCAGGTACCATGTGCATCCAGATGCCACCTCCCA 116
|||||
|||||

QY

29 SerSerLeuSerAlaSerLeuGly 36
|||||
|||||

Db

117 TCCTCCTTATCTGCCTCTCTGGGA 140
|||||
|||||

RESULT 4

BM194777/c

LOCUS

DEFINITION
L0700H12-3 NIA Mouse Germinal Center B Cell cDNA Library Mus

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BM194777 585 bp mRNA linear EST 30-JAN-2002
musculus cDNA clone L0700H12 3', mRNA sequence.

BM194777
EST.
BM194777.1 GI:17745971

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 585)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Klotz, E.,
Kelsoe, G., Hodes, R. and Ko, M.S.H.

Systematic Analyses of NIA Mouse Germinal Center B Cell cDNA
Library

Unpublished
Contact: Dawood B. Dudekula
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: L0700 row: H column: 12
Seq primer: -21M13 Forward
High quality sequence stop: 585
POLYA=Yes.

FEATURES

source

Location/Qualifiers
1. .585
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="niaEST:L0700H12-3"
/db_xref="taxon:10090"
/clone="L0700H12"
/tissue_type="Germinal Center B Cell"
/lab_host="DH108"
/clone_lib="NIA Mouse Germinal Center B Cell cDNA Library"
/note="Vector: pSPOT1 (Invitrogen); Site: 1: SalI; Site: 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>
). FACS-sorted Germinal Center B cells were provided by
Drs. Richard Hodes, Emily Klotz (National Institute on
Aging and National Cancer Institute, USA) and Garnett
Kelsoe (Duke University, USA). Double-stranded cDNAs were
synthesized from 0.46 ug of total RNA with an Oligo(dT)
primer [Invitrogen].
5'-pGACTAGTCTAGATCGGAGCGCCCTTTTCTTTTCTTTT-3'],
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker LL-Sal3 (Ref. Development 127: 1737-1749 (2000)
) (PMID: 10725249), purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, cDNAs
were amplified by long-range high fidelity PCR using Ex
Taq polymerase (Takara) and purified by phenol/chloroform,
followed by Centricon 100 purification. The cDNAs were
digested with SalI and NotI enzymes and cloned into

Sali/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is 1.2 kb. The library was constructed by Yulan Piao (NIA)."

BASE COUNT
ORIGIN

137 a 121 c 167 g 160 t

Alignment Scores:

Pred. No.: 3.49e-15 Length: 585
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-2 (1-145) x BM194777 (1-585)

QY 115 ProTyrrThrpheGlyGlyThrLysLeuGluLeuLysArgAlaAspAlaProThr 134
|||||
DB 571 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAACT 512

QY 135 ValSerIlePheProSerSer 142
|||||
DB 511 GTATCCATCTTCCACCATCACT 488

RESULT 5

BQ922747 606 bp mRNA linear EST 20-AUG-2002
LOCUS AGENCOURT_8921909 NCI_CGAP_Co24 Mus musculus cDNA clone
DEFINITION IMAGE:6395978 5', mRNA sequence.

ACCESSION BQ922747
VERSION BQ922747.1 GI:223337778
KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 606)
NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM13891 row: 1 column: 03
High quality sequence stop: 605.

FEATURES

source Location/Qualifiers
1..606
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"

/db_xref="taxon:10090"
/clone="IMAGE:6395978"

/lab_host="NCI_CGAP_Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 181 a 169 c 121 g 135 t

ORIGIN

Alignment Scores:
Pred. No.: 3.62e-15 Length: 606
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 19.31% Indels: 0
DB: 13 Gaps: 0

US-08-836-455-2 (1-145) x BQ922747 (1-606)

QY 115 ProTyrrThrpheGlyGlyThrLysLeuGluLeuLysArgAlaAspAlaProThr 134
|||||
DB 15 CCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGCTGCACCAACT 74

QY 135 ValSerIlePheProSerSer 142
|||||
DB 75 GTATCCATCTTCCACCATCACT 98

RESULT 6

BQ138788 630 bp mRNA linear EST 24-OCT-2000
LOCUS BQ138788
DEFINITION 601780387F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008404 5',
mRNA sequence.

ACCESSION BQ138788
VERSION BQ138788.1 GI:10977828
KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 630)
NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM9242 row: n column: 21

High quality sequence stop: 628.

FEATURES

source Location/Qualifiers
1..630

/organism="Mus musculus"

/mol_type="mRNA"

/strain="Czech II"

/db_xref="taxon:10090"

/clone="IMAGE:4008404"

/tissue_type="tumor, metastatic to mammary"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Lu30"

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dt. Library constructed by Life Technologies.

Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 162 a 158 c 150 g 160 t

ORIGIN

Alignment Scores:
Pred. No.: 3.77e-15 Length: 630
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-2 (1-145) x BQ138788 (1-630)

QY 76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
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DB 222 TCTGGTGTCCCAAGAGTTTCAGTGGCAGTAGGTCTGGTCTGATTTCTCACCACATC 281

QY 96 SerSerLeuGluSerGluAspPhe 103

```

Db      282  AGCAGCCTTGAGTCTGAAGACTTT 305
|||||
RESULT 7
BI250555
LOCUS
DEFINITION
602993614F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5149563 5',
mRNA sequence.
ACCESSION
BI250555
VERSION
BI250555.1 GI:14799016
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 707)
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11369 row: k column: 04
High quality sequence stop: 707.
FEATURES
source
1..707
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5149563"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
BASE COUNT 198 a 171 c 172 g 166 t
ORIGIN
Alignment Scores:
Pred. No.: 4.24e-15 Length: 707
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 12 Gaps: 0
US-08-836-455-2 (1-145) x BI250555 (1-707)
QY 115 ProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAspAlaProThr 134
|||||
Db 337 CCTACACGTCGGAGGGGGCCAAAGCTGGAATAAAGCGGCTGATGCTGCACCAACT 396
|||||
QY 135 ValSerIlePheProSerSer 142
|||||
Db 397 GTATCCATCTTCCACCACCATCCAGT 420
|||||
RESULT 8
BG963055
LOCUS
DEFINITION
602828068F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982825 5',
mRNA sequence.
ACCESSION
BG963055
VERSION
BG963055.1 GI:14350692
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 725)
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10986 row: g column: 18
High quality sequence stop: 719.
FEATURES
source
1..725
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4982825"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 195 a 182 c 174 g 174 t
ORIGIN
Alignment Scores:
Pred. No.: 4.35e-15 Length: 725
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 12 Gaps: 0
US-08-836-455-2 (1-145) x BG963055 (1-725)
QY 115 ProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAspAlaProThr 134
|||||
Db 373 CCGTACACGTCGGAGGGGGCCAAAGCTGGAATAAAGCGGCTGATGCTGCACCAACT 432
|||||
QY 135 ValSerIlePheProSerSer 142
|||||
Db 433 GTATCCATCTTCCACCACCATCCAGT 456
|||||
RESULT 9
BI454240
LOCUS
DEFINITION
603170666F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5250017 5',
mRNA sequence.
ACCESSION
BI454240
VERSION
BI454240.1 GI:15244896
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 805)
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov

```

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM1631 row: d column: 18
High quality sequence stop: 790.

FEATURES

source
1. .805
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mrna"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5250017"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
BASE COUNT 230 a 209 c 186 g 180 t
ORIGIN
Alignment Scores:
Pred. No.: 4.84e-15 Length: 805
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-2 (1-145) x BT454240 (1-805)

Qy 115 ProTyrrThrPheGlyGlyThrLysLeuGluLeuLysArgAlaAspAlaProThr 134
|||||
Db 358 CCGTACACGTTGGAGGGGGACCAAGCTGGAATAAAGGGGTGATGCTGCACCAACT 417

Qy 135 ValSerIlePheProProSerSer 142
|||||
Db 418 GTATCCATCTCCACCACCATCCAGT 441

RESULT 10
BF583521 849 bp mrna linear EST 12-DEC-2000
LOCUS 602101553f1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224853 5',
DEFINITION mRNA sequence.

ACCESSION BF583521.1 GI:11657239
VERSION BF583521
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS 1 (bases 1 to 849)
TITLE NIH-MGC <http://mgc.nci.nih.gov/>
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM9815 row: i column: 14
High quality sequence stop: 627.

FEATURES

source
1. .849
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mrna"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4224853"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 274 a 215 c 183 g 177 t
ORIGIN

Alignment Scores:
Pred. No.: 5.11e-15 Length: 849
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-2 (1-145) x BF583521 (1-849)

Qy 115 ProTyrrThrPheGlyGlyThrLysLeuGluLeuLysArgAlaAspAlaProThr 134
|||||
Db 355 CCGTACACGTTGGAGGGGGACCAACTGGAATAAAGGGGTGATGCTGCACCAACT 414

Qy 135 ValSerIlePheProProSerSer 142
|||||
Db 415 GTATCCATCTCCACCACCATCCAGT 438

RESULT 11

BQ947692 854 bp mrna linear EST 21-AUG-2002
LOCUS AGENCOURT_8909039 NCI_CGAP_Mam2 Mus musculus cDNA clone
DEFINITION IMAGE:6441024 5', mRNA sequence.

ACCESSION BQ947692
VERSION BQ947692.1 GI:22363170
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS 1 (bases 1 to 854)
TITLE NIH-MGC <http://mgc.nci.nih.gov/>
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM13963 row: j column: 01
High quality sequence stop: 671.

FEATURES

source
1. .854
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mrna"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:6441024"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH

BASE COUNT 234 a 237 c 190 g 193 t

ORIGIN

Alignment Scores:

Pred. No.: 5,14e-15 Length: 854
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 13 Gaps: 0

US-08-836-455-2 (1-145) x BQ947692 (1-854)

QY 115 ProTyrrThrpheGlyGlyThrLysLeuGlulleylSargAlaAspAlaAProThr 134
|||||
Db 361 CCGTACACGTTCGGAGGGGGACCAAGCTGGAATAAAACGGGCTGATGTCGCCCAACT 420
|||||

QY 135 ValSerIlePheProSerSer 142
|||||

Db 421 GTATCCATCTTCCACCACCATCAGT 444
|||||

RESULT 12

BQ940987

LOCUS

DEFINITION BQ940987 886 bp mRNA linear EST 21-AUG-2002
IMAGE: 6476176 5', mRNA sequence.

ACCESSION BQ940987.1 GI:22356465

VERSION EST.

KEYWORDS

SOURCE

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 886)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@email.nih.gov

Tissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLMI4016 row: b column: 17

High quality sequence stop: 626.

FEATURES

source

1..886

Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:6476176"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

2 others

BASE COUNT 242 a 243 c 183 g 216 t

ORIGIN

Alignment Scores:

Pred. No.: 5,33e-15 Length: 886

Score: 28.00 Matches: 28

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 19.31% Indels: 0

DB:

13

Gaps: 0

US-08-836-455-2 (1-145) x BQ940987 (1-886)

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

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QY

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QY

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QY

Db

QY

Db

QY

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QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

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RESULT 14
BF785914
LOCUS
DEFINITION 602112548F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240762
5', mRNA sequence.
ACCESSION BF785914
VERSION BF785914.1 GI:12090950
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 906)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
JOURNAL DNA Sequencing by: Incyte Genomics, Inc.
COMMENT Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9855 row: p column: 11
High quality sequence stop: 718.
FEATURES
source
1..906
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4240762"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 243 a 232 c 237 g 194 t
ORIGIN
Alignment Scores:
Pred. No.: 5,46e-15 Length: 906
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 10 Gaps: 0
US-08-836-455-2 (1-145) x BF785914 (1-906)
QY 115 ProTyrrPheGlyGlyThrLysLeuGlulileysArgAlaaspAlaAProThr 134
|||||
Db 372 CCGTACACGTTCGGAGGGGGACCAAGCTGGAATAAAGCGGCTGATGCTGCCACCAACT 431
|||||
QY 135 ValSerIlePheProSerSer 142
|||||
Db 432 GTATCCATCTTCCACCATCCAGT 455
|||||
RESULT 15
BU524124
LOCUS
DEFINITION BU524124 908 bp mRNA linear EST 13-SEP-2002
AGENCOURT_10126425 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6530882 5', mRNA sequence.
ACCESSION BU524124
VERSION BU524124.1 GI:22834563
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE 1 (bases 1 to 908)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM14133 row: f column: 02
High quality sequence stop: 604.
FEATURES
source
1..908
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6530882"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 238 a 270 c 194 g 206 t
ORIGIN
Alignment Scores:
Pred. No.: 5,47e-15 Length: 908
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 13 Gaps: 0
US-08-836-455-2 (1-145) x BU524124 (1-908)
QY 115 ProTyrrPheGlyGlyThrLysLeuGlulileysArgAlaaspAlaAProThr 134
|||||
Db 173 CCGTACACGTTCGGAGGGGGACCAAGCTGGAATAAAGCGGCTGATGCTGCCACCAACT 232
|||||
QY 135 ValSerIlePheProSerSer 142
|||||
Db 233 GTATCCATCTTCCACCATCCAGT 256
|||||
Search completed: August 31, 2003, 02:16:24
Job time : 1747.87 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2003, 19:50:30 ; Search time 34.547 Seconds
(without alignments)
666.204 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 740

Sequence: 1 MGAPQILGFLLLFPETRC.....IKRAAPVSIPTPPSSKLG 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863-seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	740	100.0	145	AAW27119	Murine monoclonal
2	740	100.0	145	AA016292	Mouse 11D10 antibo
3	727	98.2	145	AAW87593	Antibody 11D10 lig
4	662	89.5	146	AAAP30251	Sequence of the le
5	633	85.5	135	AAV44599	Mouse light chain
6	527	71.2	129	AAW22537	Murine anti-human
7	527	71.2	129	AAE20200	Murine 44H104 mab
8	518	70.0	129	AAE20204	Murine 44H104 mab
9	508	68.6	246	AAE39569	Sequence of 520C9

10	507	68.5	243	17	AAW02280	520C9 anti-c-erbB-
11	507	68.5	243	19	AAW53170	520C9 anti-c-erbB-
12	507	68.5	243	20	AAW80424	520C9 sfv sequence
13	506	68.4	108	21	AAV44587	Mouse anti-IL-18 a
14	505	68.2	252	23	AAU72863	P4-14 single chain
15	505	68.2	439	23	AAU72872	3B10xP4-14 bispeci
16	504	68.1	107	18	AAW27121	Murine antibody 11
17	503	68.0	108	13	AAW21310	Light chain of M1f
18	503	68.0	144	12	AAW15322	IL-2 chimeric anti
19	503	68.0	146	22	AAW99115	Human protein SEQ
20	502	67.8	236	23	ABG77160	Germline protein s
21	502	67.8	237	21	AAV44595	EscFv#125-2H recom
22	502	67.8	243	21	AAV44596	EscFv#125-2H.Hr re
23	502	67.8	257	23	AAU72869	P5-11 single chain
24	497	67.2	144	12	AAW15321	IL-2 chimeric anti
25	496	67.0	109	18	AAW18271	Prp 37 light chain
26	496	67.0	109	20	AAW85910	Prp 37 light chain
27	496	67.0	109	22	AGC65862	Anti-Prp antibody
28	496	67.0	109	23	ABF51796	Anti-prion protein
29	496	67.0	109	24	ABU58877	Anti-prion protein
30	495	66.9	534	14	AAW39571	Sequence of G-FIT.
31	494	66.8	236	23	ABG77164	Germline protein s
32	492	66.5	107	21	AAV90824	520C9 hybridoma VL
33	483	65.3	138	15	AAW62881	Murine anti-human
34	482	65.1	236	21	AAV96297	Human TGFAM-9 immu
35	479	64.7	148	22	AAW35096	Filamentous phage
36	479	64.7	236	14	AAW42065	Human anti-HBs lig
37	479	64.7	287	22	AAW35102	Antibody variable
38	475	64.2	236	23	ABG77163	Amino acid sequenc
39	473	63.9	236	23	ABG77159	Amino acid sequenc
40	473	63.9	236	23	AAU74297	Anti-human AILIM m
41	471	63.6	112	23	AAW50879	Anti-bovine prion
42	471	63.6	142	17	AAW99686	Monoclonal anti-id
43	471	63.6	142	17	AAW98410	3H1 light chain va
44	471	63.6	142	18	AAW26728	Anti-idiotypic anti
45	471	63.6	142	21	AAW49961	Murine MAB against

ALIGNMENTS

```

RESULT 1
AAW27119
ID AAW27119 standard; Protein; 145 AA.
XX AC AAW27119;
XX AC
XX 25-MAR-2003 (updated)
DT 04-JAN-1998 (first entry)
XX
XX Murine monoclonal anti-idiotypic antibody 11D10 VL region.
DE Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
KW human milk fat globule; HMF; tumour; breast cancer; vaccine.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX Protein 21..145
XX Region 21..43
XX /label= Frl
XX /note= "framework region 1"
XX Region 44..54
XX /label= CDR1
XX /note= "complementarity determining region 1"
XX Region 55..69
XX /label= FR2
XX /note= "framework region 2"
XX Region 70..76
XX /label= CDR2

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 FT 77..108
 FT /label= FR3
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 FT 109..117
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT 118..127
 FT /label= FR1
 FT /note= "framework region 4"
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 PN WO9722699-A2.
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 XX 26-JUN-1997.
 XX
 XX 19-DEC-1996; 96WO-US20757.
 XX
 PR 20-DEC-1995; 95US-0575762.
 PR 26-JAN-1996; 96US-0591965.
 PR 13-DEC-1996; 96US-0766350.
 XX
 XX (KENT) UNIV KENTUCKY.
 XX
 XX Chatterjee M, Chatterjee SK, Foon KA;
 PI WPI; 1997-341690/31.
 XX N-PSDB; AAT85149.
 DR
 XX Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
 PT against human milk fat globule disease associated tumours,
 PT especially breast cancer
 XX
 PS Claim 9; Page 94; 130pp; English.
 XX
 XX This polypeptide sequence comprises the light chain variable region
 CC (VL) of monoclonal anti-idiotypic antibody 11D10 produced by
 CC hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
 CC naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotypic
 CC response. It elicits an immune response against a specific epitope
 CC of a high mol.wt. mucin of human milk fat globule (HMFG). It
 CC induces an immunological response to HMFG in mice, rabbits, monkeys
 CC and patients with advanced HMFG-associated tumours. Pharmaceutical
 CC compositions and vaccines comprising 11D10, 11D10 polypeptides
 CC and/or 11D10 polynucleotides (see also AAT85149-50) are claimed.
 CC Also claimed are diagnostic kits and methods of using 11D10, 11D10
 CC polypeptides and/or 11D10 polynucleotides, including methods of
 CC treating HMFG-associated tumours. 11D10 is also used in a claimed
 CC method of palliating HMFG-associated disease and in claimed kits to
 CC detect or quantify anti-HMFG antibody.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 145 AA;
 Query Match 100.0%; Score 740; DB 18; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1.5e-48;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAQILGFLLLFPCTGCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQPEP 60
 DB 1 MGAPAQILGFLLLFPCTGCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQPEP 60
 QY 61 DGTIKRIIYATSSILGSGVPRFRFSGSRGSDYSLTISSEDFVAYYCLQYASSPYTFGG 120
 DB 61 DGTIKRIIYATSSILGSGVPRFRFSGSRGSDYSLTISSEDFVAYYCLQYASSPYTFGG 120
 QY 121 GTKLEIKRADAAPTVSIFFPPSSKLG 145
 DB 121 GTKLEIKRADAAPTVSIFFPPSSKLG 145
 RESULT 2
 AAO16292
 ID AAO16292 standard; Protein; 145 AA.

XX AAO16292;
 AC 20-MAR-2003 (first entry)
 DT
 XX Mouse 11D10 antibody light chain variable region.
 DE
 XX Mouse; murine; vaccine; tumour; human milk fat globules; HMFG;
 KW carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour;
 KW CEA-associated tumour; anti-idiotypic antibody.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT 1..20
 FT Peptide /label= signal_peptide
 FT 21..145
 FT Protein /note= "Mature murine 11D10 antibody light chain variable
 FT region"
 FT
 PN WO200292012-A2.
 XX
 XX 21-NOV-2002.
 XX
 XX 17-MAY-2002; 2002WO-US15840.
 PF
 XX 17-MAY-2001; 2001US-0861294.
 PR
 XX (KENT) UNIV KENTUCKY RES FOUND.
 PA
 XX Chatterjee M, Foon KA;
 PI WPI; 2003-129216/12.
 XX N-PSDB; AAL51273.
 DR
 XX Use of anti-idiotypic antibodies for human milk fat globules (HMFG)- or
 PT carcinoembryonic antigen (CEA)-associated tumor for delaying the
 PT development of, or treating a HMFG- or CEA-associated tumor (e.g.
 PT breast tumor) in humans
 XX
 PS Claim 2; Fig 1; 98pp; English.
 XX
 CC The invention comprises a method for delaying the development of, or
 CC treating a tumor that is associated with human milk fat globules (HMFG)
 CC or carcinoembryonic antigen (CEA). The method of the invention involves
 CC administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an
 CC anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for
 CC delaying the development, of or treating HMFG/CEA-associated tumours. The
 CC present amino acid sequence represents the light chain variable region of
 CC the mouse 11D10 anti-idiotypic antibody.
 XX
 SQ Sequence 145 AA;
 Query Match 100.0%; Score 740; DB 24; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1.5e-48;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAQILGFLLLFPCTGCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQPEP 60
 DB 1 MGAPAQILGFLLLFPCTGCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQPEP 60
 QY 61 DGTIKRIIYATSSILGSGVPRFRFSGSRGSDYSLTISSEDFVAYYCLQYASSPYTFGG 120
 DB 61 DGTIKRIIYATSSILGSGVPRFRFSGSRGSDYSLTISSEDFVAYYCLQYASSPYTFGG 120
 QY 121 GTKLEIKRADAAPTVSIFFPPSSKLG 145
 DB 121 GTKLEIKRADAAPTVSIFFPPSSKLG 145
 RESULT 3
 AAW87593
 ID AAW87593 standard; Protein; 145 AA.

AAW87593;
 16-MAR-1999 (first entry)
 Antibody 11D10 light chain variable region.
 Murine; mouse; antibody; light chain; variable region; anti-idiotypic;
 human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
 Mus sp.
 Key Location/Qualifiers
 Peptide 1..20
 Protein /note= "signal peptide"
 Region /note= "mature protein"
 Domain /label= framework_1
 /label= CDR1
 Region /note= "complementarity determining region 1"
 /label= framework_2
 Misc-difference 55
 /note= "encoded by TGG"
 Domain /note= "CDR2"
 Region /note= "complementarity determining region 2"
 /label= framework_3
 Domain /label= CDR3
 Region /note= "complementarity determining region 3"
 /label= framework_4
 WO9856419-A1.
 17-DEC-1998.
 12-JUN-1998; 98WO-US12250.
 11-JUN-1998; 98US-0096244.
 13-JUN-1997; 97US-0049540.
 (KENT) UNIV KENTUCKY RES FOUND.
 Chatterjee M, Foon KA;
 WPI; 1999-060029/05.
 N-PSDB; AAV83772.
 Delaying development of, or treating, HMFg-associated tumours -
 using anti-idiotypic antibody 11D10 raised against antibodies to
 human milk fat globule protein
 Disclosure; Fig 1; 54pp; English.
 This sequence represents the light chain variable region of the murine
 antibody 11D10. This anti-idiotypic antibody is used to delay the
 development of, or treat, a human milk fat globule (HMFg) associated
 tumour in an individual having low tumour burden. The antibody 11D10
 is used to prevent the recurrence of HMFg-associated tumours e.g.
 ovarian, non-small cell lung and pancreatic carcinoma, especially for
 treating breast tumours.
 Sequence 145 AA;
 Query Match 98.2%; Score 727; DB 20; Length 145;
 Best Local Similarity 99.3%; Pred. No. 1.4e-47;
 Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGAPAOILGFLLLFFETGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60
 DB 1 MGAPAOILGFLLLFFETGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60
 QY 61 DGTIKELIYATSSLSGSGVPRFSGSGSDYSLTISLSLESDRFVAYCYQYASSPYTFGG 120
 DB 61 DGTIKELIYATSSLSGSGVPRFSGSGSDYSLTISLSLESDRFVAYCYQYASSPYTFGG 120
 QY 121 GYKLEIKRADAAPTVSIFPPSSKLG 145
 DB 121 GYKLEIKRADAAPTVSIFPPSSKLG 145
 RESULT 4
 AAP30251
 ID AAP30251 standard; peptide; 146 AA.
 XX AAP30251;
 AC AAP30251;
 XX 25-MAY-1992 (first entry)
 DT Sequence of the leader, variable region and first 16 AAs of
 DE the constant region of the kappa-chain (light chain) of MOPC41.
 DE
 XX Diagnosis; therapy; immunoglobulin.
 KW Homo sapiens.
 XX
 OS Key Location/Qualifiers
 FH Region 1..22
 FT /label= leader
 FT Region 23..130
 FT /label= variable
 FT Region 131..146
 FT /label= constant
 XX EP88994-A.
 PN 21-SEP-1983.
 XX 10-MAR-1983; 83EP-0001655.
 XX 15-MAR-1982; 82US-0358414.
 PR 05-DEC-1983; 83US-0558551.
 XX (SCHE) SCHERING CORP.
 PA (DNAX-) DNAX RES INST.
 XX Moore KW, Zaffaroni A;
 PI WPI; 1983-772290/39.
 XX N-PSDB; AAN30165.
 DR Transformed expression vectors or plasmid(s) - with double
 PT stranded DNA sequence coding only for desired part of polypeptide
 PT chain
 XX Example; Page 40-41; 68pp; English.
 PS The pref. vector or plasmid of the invention has a double-stranded
 CC DNA seq. coding for a variable region of a light or heavy chain of
 CC IgG, or for a variable region of a light or heavy chain of an
 CC immunoglobulin specific for an enzyme or surface protein. The
 CC sequence esp. codes for a variable region of a light chain having 95-
 CC 115 AAs or for a variable region of a heavy chain having 110-125 AAs
 CC esp. including the D region of the heavy chain.
 XX Sequence 146 AA;
 SQ Query Match 89.5%; Score 662; DB 4; Length 146;
 Best Local Similarity 91.6%; Pred. No. 1.1e-42;
 Matches 131; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MGAPAIQLGFLLLFPCTRCIDIQMTQSPSSLSASLGQVSLTCRASODIGINLHWLQOEP 60
 Db 3 MRAPAIQIFGFLLLFQCTRCIDIQMTQSPSSLSASLGQVSLTCRPSODIGSSLNWLQOEP 62
 QY 61 DGTIKRLIYATSLGSGVPRFSGSRGSDYSLTISSEDFVAYICLOYASSPYTFGG 120
 Db 63 DGTIKRLIYATSLDGSVPRFSGSRGSDYSLTISSEDFVDYICLOYASSPYTFGG 122
 QY 121 GTKLEIKRADAAPTYSIFPPSSK 143
 Db 123 GTKLEIKRADAAPTYSIFPPSSE 145

RESULT 5
 AAY44599
 ID AAY44599 standard; Protein: 135 AA.
 XX
 AC AAY44599;
 DT 04-APR-2000 (first entry)
 XX Mouse light chain variable region encoded by PCR A product.
 DE Mouse light chain variable region; VL; variable region light chain;
 KW interleukin-18; immunopathies; inflammatory disorder; autoimmune disease;
 KW mouse; anti-allergic; anti-inflammatory; immunosuppressive;
 KW hematopoietic; leukocytopenic; antialgic; antipyretic.
 XX Mus musculus.
 OS Synthetic.
 XX
 PN EP974600-A2.
 XX
 PD 26-JAN-2000.
 XX
 XX 24-JUN-1999; 99EP-0304977.
 XX
 XX 24-JUN-1998; 98JP-0177580.
 PR 12-OCT-1998; 98JP-0289044.
 PR 22-DEC-1998; 98JP-0365023.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
 XX
 DR WPI; 2000-118341/11.
 DR N-PSDB; AAZ49548.
 XX
 XX New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases -
 XX
 PS Disclosure; Page 28-29; 32pp; English.
 CC
 CC The present sequence is the mouse light chain variable region. This was
 CC encoded by a recombinant DNA is derived from PCR A which amplifies
 CC antibody light chain variable region (VL). The transformant produced
 CC using the VL gene was used to transform competent E. coli cells. The peptide
 CC produced by transformants neutralises interleukin-18. This is useful for
 CC treating and preventing immunopathies, inflammatory disorders and
 CC autoimmune diseases which are caused by excessive immunoreaction. The
 CC peptide has anti-allergic, anti-inflammatory, immunosuppressive,
 CC hematopoietic, leukocytopenic, antialgic, antipyretic and hepatic
 CC -function improving activities.
 XX
 SQ Sequence 135 AA;

Query Match 85.58; Score 633; DB 21; Length 135;
 Best Local Similarity 92.6%; Pred. No. 1.6e-40;
 Matches 125; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MGAPAIQLGFLLLFPCTRCIDIQMTQSPSSLSASLGQVSLTCRASODIGINLHWLQOEP 60
 Db 1

Db 1 MRAPAIQIFGFLLLFPCTRCIDIQMTQSPSSLSASLGQVSLTCRASODIGSKLYWLQOEP 60
 QY 61 DGTIKRLIYATSLGSGVPRFSGSRGSDYSLTISSEDFVAYICLOYASSPYTFGG 120
 Db 61 DGTIKRLIYATSLDGSVPRFSGSRGSDYSLTISSEDFVDYICLOYASSPYTFGG 120
 QY 121 GTKLEIKRADAAPT 135
 Db 121 GTKLAIKRADAAPT 135

RESULT 6
 AAW22537
 ID AAW22537 standard; Protein: 129 AA.
 XX
 AC AAW22537;
 DT 03-NOV-1997 (first entry)
 XX Murine anti-human class II monoclonal antibody 44H104 VL chain.
 DE
 DE Antibody; light chain; variable region; hybridoma cell line 44H104;
 KW immune response; enhance; stimulate; vaccine; immunodiagnosis;
 KW antigen delivery.
 XX
 OS Mus musculus.
 XX WO9640941-A1.
 PN 19-DEC-1996.
 PD
 PF 07-JUN-1996; 96WO-CA00400.
 XX
 XX 07-JUN-1995; 95US-0483576.
 XX
 XX (CONN-) CONNAUGHT LAB LTD.
 PA
 PI Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH;
 XX
 DR WPI; 1997-077271/07.
 DR N-PSDB; AAT77851.
 XX
 XX Recombinant conjugate antibody mol., modified for delivering an
 PT antigen - elicits enhanced immune response without the use of
 PT adjuvant to generate antibodies which are useful in vaccines or
 PT immuno:diagnosis
 XX
 PS Example 1; Fig 1A; 64pp; English.
 CC
 CC Novel recombinant conjugate antibody molecules comprise a monoclonal
 CC antibody specific for a surface structure of antigen presenting
 CC cells (APC), genetically modified to contain at least one antigen
 CC exclusively at one or more preselected sites. The conjugate is capable
 CC of delivering the antigen to APC and eliciting an immune response to
 CC the antigen. The new conjugates are useful as vaccines and are able
 CC to elicit an enhanced immune response without the use of an adjuvant.
 CC In a specific example, a conjugate was constructed using the murine
 CC anti-human class II monoclonal antibody secreted by hybridoma
 CC 44H104. The peptide CLTB36 was chosen as antigen; it consists of
 CC a tandemly linked T and B cell epitope derived from HIV MN strain.
 CC The present sequence represents the light chain variable region
 CC from 44H104 which was used in the preparation of a conjugate with
 CC antigen CLTB36.
 XX
 SQ Sequence 129 AA;

Query Match 71.28; Score 527; DB 18; Length 129;
 Best Local Similarity 81.1%; Pred. No. 1.5e-32;
 Matches 103; Conservative 7; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MGAPAIQLGFLLLFPCTRCIDIQMTQSPSSLSASLGQVSLTCRASODIGINLHWLQOEP 60
 Db 3 MRPAHVFGFLLLWFFCTRCIDIQMTQSPSSLSASLGQVSLTCRASOEISGLYTLWLOKP 62


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QY      81  RFGSGRSGDYSLTISSESEDFVAYICLQYASSPYTFGGTKLEIKRAD 130
      |||||||
Db      194  RFGSGRSGDYSLTISSESEDFVAYICLQYAIFFYTFGGTNLEIKRAD 243

RESULT 11
AAW53170
ID      AAW53170 standard; Protein; 243 AA.
XX
AC      AAW53170;
XX
DT      16-JUL-1998 (first entry)
XX
DE      520C9 anti-c-erbB-2 sfv' dimeric construct protein sequence.
XX
KW      Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer;
KW      c-erbB-2; tumour; diagnosis; ss.
XX
OS      Synthetic.
OS      Mus sp.
XX
PN      US5753204-A.
XX
PD      19-MAY-1998.
XX
PF      05-JUN-1995; 95US-0461838.
XX
PR      07-OCT-1993; 93US-0133804.
PR      06-FEB-1992; 92US-0831967.
PR      05-JUN-1995; 95US-0461838.
XX
PA      (CHIR ) CHIRON CORP.
PA      (CREA-) CREATIVE BIOMOLECULES INC.
XX
PI      Houston LL, Huston JS, Oppermann H, Ring DB;
XX
DR      WPI; 1998-311318/27.
DR      N-PSDB; AAV21798.
XX
PT      Imaging of antigens in vivo - using dimers of single-chain antibody
PT      Fv fragments
XX
PS      Example 1; Columns 33-36; 30pp; English.
XX
CC      This represents the protein sequence of a 520C9 sfv' (single chain Fv)
CC      construct. This was constructed by connecting the Vh and Vl genes with
CC      a DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal
CC      antibody useful in targeting c-erbB-2 antigen. This dimeric construct
CC      can be used in the methods of invention of imaging a preselected antigen
CC      expressed in a mammal. The methods are used in magnetic resonance imaging
CC      of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic
CC      constructs have enhanced properties as in vivo targeting agents in
CC      comparison with intact monoclonal antibodies or their Fab fragments. The
CC      dimeric constructs permit the in vivo targeting of an epitope on an
CC      antigen with greater apparent avidity, including greater tumour
CC      specificity, tumour localisation and tumour retention properties than
CC      that of the Fab fragment having the same CDRs as the construct.
XX
SQ      Sequence 243 AA;
      Query Match 68.5%; Score 507; DB 19; Length 243;
      Best Local Similarity 91.8%; Pred. No. 8.9e-31;
      Matches 101; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      21  DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQEPDGTIKRLIYATSSLSGSGVPK 80
      |||||||
Db      134  DIQMTQSPSSLSASLGQRVSLTCRASQDIGNSLTWLQEPDGTIKRLIYATSSLSGSGVPK 193

QY      81  RFGSGRSGDYSLTISSESEDFVAYICLQYASSPYTFGGTKLEIKRAD 130
      |||||||
Db      194  RFGSGRSGDYSLTISSESEDFVAYICLQYAIFFYTFGGTNLEIKRAD 243

RESULT 12
AAW80424
ID      AAW80424 standard; Protein; 243 AA.
XX
AC      AAW80424;
XX
DT      28-JAN-1999 (first entry)
XX
DE      520C9 sfv sequence.
XX
KW      520C9 sfv; antigen; tumour cell; antibody 520C9;
KW      targeted delivery; antigen-expressing cell.
XX
OS      Synthetic.
XX
PN      US5837846-A.
XX
PD      17-NOV-1998.
XX
PF      05-JUN-1995; 95US-0461386.
XX
PR      07-OCT-1993; 93US-0133804.
PR      06-FEB-1992; 92US-0831967.
PR      05-JUN-1995; 95US-0461386.
XX
PA      (CHIR ) CHIRON CORP.
PA      (CREA-) CREATIVE BIOMOLECULES INC.
XX
PI      Houston LL, Huston JS, Oppermann H, Ring DB;
XX
DR      WPI; 1999-023541/02.
DR      N-PSDB; AAV63399.
XX
PT      Nucleic acid encoding single-chain Fv fragment specific for antigens
PT      - and having C-terminal tail for crosslinking to form dimer with
PT      improved pharmacokinetic properties, used to deliver drugs and
PT      imaging agents, especially to tumours
XX
PS      Example 1; Columns 35-36; 29pp; English.
XX
CC      The present sequence represents an antibody 520C9 sfv. Variable heavy
CC      and light sequences of antibody 7520C9 are connected, together with a
CC      serine linker, to produce the present single chain Fv gene. The present
CC      sequence exemplifies the invention. Dimers of the single chain Fv are
CC      used for targeted delivery of drugs or imaging agents (e.g. cytotoxins,
CC      prodrugs or 99m-technetium) to antigen-expressing cells, particularly
CC      for treatment or diagnosis of tumours (especially of ovary or breast).
XX
SQ      Sequence 243 AA;
      Query Match 68.5%; Score 507; DB 20; Length 243;
      Best Local Similarity 91.8%; Pred. No. 8.9e-31;
      Matches 101; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      21  DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQEPDGTIKRLIYATSSLSGSGVPK 80
      |||||||
Db      134  DIQMTQSPSSLSASLGQRVSLTCRASQDIGNSLTWLQEPDGTIKRLIYATSSLSGSGVPK 193

QY      81  RFGSGRSGDYSLTISSESEDFVAYICLQYASSPYTFGGTKLEIKRAD 130
      |||||||
Db      194  RFGSGRSGDYSLTISSESEDFVAYICLQYAIFFYTFGGTNLEIKRAD 243

RESULT 13
AAW44587
ID      AAW44587 standard; Protein; 108 AA.
XX
AC      AAW44587;
XX
DT      04-APR-2000 (first entry)
XX
DE      Mouse anti-IL-18 antibody light chain variable region.

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XX Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
 KW Hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18;
 KW antiinflammatory; immunosuppressive; leucocytopenetic; antiallgic;
 KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
 KW immunopathy; inflammatory disorder; immunoreaction.
 OS Mus musculus.
 XX
 XX EP974600-A2.
 XX
 XX 26-JAN-2000.
 XX
 XX 24-JUN-1999; 99EP-0304977.
 XX
 XX 24-JUN-1998; 98JP-0177580.
 PR 12-OCT-1998; 98JP-0289044.
 PR 22-DEC-1998; 98JP-0365023.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;
 PI
 XX
 DR WPI; 2000-118341/11.
 DR N-PSDB; AAZ49534.
 XX
 PT New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases -
 XX
 PS Claim 5; Page 17; 36pp; English.
 XX
 CC The present protein sequence is the mouse anti-Interleukin-18 antibody
 CC light chain variable region (VL) encoded by cDNA derived from hybridoma
 CC #125-2H. The nucleotide sequence is used in the production of recombinant
 CC monoclonal antibody #125-2HmAb, which is capable of neutralising
 CC biological activities of interleukin-18. The antibody has antiallgic,
 CC antiinflammatory, immunosuppressive, leucocytopenetic, antipyretic,
 CC antiallergic and hepatotropic activity and can be used for prevention and
 CC treatment of autoimmune diseases, immunopathies and inflammatory
 CC disorders caused by excessive immunoreaction.
 XX
 SQ Sequence 108 AA;
 Query Match 68.4%; Score 506; DB 21; Length 108;
 Best Local Similarity 92.6%; Pred. No. 4.8e-31;
 Matches 100; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 21 DIQWTSPLSASLGORVSLTCRASODIGINLHWLQOEPDGTIKRLIYATSSLGSPVK 80
 Db 1 DIQWTSPLSASLGORVSLTCRASODIGSKLYLWLOQEPDGTIKRLIYATSSLDGSPVK 60
 QY 81 RFGSRSGSDYSLTISSEDFVAYYCLQYASSPYTFGGGTKLEIKR 128
 Db 61 RFGSRSGSDYSLTISSEDFVYCYLQYASSPYTFGGGTKLAIR 108
 RESULT 14
 AAU72863
 ID AAU72863 standard; Protein; 252 AA.
 XX
 AC AAU72863;
 XX
 XX 26-FEB-2002 (first entry)
 XX
 DE P4-14 single chain Fv.
 XX
 KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
 KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
 KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
 KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
 KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10;
 KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;

KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
 KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
 KW p53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
 XX Homo sapiens.
 XX WO200171005-A2.
 PN
 XX 27-SEP-2001.
 XX
 XX 26-MAR-2001; 2001WO-EP03414.
 PF
 XX 24-MAR-2000; 2000EP-0106467.
 PR
 XX (KUFE/) KUFER P.
 PA
 XX Kufer P, Riethmueller G, Lutterbuese R, Borschert K, Kischel R;
 PI Mayer M, Hofmeister R;
 PI
 XX WPI; 2002-055119/07.
 DR N-PSDB; AAS97137.
 DR
 XX Multifunctional polypeptides comprising binding sites that specifically
 PT recognise extracellular groups of the NKG2D receptor complex and
 PT domains which function as receptors or ligands, useful for treating
 PT cancers and infectious diseases -
 XX
 PS Example 7; Fig 16; 114pp; English.
 XX
 CC The invention relates to a multifunctional polypeptide comprising a
 CC domain with a binding site that specifically recognises an extracellular
 CC group of the NKG2D receptor complex and a second domain which functions
 CC as a receptor or ligand. The polypeptide and its associated
 CC polynucleotide are used for the preparation of a pharmaceutical
 CC composition for the treatment of cancer, infections and/or autoimmune
 CC conditions. The cancer may be a tumour of the head and neck, stomach,
 CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
 CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
 CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
 CC The infectious diseases can be caused by viruses, bacteria, fungi,
 CC protozoa or helminths. The autoimmune diseases include multiple
 CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
 CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
 CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
 CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
 CC receptor and the polypeptides of the invention.
 XX
 SQ Sequence 252 AA;
 Query Match 68.2%; Score 505; DB 23; Length 252;
 Best Local Similarity 86.2%; Pred. No. 1.3e-30;
 Matches 100; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 17 GTRCDIQMTQSPSSLSASLGORVSLTCRASODIGINLHWLQOEPDGTIKRLIYATSSLSGS 76
 Db 130 GGSSELVMTQSPSSLSASLGORVSLTCRASODIGSSLNWLOQEPDGTIKRLIYATSSLSGS 189
 QY 77 GVPKRFSGSRGSDYSLTISSEDFVAYYCLQYASSPYTFGGGTKLEIKRADA 132
 Db 190 GVPKRFSGSRGSDYSLTISSEDFVDYCYLQYASSPYTFGGGTKLEIKRTSS 245
 RESULT 15
 AAU72872
 ID AAU72872 standard; Protein; 499 AA.
 XX
 AC AAU72872;
 XX
 XX 26-FEB-2002 (first entry)
 DT
 XX 3B10xP4-14 bispecific single chain Fv.
 DE
 XX Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;

KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; FV;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10;
KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 8E5A7x4-7; P4-2; P4-3; P4-14;
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10XP4-3; 3B10XP4-14;
KW P53 tetramerisation domain; 3B10XP5-2; 3B10XP5-23.
XX Homo sapiens.
OS
XX
XX WO200171005-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 26-MAR-2001; 2001WO-EP03414.
PF
XX
XX 24-MAR-2000; 2000EP-0106467.
PR
XX
XX (KUFE/) KUFER P.
PA
XX
XX Kufer P, Riethmuller G, Lutterbuese R, Borschert K, Kischel R;
PI Mayer M, Hofmeister R;
XX
XX WPI; 2002-055119/07.
DR N-PSDB; AAS97146.
DR
XX
XX Multifunctional polypeptides comprising binding sites that specifically
PT recognise extracellular groups of the NKG2D receptor complex and
PT domains which function as receptors or ligands, useful for treating
PT cancers and infectious diseases -
XX
PS Example 5; Fig 16; 114pp; English.
XX
CC The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NKG2D receptor complex and a second domain which functions
CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
CC receptor and the polypeptides of the invention.
XX
SQ Sequence 499 AA;

Query Match 68.2%; Score 505; DB 23; Length 499;
Best Local Similarity 86.2%; Pred. No. 2.5e-30;
Matches 100; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 17 GTRCDIQTQSPSSLSASIGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLSGS 76
Db 377 GGSSELVMTQSPSSLSASIGERVSLTCRASQDIGSNLWVQQEPDGTIKRLIYATSSLSGS 436
QY 77 GVPKRFSGSGSDYSLTISSESEDFVAYCYQYASSPYTFGGGTKEIKRADAA 132
Db 437 GVPKRFSGSGSDYSLTISSESEDFVDYCYQYASSPYTFGGGTKEIKRTSS 492

Search completed: August 30, 2003, 22:04:04
Job time : 36.547 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2003, 21:57:15 ; Search time 23.3557 Seconds
(without alignments)
849.188 Million cell updates/sec

Title: US-08-836-455-2
Perfect score: 740
Sequence: 1 MGAPAIQLGFLLLFPCTRC.....IKRADAPTIVIPPPSKLG 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0

Maximum Match 100%

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published:Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	740	100.0	145	9	US-09-861-294-2
2	740	100.0	145	12	US-10-367-506-2
3	601	81.2	130	8	US-08-779-784-35
4	541	73.1	130	12	US-10-268-883-11
5	518	70.0	129	9	US-09-007-093-2
6	507	68.5	243	10	US-09-887-853-6
7	506	68.4	108	10	US-09-924-099-1
8	502	67.8	237	10	US-09-924-099-9
9	502	67.8	243	10	US-09-924-099-10
10	496	67.0	109	10	US-09-943-906-74
11	473	63.9	236	10	US-09-859-053-30
12	471	63.6	112	12	US-10-355-780-1
13	471	63.6	142	9	US-09-797-481-2
14	471	63.6	142	9	US-09-844-736-4
15	471	63.6	142	15	US-10-162-396-4

16	464	62.7	108	12	US-10-268-883-12	Sequence 12, Appl
17	461	62.3	131	8	US-08-779-784-21	Sequence 21, Appl
18	455.5	61.6	241	15	US-10-221-945-1	Sequence 1, Appl
19	445	60.1	234	9	US-09-740-002-24	Sequence 24, Appl
20	444	60.0	276	9	US-09-766-543-12	Sequence 12, Appl
21	442	59.7	109	10	US-09-943-906-73	Sequence 73, Appl
22	439	59.3	127	12	US-10-268-883-5	Sequence 5, Appl
23	438	59.2	236	15	US-10-006-593-69	Sequence 69, Appl
24	436	58.9	128	9	US-09-764-304-10	Sequence 10, Appl
25	436	58.9	128	9	US-09-764-304-19	Sequence 19, Appl
26	436	58.9	128	15	US-10-265-713-10	Sequence 10, Appl
27	436	58.9	128	15	US-10-265-713-19	Sequence 19, Appl
28	433	58.5	127	15	US-10-084-139-2	Sequence 2, Appl
29	423.5	57.2	234	9	US-09-740-002-26	Sequence 26, Appl
30	422	57.0	214	15	US-10-153-382-19	Sequence 19, Appl
31	421	56.9	237	9	US-09-056-160B-100	Sequence 100, App
32	421	56.9	491	14	US-10-011-125-2	Sequence 2, Appl
33	419	56.6	237	15	US-10-020-786-8	Sequence 8, Appl
34	419	56.6	237	15	US-10-227-694-4	Sequence 4, Appl
35	417	56.4	214	9	US-09-754-998-1	Sequence 1, Appl
36	416	56.2	237	15	US-10-020-786-10	Sequence 10, Appl
37	415	56.1	121	10	US-09-797-941A-4	Sequence 4, Appl
38	409	55.3	237	9	US-09-940-166A-6	Sequence 6, Appl
39	409	55.3	237	15	US-10-227-694-1	Sequence 1, Appl
40	407	55.0	214	9	US-09-940-166A-2	Sequence 2, Appl
41	407	55.0	214	9	US-09-811-384-11	Sequence 11, Appl
42	407	55.0	214	12	US-10-356-974-1	Sequence 1, Appl
43	407	55.0	214	15	US-10-253-366-1	Sequence 1, Appl
44	407	55.0	214	15	US-10-316-694-1	Sequence 1, Appl
45	406	54.9	107	15	US-10-056-794-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-09-861-294-2
; Sequence 2, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFQ AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-09-861-294-2

Query Match	100.0%;	Score 740;	DB 9;	Length 145;
Best Local Similarity	100.0%;	Pred. No. 8.9e-59;		
Matches 145;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1	MGAPAIQLGFLLLFPCTRCDIOMTQSPSSLSASLGQSVSLTCRASODIGINLHLWQEP	60	
Db	1	MGAPAIQLGFLLLFPCTRCDIOMTQSPSSLSASLGQSVSLTCRASODIGINLHLWQEP	60	
Oy	61	DGTLKRLIYATSSILGSGVGPKRFRSGSRGSDYSLTISSEDFVAYCYCLQYASSPYTFGG	120	
Db	61	DGTLKRLIYATSSILGSGVGPKRFRSGSRGSDYSLTISSEDFVAYCYCLQYASSPYTFGG	120	

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RESULT 4
US-10-268-893-11
; Sequence 11, Application US/10268883
; Publication No. US20030138862A1
; GENERAL INFORMATION:
; APPLICANT: Iso, J. Yun
; APPLICANT: Green, Jennifer Macphat
; TITLE OF INVENTION: Anti-HLA-DR Ant
; FILE REFERENCE: 05982.0052.NPUS01
; CURRENT APPLICATION NUMBER: US/10/2-26
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: USSN 60/3
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: USSN 60/3
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mouse
US-10-268-893-11

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Db 63 DGIKRLVYAASTLDSGVPKRFSGRSQDTSLTSSLESEDFADYYCLQYTNYPITFGA 122

QY 121 GTKLEIK 127
Db 123 GTKLEIK 129

RESULT 6
US-09-887-853-6
; Sequence 6, Application US/09887853
; Patent No. US20020168375A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; Oppermann, Hermann
; Houston, L. L.
; Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/887,853
; FILING DATE: 21-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6

Query Match 68.5%; Score 507; DB 10; Length 243;
Best Local Similarity 91.8%; Pred. No. 9.6e-38;
Matches 101; Conservative 2; Mismatches 7; Indels 0; Gaps 0

QY 21 DIQWTQPSLSASLGRVSLTCRASQDIGNLHWLQOEPDGTIKRLIYATSSLSGVPK 80
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Db 134 DIQWTQPSLSASLGRVSLTCRASQDIGNLHWLQOEPDGTIKRLIYATSSLSGVPK 193
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QY 81 RFGSGRSQDYSLTSSLESEDFVAYCYLOYASSPYTFGGGTKLEIKRAD 130
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Db 194 RFGSGRSQDYSLTSSLESEDFVYVYCLQYAIFFYTFGGGNTLEIKRAD 243
|||||:| | :| ||||||||| ||||||||| ||||||| :| |||

RESULT 7
US-09-924-099-1
; Sequence 1, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:

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; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-1

Query Match      68.4%; Score 506; DB 10; Length 108;
Best Local Similarity 92.6%; Pred. No. 4.8e-38;
Matches 100; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQOEPDGTIKRLIYATSSLGSGVPK 80
Db 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQOEPDGTIKRLIYATSSLGSGVPK 60

Qy 81 RFGSGRSGSDYSLTISSEDFVAYYCLQYASSPYTFGGGKLEIKR 128
Db 61 RFGSGRSGSDYSLTISSEDFVAYYCLQYASSPYTFGGGKLEIKR 108

RESULT 8
US-09-924-099-9
; Sequence 9, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 9
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-9

Query Match      67.8%; Score 502; DB 10; Length 237;
Best Local Similarity 90.1%; Pred. No. 2.6e-37;
Matches 100; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 17 GTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQOEPDGTIKRLIYATSSLG 76
Db 127 GGSQDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQOEPDGTIKRLIYATSSLD 186

Qy 77 GVPKRFSGRSGSDYSLTISSEDFVAYYCLQYASSPYTFGGGKLEIK 127
Db 77 GVPKRFSGRSGSDYSLTISSEDFVAYYCLQYASSPYTFGGGKLEIK 127

US-09-924-099-9
; Sequence 9, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 9
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-9

Query Match      67.8%; Score 502; DB 10; Length 237;
Best Local Similarity 90.1%; Pred. No. 2.6e-37;
Matches 100; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 17 GTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQOEPDGTIKRLIYATSSLG 76
Db 127 GGSQDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQOEPDGTIKRLIYATSSLD 186

Qy 77 GVPKRFSGRSGSDYSLTISSEDFVAYYCLQYASSPYTFGGGKLEIK 127
Db 77 GVPKRFSGRSGSDYSLTISSEDFVAYYCLQYASSPYTFGGGKLEIK 127

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Db 187 GVPKRFSGRSGSDYSLTISSEDFVAYYCLQYASSPYTFGGGKLEIK 237

RESULT 9
US-09-924-099-10
; Sequence 10, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 10
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-10

Query Match      67.8%; Score 502; DB 10; Length 243;
Best Local Similarity 90.1%; Pred. No. 2.7e-37;
Matches 100; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 17 GTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQOEPDGTIKRLIYATSSLG 76
Db 127 GGSQDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQOEPDGTIKRLIYATSSLD 186

Qy 77 GVPKRFSGRSGSDYSLTISSEDFVAYYCLQYASSPYTFGGGKLEIK 127
Db 187 GVPKRFSGRSGSDYSLTISSEDFVAYYCLQYASSPYTFGGGKLEIK 237

RESULT 10
US-09-943-906-74
; Sequence 74, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-162-396-4

Query Match          63.6%; Score 471; DB 15; Length 142;
Best Local Similarity 67.6%; Pred. No. 8.6e-35;
Matches 96; Conservative 13; Mismatches 33; Indels 0; Gaps 0;

QY 1 MGAPAQILGELLFFCTRCIDIOMTQSPSSLSASLGORVSLTCRASODIGINLHWLQOEP 60
Db 1 MVSTAQFLGILLWFFPGIKSDIKMTQSPSSMYASLAGERVITTCASODINGYLNWFQOEP 60

QY 61 DGTIKRLIYATSSILGSGVPRKFRSGSRGSDYSLTISSESEDFVAYYCLQYASSPYTFGG 120
Db 61 GKSPKTLIYRANRLIDGVPRFSGSGGQYISLTISSEYEDMGTYCYCLOFDEFPWMFEG 120

QY 121 GTKLEIKRADAPTVSIFPPSS 142
Db 121 GTKLEIKRADAPTVSIFPPSS 142
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2003, 22:02:45 ; Search time 17.5168 Seconds
(without alignments)
796.063 Million cell updates/sec

Title: US-08-836-455-2
Perfect score: 740
Sequence: 1 MGAPAIILGFLLLFPGRNC.....IKRADAPTIVTFPPSKLG 145
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

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2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	596	80.5	130	1 KVM5M4	Ig kappa chain pre
2	501	67.7	106	2 PL0260	Ig kappa chain v r
3	497	67.2	106	2 PL0259	Ig kappa chain v r
4	496	67.0	234	2 S14237	Ig kappa chain pre
5	478	64.6	129	2 D32513	Ig kappa chain pre
6	459	62.0	106	2 PL0262	Ig kappa chain v r
7	452	61.1	117	1 KVM53B	Ig kappa chain pre
8	447	60.4	234	2 S01320	Ig kappa chain pre
9	445	60.1	108	4 B47271	Ig kappa chain pre
10	443	59.9	128	2 A26406	nitrophenyl phosph
11	439	59.3	127	2 PH1224	Ig kappa chain v r
12	438	59.2	129	2 S40369	Ig kappa chain pre
13	435	58.8	98	2 PH1062	Ig kappa chain - h
14	435	58.8	126	2 A34904	Ig kappa chain v r
15	434	58.6	125	2 S40353	Ig kappa chain pre
16	434	58.6	130	2 S40368	Ig kappa chain v-J
17	433	58.5	129	2 B23986	Ig kappa chain - h
18	431	58.2	122	2 A29380	Ig kappa chain pre
19	429	58.0	141	2 A49134	Ig kappa chain v r
20	428.5	57.9	230	2 S33161	Ig kappa chain - s
21	428	57.8	129	2 S40317	Ig kappa chain - h
22	426	57.6	127	2 S52447	Ig kappa chain v r
23	425	57.4	132	2 S40334	Ig kappa chain - h
24	424	57.3	115	2 JL0080	Ig kappa chain pre
25	422	57.0	123	2 S40313	Ig kappa chain v-J
26	419	56.6	88	2 PL0261	Ig kappa chain v r
27	419	56.6	129	2 S52789	Ig kappa chain v r
28	419	56.6	131	2 S40352	Ig kappa chain v-J
29	418	56.5	125	2 S40349	Ig kappa chain v-J

ALIGNMENTS

RESULT 1
KVM5M4

Ig kappa chain precursor V region (MOPC 41) - mouse
N:Contains: Ig kappa chain precursor V region VK41
C:Species: Mus musculus (house mouse)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 28-May-1999
C:Accession: A93211; B93211; A93815; A94239; A01922; A01923
R:Seidman, J.G.; Max, E.E.; Leder, P.
Nature 280, 370-375, 1979

A:Title: A kappa-immunoglobulin gene is formed by site-specific recombination without
A:Reference number: A93211; MUID:79221900; PMID:111146
A:Accession: A93211
A:Molecule type: DNA
A:Residues: 1-130 <PC41>
A:Accession: B93211
A:Molecule type: DNA
A:Residues: 1-117 <VK41>
A:Cross-references: GB:V00804; GB:J00566; NID:952127; PIDN:CAA24186.1; PID:g575660
A:Note: the sequences were determined from the differentiated gene MOPC 41 and the ge
R:Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A:Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precurs
A:Reference number: A93815; MUID:77148916; PMID:403522
A:Accession: A93815
A:Molecule type: protein
A:Residues: 1-33 <BUR>
A:Note: Met-3 is apparently used as an alternative initiator in 25% of the chains
R:Gray, W.R.; Dreyer, W.J.; Hood, L.
Science 155, 465-467, 1967
A:Title: Mechanism of antibody synthesis: size differences between mouse kappa chains
A:Reference number: A94239; MUID:67056897; PMID:4162931
A:Accession: A94239
A:Molecule type: protein
A:Residues: 23-49, 'B', '51-53, 'LSB', '57-58, '22', '61-62, 'BZ', '65-76, 'B', '78-108, 110-130 <GRA
A:Experimental source: Bence Jones protein MOPC 41
C:Genetics: 19/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

Query Match 80.5%; Score 596; DB 1; Length 130;
Best Local Similarity 92.2%; Pred. No. 3.7e-42;
Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGAPAIILGFLLLFPGRNCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHLWQQEP 60

Db 3 MRAPAFGLFLLFQGTCDIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLOQEP 62
 QY 61 DGTIKRLIYATSSLSGSGVPRFSGSRGSDYSLTISSESEDFVAYYCLOYASSPYTFGG 120
 Db 63 DGTIKRLIYATSSLDGSGVPRFSGSRGSDYSLTISSESEDFVAYYCLOYASSPYTFGG 122
 QY 121 GTKLEIKR 128
 Db 123 GTKLEIKR 130

RESULT 2

PL0260
 Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 C:Accession: PL0260
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618; PMID:2104919
 A:Accession: PL0260
 A:Molecule type: mRNA
 A:Residues: 1-106 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:24-34/Region: complementarity-determining 1
 F:35-49/Region: framework 2
 F:50-56/Region: complementarity-determining 2
 F:57-88/Region: framework 3
 F:89-97/Region: complementarity-determining 3
 F:98-106/Region: framework 4

Query Match 67.7%; Score 501; DB 2; Length 106;
 Best Local Similarity 93.4%; Pred. No. 1.9e-34;
 Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 21 DIQMTQSPSSLSASLGERVSLTCRASQDIGINLHWLOQEPDGTIKRLIYATSSLSGSGVPR 80
 Db 1 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLOQEPDGTIKRLIYATSSLDGSGVPR 60
 QY 81 RFGSGRSGSDYSLTISSESEDFVAYYCLOYASSPYTFGGGTGLEI 126
 Db 61 RFGSGRSGSDYSLTISSESEDFVAYYCLOYASSPYTFGGGTGLEI 106

RESULT 3

PL0259
 Ig kappa chain V region (anti-DNA, DP1LVK) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 C:Accession: PL0259
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618; PMID:2104919
 A:Accession: PL0259
 A:Molecule type: mRNA
 A:Residues: 1-106 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:24-34/Region: complementarity-determining 1
 F:35-49/Region: framework 2
 F:50-56/Region: complementarity-determining 2
 F:57-88/Region: framework 3
 F:89-97/Region: complementarity-determining 3
 F:98-106/Region: framework 4

Query Match 67.2%; Score 497; DB 2; Length 106;
 Best Local Similarity 92.5%; Pred. No. 4.1e-34;
 Matches 98; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 21 DIQMTQSPSSLSASLGERVSLTCRASQDIGINLHWLOQEPDGTIKRLIYATSSLSGSGVPR 80
 Db 1 DIQMTQSPSSLSASLGERVSLTCRASQDIGRSLNWLOQEPDGTIKRLIYATSSLDGSGVPR 60
 QY 81 RFGSGRSGSDYSLTISSESEDFVAYYCLOYASSPYTFGGGTGLEI 126
 Db 61 RFGSGRSGSDYSLTISSESEDFVAYYCLOYASSPYTFGGGTGLEI 106

RESULT 4

SL4237
 Ig kappa chain precursor (15C5) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: SL4237
 R:Vandamme, A.M.; Bullens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
 Eur. J. Biochem. 192, 767-775, 1990
 A:Title: Construction and characterization of a recombinant murine monoclonal antibody
 A:Reference number: SL4236; MUID:91006173; PMID:2209622
 A:Accession: SL4237
 A:Molecule type: mRNA
 A:Residues: 1-234 <VAN>
 A:Cross-references: EMBL:X56394; NID:g51622; PID:CAA39805.1; PID:g51623
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 67.0%; Score 496; DB 2; Length 234;
 Best Local Similarity 68.5%; Pred. No. 1.1e-33;
 Matches 98; Conservative 15; Mismatches 30; Indels 0; Gaps 0;
 QY 1 MGAPAILGFLLLFPCTRCDIQMTQSPSSLSASLGERVSLTCRASQDIGINLHWLOQEP 60
 Db 1 MRPAPQFLGILLWFFPGIKCDIKMTQSPSSMYASLGERVTVTCRASQDINSYLSWIOQKP 60
 QY 61 DGTIKRLIYATSSLSGSGVPRFSGSRGSDYSLTISSESEDFVAYYCLOYASSPYTFGG 120
 Db 61 GKSPKTLIYGRNLRVAGVPSRFGSGSGQDYSLTISSESEDFVAYYCLOYASSPYTFGG 120
 QY 121 GTKLEIKRADAAAPTTSIFPPSSK 143
 Db 121 GTKLEIKRADAAAPTTSIFPPSE 143

RESULT 5

D32513
 Ig kappa chain precursor V region (BXW16) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
 C:Accession: D32513
 R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A
 J. Clin. Invest. 82, 852-860, 1988
 A:Title: Immunoglobulin kappa light chain variable region gene complex organization a
 A:Reference number: A94689; MUID:88331394; PMID:3138286
 A:Accession: D32513
 A:Molecule type: DNA
 A:Residues: 1-129 <KOF>
 A:Cross-references: GB:M20832; NID:g196941; PID:AAA38845.1; PID:g196942
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 64.6%; Score 478; DB 2; Length 129;
 Best Local Similarity 76.8%; Pred. No. 1.8e-32;
 Matches 96; Conservative 6; Mismatches 23; Indels 0; Gaps 0;
 QY 3 APAQILGFLLLFPFGTRCDIQMTQSPSSLSASLGERVSLTCRASQDIGINLHWLOQEPDG 62
 Db 5 APAQFLGILLWFFPGARCDIQMTQSPSSMFGSLGDRVSLSCRASQDIGINLHWLOQEPDG 64

Query Match 60.1%; Score 445; DB 4; Length 108;
Best Local Similarity 83.2%; Pred. No. 7.7e-30;
Matches 89; Conservative 7; Mismatches 11; Indels

QY 21 DIQWQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEPDGTIKRLIYATSSLSGSGVPG 80
 Db 2 ELVLTQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEPDGTIKRLIYATSSLSGSGVPG 61
 QY 81 RFGSGRSGDYSLTSSLESEDFVAYYCLOYASSPYTFGGGTTKLEIK 127
 Db 62 RFGSGRSGDYSLTSSLESEDFVAYYCLOYASSPYTFGGGTTKLEIK 108

RESULT 10

A26406
 Ig kappa chain V region (Ara-A) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 21-Jan-2000
 C:Accession: A26406
 R:Sanz, I.; Capra, J.D.
 A:Title: V-K and J-K gene segments of A/J Ara-A antibodies: somatic recombination generated
 A:Reference number: A26406; MUID:87147197; PMID:3103124
 A:Accession: A26406
 A:Molecule type: DNA
 A:Residues: 1-128 <SAN>
 A:Cross-references: GB:M15519
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 59.9%; Score 443; DB 2; Length 128;
 Best Local Similarity 70.3%; Pred. No. 1.3e-29;
 Matches 90; Conservative 11; Mismatches 27; Indels 0; Gaps 0;
 QY 1 MGPAQILGFLLLFPQTRCDIQWQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEP 60
 Db 1 MIASAOPLGLLLCFQGTCTDIQWQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEP 60
 QY 61 DGTIKRLIYATSSLSGSGVPGKRFSGSGSGDYSLTSSLESEDFVAYYCLOYASSPYTFGG 120
 Db 61 DGTIKRLIYATSSLSGSGVPGKRFSGSGSGDYSLTSSLESEDFVAYYCLOYASSPYTFGG 120
 QY 121 GTKLEIKR 128
 Db 121 GTKLEIKR 128

RESULT 11

PH1224
 Ig kappa chain precursor V region (M-T151) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
 C:Accession: PH1224
 R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz
 Gene 121, 271-278, 1992
 A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on
 A:Reference number: PH1224; MUID:93077041; PMID:1446824
 A:Accession: PH1224
 A:Molecule type: mRNA
 A:Residues: 1-127 <WEI>
 A:Cross-references: NID:g260761; PIDN:AAB24318.1; PID:g260762
 A:Note: This mouse sequence was hybridized and fused with a human constant region gene
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-127/Product: Ig light chain V region #status predicted <MAT>
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 59.3%; Score 439; DB 2; Length 127;
 Best Local Similarity 69.3%; Pred. No. 2.8e-29;
 Matches 88; Conservative 12; Mismatches 27; Indels 0; Gaps 0;
 QY 1 MGPAQILGFLLLFPQTRCDIQWQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEP 60
 Db 1 MMSSAOPLGLLLCFQGTCTDIQWQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEP 60

QY 61 DGTIKRLIYATSSLSGSGVPGKRFSGSGSGDYSLTSSLESEDFVAYYCLOYASSPYTFGG 120
 Db 61 DGTIKRLIYATSSLSGSGVPGKRFSGSGSGDYSLTSSLESEDFVAYYCLOYASSPYTFGG 120
 QY 121 GTKLEIK 127
 Db 121 GTKLEIK 127

RESULT 12

S40369
 Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40369
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891; PMID:8258341
 A:Accession: S40369
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-129 <KLE>
 A:Cross-references: EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PID:g441427
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 59.2%; Score 438; DB 2; Length 129;
 Best Local Similarity 70.2%; Pred. No. 3.4e-29;
 Matches 87; Conservative 11; Mismatches 26; Indels 0; Gaps 0;
 QY 5 AQLIGFLLLPQTRCDIQWQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEPDGTI 64
 Db 6 AQLIGFLLLPQTRCDIQWQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEPDGTI 64
 QY 65 KRLIYATSSLSGSGVPGKRFSGSGSGDYSLTSSLESEDFVAYYCLOYASSPYTFGGGTKL 124
 Db 66 KSLIYATSSLSGSGVPGKRFSGSGSGDYSLTSSLESEDFVAYYCLOYASSPYTFGGGTKL 125
 QY 125 EIKR 128
 Db 126 EIKR 129

RESULT 13

PH1062
 Ig light chain V region (clone 202.105) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PH1062
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1062
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-98 <TII>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 58.8%; Score 435; DB 2; Length 98;
 Best Local Similarity 87.8%; Pred. No. 4.6e-29;
 Matches 86; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 21 DIQWQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEPDGTIKRLIYATSSLSGSGVPG 80
 Db 1 DIQWQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEPDGTIKRLIYATSSLSGSGVPG 60
 QY 81 RFGSGRSGDYSLTSSLESEDFVAYYCLOYASSPYTF 118

Search completed: August 30, 2003, 22:08:53
Job time : 18.5168 secs

Db	61	RFGSGRSGDYSLTISSESEDFADYCYLQYASSPYTF	98
RESULT 14			
A34904			
Ig kappa chain precursor V region (5-27) - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000			
C:Accession: A34904			
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.			
J. Biol. Chem. 265, 133-138, 1990			
A:Title: Active site structure and antigen binding properties of idiotypically cross-reactive			
A:Reference number: A34903; PMID:90094387; PMID:2104617			
A:Accession: A34904			
A:Status: preliminary; not compared with conceptual translation			
A:Molecule type: mRNA			
A:Residues: 1-126 <BED>			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
F:35-109/Domain: immunoglobulin homology <IMM>			
Query Match 58.8%; Score 435; DB 2; Length 126;			
Best Local Similarity 70.5%; Pred. No. 5.9e-29;			
Matches 86; Conservative 12; Mismatches 24; Indels 0; Gaps 0;			
QY	5	AQILGLFLLLPCTGCDIQMTQSPSSLSASLGQVSLTCSRASODIGINLHWLQEPDGTI	64
Db	4	AQFLGLLLLCFQGTCDIQMTQSPSSLSASLGQVSLTCSRASODINNLYNWYQKPDGTV	63
QY	65	KRLIYATSSLGSGVPRFSGSGSDYSLTISSESEDFVAYCYLQYASSPYTFGGGTKL	124
Db	64	KLLIYTSKLGSGVPRFSGSGSDYSLTISNLEQEDIATYFCQGGNTLPWTFGGGTKL	123
QY	125	EI 126	
Db	124	EI 125	
RESULT 15			
S40353			
Ig kappa chain V-J-C region - human			
C:Species: Homo sapiens (man)			
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000			
C:Accession: S40353			
R:Klein, R.; Jaenichen, R.; Zachau, H.G.			
Eur. J. Immunol. 23, 3248-3271, 1993			
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.			
A:Reference number: S40312; PMID:94080891; PMID:8258341			
A:Accession: S40353			
A:Status: preliminary; translation not shown			
A:Molecule type: mRNA			
A:Residues: 1-125 <KLE>			
A:Cross-references: EMBL:X72463			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
F:30-104/Domain: immunoglobulin homology <IMM>			
Query Match 58.6%; Score 434; DB 2; Length 125;			
Best Local Similarity 68.0%; Pred. No. 7.1e-29;			
Matches 85; Conservative 14; Mismatches 26; Indels 0; Gaps 0;			
QY	7	ILGLFLLLPCTGCDIQMTQSPSSLSASLGQVSLTCSRASODIGINLHWLQEPDGTIKR	66
Db	1	LLGLLLWFFGACDIQMTQSPSSLSASVGDRTYTCRASQIGNDLGWTQQRPGKAPKR	60
QY	67	LIYATSSLGSGVPRFSGSGSDYSLTISSESEDFVAYCYLQYASSPYTFGGGTKLEI	126
Db	61	LIYAASFQSGVPRFSGSGGTEFTLTISGLQPEDFATYCYLQHNSYPLTFGGGTRVEI	120
QY	127	KRADA 131	
Db	121	KRTVA 125	

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OM protein - protein search, using sw model

Run on: August 30, 2003, 19:57:10 ; Search time 10.2181 Seconds
(without alignments)
667.331 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 740

Sequence: 1 MGAPQILGFLLLFPGRRC.....IKRADAAPTVSIFPPSSKLG 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	596	80.5	130	1	KV5G_MOUSE
2	452	61.1	117	1	KV5H_MOUSE
3	412	55.7	128	1	KV5E_MOUSE
4	394	53.2	129	1	KV1W_HUMAN
5	389	52.6	108	1	KV5J_MOUSE
6	384	51.9	108	1	KV5K_MOUSE
7	383	51.8	108	1	KV5Q_MOUSE
8	382	51.6	108	1	KV5M_MOUSE
9	382	51.6	108	1	KV5N_MOUSE
10	381	51.5	117	1	KV1I_HUMAN
11	379	51.2	108	1	KV5L_MOUSE
12	373	50.4	108	1	KV1R_HUMAN
13	370	50.0	115	1	KV5F_MOUSE
14	368	49.7	129	1	KV1X_HUMAN
15	367	49.6	108	1	KV5S_MOUSE
16	365	49.3	108	1	KV5O_MOUSE
17	364	49.2	108	1	KV5Q_MOUSE
18	363	49.1	108	1	KV5T_MOUSE
19	362	48.9	117	1	KV1J_HUMAN
20	354	47.8	108	1	KV1O_HUMAN
21	353.5	47.8	129	1	KV3H_HUMAN
22	353.5	47.8	129	1	KV3M_HUMAN
23	353	47.7	108	1	KV5R_MOUSE
24	352.5	47.6	129	1	KV3L_HUMAN
25	351	47.4	108	1	KV1Y_HUMAN
26	350	47.3	128	1	KV3K_HUMAN
27	348	47.0	108	1	KV1L_HUMAN
28	348	47.0	108	1	KV1L_HUMAN
29	348	47.0	108	1	KV1P_HUMAN
30	346	46.8	108	1	KV1H_HUMAN
31	346	46.8	108	1	KV1V_HUMAN
32	341	46.1	108	1	KV1B_HUMAN
33	339	45.8	108	1	KV1C_HUMAN

ALIGNMENTS

RESULT 1

ID	KV5G_MOUSE	STANDARD;	PRT;	130 AA.
AC	P01639; P01640;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-V region MOPC 41 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=79221900; PubMed=111146;			
RA	Seidman J.G., Max E.E., Leder P.;			
RT	"A kappa-immunoglobulin gene is formed by site-specific recombination			
RT	without further somatic mutation.";			
RL	Nature 280:370-375(1979).			
RN	[2]			
RP	SEQUENCE OF 1-33.			
RX	MEDLINE=77148916; PubMed=403522;			
RA	Burstein Y., Schechter I.;			
RT	"Amino acid sequence of the NH2-terminal extra piece segments of the			
RT	precursors of mouse immunoglobulin lambdaI-type and kappa-type light			
RL	chains.";			
Proc.	Natl. Acad. Sci. U.S.A. 74:716-720(1977).			
RN	[3]			
RP	SEQUENCE OF 23-130.			
RX	MEDLINE=67056897; PubMed=4162931;			
RA	Gray W.R., Dreyer W.J., Hood L.;			
RT	"Mechanism of antibody synthesis: size differences between mouse			
RT	kappa chains.";			
Science	155:465-467(1967).			
CC	-I- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE			
CC	SYSTEM DIRECTED BY MENA ISOLATED FROM MYELOMA POLYSOMES.			
CC	-I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
DR	PIR; A93211; KVM5M4.			
DR	HSSP; P01607; IREI.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
DR	Immunoglobulin V region; Signal; Bence-Jones protein.			
FT	SIGNAL	1	22	
FT	CHAIN	23	130	IG KAPPA CHAIN V-V REGION MOPC 41.
FT	DOMAIN	23	45	FRAMEWORK-1.
FT	DOMAIN	46	56	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	57	71	FRAMEWORK-2.
FT	DOMAIN	72	78	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	79	110	FRAMEWORK-3.
FT	DOMAIN	111	119	COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN	120	129	FRAMEWORK-4.
FT	DISULFID	45	110	BY SIMILARITY.

P01597 homo sapien
P01606 homo sapien
P01596 homo sapien
P01611 homo sapien
P01593 homo sapien
P01649 mus musculu
P01612 homo sapien
P01605 homo sapien
P06310 homo sapien
P01603 homo sapien
P01598 homo sapien
P01609 homo sapien

KV1E_HUMAN
KV1D_HUMAN
KV1S_HUMAN
KV1A_HUMAN
KV5P_MOUSE
KV1T_HUMAN
KV1M_HUMAN
KV2F_HUMAN
KV1K_HUMAN
KV1E_HUMAN
KV1Q_HUMAN

34 339 45.8 108 1
35 339 45.8 108 1
36 338.5 45.7 107 1
37 338 45.7 108 1
38 337 45.5 108 1
39 332 44.9 108 1
40 331.5 44.8 109 1
41 331 44.7 108 1
42 330.5 44.7 133 1
43 327 44.2 108 1
44 326 44.1 108 1
45 325 43.9 108 1

FT VARIANT 1 2 MISSING (IN 25% OF THE MOLECULES).

FT NON_TER 130 130

SQ SEQUENCE 130 AA; 14311 MW; 5EPE0FE71D5F1BEC CRC64;

Query Match 80.5%; Score 596; DB 1; Length 130;

Best Local Similarity 92.2%; Pred. No. 2.9e-52;

Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGAPAIIGLGLLLFPPTGTRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEP 60

DB 3 MRAPAIIFGILLFPPTGTRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEP 62

QY 61 DGTIKRLIYATSSLSGSGVPRKFSRSGSDYSLTISSESEDFVAYYCLQYASSPYTFGG 120

DB 63 DGTIKRLIYATSSLSGSGVPRKFSRSGSDYSLTISSESEDFVAYYCLQYASSPYTFGG 122

QY 121 GTKLEIKR 128

DB 123 GTKLEIKR 130

RESULT 2

KV5H_MOUSE

ID KV5H_MOUSE STANDARD; PRT; 117 AA.

AC P01641;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-V region MOPC 173B precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ON NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=81064681; PubMed=6777049;

RA Max E.E., Seidman J.G., Miller H., Leder P.;

RT "Variation in the crossover point of kappa immunoglobulin gene V-J

recombination: evidence from a cryptic gene.";

RL Cell 21:793-799(1980).

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CC -----

DR EMBL; K00880; AAA39031.1; -.

DR PIR; A01924; KVM53B.

DR HSSP; P01607; IREI.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IgV; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 22

FT CHAIN 23 117 IG KAPPA CHAIN V-V REGION MOPC 173B.

FT DOMAIN 23 45 FRAMEWORK-1.

FT DOMAIN 23 45 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 46 56 FRAMEWORK-2.

FT DOMAIN 57 71 FRAMEWORK-3.

FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 79 110 FRAMEWORK-3.

FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 45 110 BY SIMILARITY.

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12954 MW; 24B3D4B9AC2EAD6C CRC64;

Query Match

Best Local Similarity 61.1%; Score 452; DB 1; Length 117;

Matches 92; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 MGAPAIIGLGLLLFPPTGTRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEP 60

DB 3 MRAPAVEGFLLLFPPTGTRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEP 62

QY 61 DGTIKRLIYATSSLSGSGVPRKFSRSGSDYSLTISSESEDFVAYYCLQYASSP 115

DB 63 GETIKHLIYETSNLSDGVPKFSRSGSDYSLTISSESEDFVAYYCLQYASSP 117

RESULT 3

KV5E_MOUSE

ID KV5E_MOUSE STANDARD; PRT; 128 AA.

AC P01637;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-V region T1 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ON NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=81052342; PubMed=6776411;

RA Altenburger W., Steinmetz M., Zachau H.G.;

RT "Functional and non-functional joining in immunoglobulin light chain

genes of a mouse myeloma.";

RL Nature 287:603-607(1980).

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CC -----

DR EMBL; V00772; CAA24150.1; -.

DR PIR; A01920; KVM5T1.

DR HSSP; P80362; 1WTL.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION T1.

FT DOMAIN 21 43 FRAMEWORK-1.

FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 55 69 FRAMEWORK-2.

FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 77 108 FRAMEWORK-3.

FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 118 127 FRAMEWORK-4.

FT DISULFID 43 108 BY SIMILARITY.

FT NON_TER 128 128

SQ SEQUENCE 128 AA; 14385 MW; AFA563D31BB7E05 CRC64;

Query Match

Best Local Similarity 55.7%; Score 412; DB 1; Length 128;

Matches 81; Conservative 14; Mismatches 33; Indels 0; Gaps 0;

QY 1 MGAPAIIGLGLLLFPPTGTRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEP 60

DB 1 MRPAPFLGILLFPPTGTRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQOEP 60

QY 61 DGTIKRLIYATSSLSGSGVPRKFSRSGSDYSLTISSESEDFVAYYCLQYASSPYTFGG 120

DB 61 GKSPKTLIYANRLVDPVPSRSGSDYSLTISSESEDFVAYYCLQYASSPYTFGG 120

QY 121 GTKLEIKR 128


```
KV5N_MOUSE
ID KV5N_MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP 124E1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR HSSP; P01607; IREI.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEFA2 CRC64;

Query Match
Best Local Similarity 70.4%; Score 382; DB 1; Length 108;
Matches 76; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 21 DIQMTQSPSSLSASLGQRVSLTCSRASQDIGINLHWLQEPDGTIKRLIYATSLGSGVPK 80
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 DIQMTQTSLSASLGDRVTISCRASQDINNLYNQKPDGTIVKLLIYTSKRLHSGVPS 60

QY 81 RESGSRGSDYSLTISSESEDFVAYCYQYASSPYTFGGGKLEIKR 128
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 RESGSGGPDYSLTISLNLEQDIATYFCQGGKTLPRTFGGGKLEIKR 108

RESULT 10
KVIL_HUMAN
ID KVIL_HUMAN STANDARD; PRT; 117 AA.
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RT kappa genes and a pseudogene.";
RL Nature 288:730-733(1980).
RN [2]

SEQUENCE FROM N.A.
RP MEDLINE=83129397; PubMed=6402305;
RA Bentley D.L., Rabbitts T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
RT recently duplicated human V kappa sequences have diverged by gene
RT conversion.";
RL Cell 32:181-189(1983).
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CC -----
CC EMBL; K01322; AAA58930.1; -
CC EMBL; K01324; AAA58932.1; -
CC EMBL; V00558; CAA23824.1; -
CC PIR; A01881; K1H011.
CC HSSP; P01607; IREI.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding activity; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro: IPR007110; Ig-Like.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION HK101.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12799 MW; D7DOFF3718CEP587 CRC64;

Query Match
Best Local Similarity 51.5%; Score 381; DB 1; Length 117;
Matches 76; Conservative 10; Mismatches 25; Indels 0; Gaps 0;

QY 5 AQILGFLLLFPCTRCDIQMTQSPSSLSASLGQRVSLTCSRASQDIGINLHWLQEPDGTI 64
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7 AQLLGLLLCFPGARCDIQMTQSPSSLSASVGRVITTCRARGISGLWLAWYQOKPEKAP 66

QY 65 KRLIYATSLGSGVPKRFRSGSRGSDYSLTISSESEDFVAYCYQYASSPY 115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 KSLIYAASSLQSGVPSRFRSGSGSGTDTLTLSLQPEDFATYCYQYNSYP 117

RESULT 11
KV5L_MOUSE
ID KV5L_MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
```

RT *Complete amino acid sequence of light chain variable regions derived
 RT from five monoclonal anti-p-azophenylarsenate antibodies differing
 RT with respect to a crossreactive idiotype.*;
 CC Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 RL -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR HSP; P01607; IREI.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region.

FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;
 Query Match 51.2%; Score 379; DB 1; Length 108;
 Best Local Similarity 70.4%; Pred. No. 7.9e-31;
 Matches 76; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 21 DIQMTSPSSLSASLGORVSLTCSRASODIGINLHWLQOEPDGTIKRLIYATSSLSGVK 80
 DB 1 DIQMTSSLSASLGDRVTITCRASQDINSYLNWYQKPGDGVKLIYITSLRHSGVPS 60
 QY 81 RFGSGSGSDYSLTISSESEDFVAYCYQYASSPYTFGGTKLEIKR 128
 DB 61 RFGSGSGSDYSLTISNLEQDIATYFCQGNMLPRTFGGTKLEIKR 108

RESULT 12

KVIR_HUMAN
 ID KVIR_HUMAN STANDARD; PRT; 108 AA.
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 RT (protein WEA) with antibody activity against 3,4-pyruvylated
 RT galactose in Klebsiella polysaccharides K30 and K33.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
 CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 CC WALDENSTROM'S MACROGLOBULINEMIA.
 DR PIR: A01876; KIHUWE.
 DR HSP; P80362; IWL.
 DR GO: 0005576; C:extracellular; NAS.
 DR GO: 0003823; F:antigen binding activity; NAS.
 DR GO: 0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; Monoclonal antibody.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;

FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;
 Query Match 50.4%; Score 373; DB 1; Length 108;
 Best Local Similarity 66.7%; Pred. No. 3.1e-30;
 Matches 72; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

RESULT 13

KVSF_MOUSE
 ID KVSF_MOUSE STANDARD; PRT; 115 AA.
 AC P01638;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region L6 precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81220975; PubMed=6264318;
 RA Pech M., Hochtl J., Schnell H., Zachau H.G.;
 RT "Differences between germ-line and rearranged immunoglobulin V kappa
 RT coding sequences suggest a localized mutation mechanism.";
 RL Nature 291:668-670(1981).
 DR PIR: A01921; KMSL6.
 DR HSP; P01607; IREI.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 >115
 FT DOMAIN 21 43
 FT DOMAIN 44 54
 FT DOMAIN 55 69
 FT DOMAIN 70 76
 FT DOMAIN 77 108
 FT DOMAIN 109 >115
 FT DISULFID 43 108
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12986 MW; BA852C58F328E1C3 CRC64;
 Query Match 50.0%; Score 370; DB 1; Length 115;
 Best Local Similarity 64.3%; Pred. No. 6.7e-30;
 Matches 74; Conservative 10; Mismatches 31; Indels 0; Gaps 0;

QY 1 MGAPAQILGELLFLPCTRCDIQMTQSPSSLSASLGORVSLTCSRASODIGINLHWLQOEP 60
 DB 1 MRPAPQFLGILLFLWPGIKCDIKMTQSPSSMSALGSRVITTCRASODINSYLSWFOQKP 60
 QY 61 DGTIKRLIYATSSLSGVKPRFSGSGSDYSLTISSESEDFVAYCYQYASSPYTFGGTKLEIKR 115

```
Db 61 GSKPTLIYRANRLVDGVPSPSGSGQDYSLTISSEYEDMGIIYCLQYDEFP 115

RESULT 14
KVIX_HUMAN STANDARD; PRT; 129 AA.
AC P04432;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Daudi precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G.; Combriato G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC -----
DB EMBL; X00966; CA245748.1; ALT_TERM.
DR PIR; A01884; KIHUDI.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION DAUDI.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14235 MW; CAF076BCE5574C8 CRC64;

Query Match 49.7%; Score 368; DB 1; Length 129;
Best Local Similarity 59.1%; Pred. No. 1.2e-29;
Matches 75; Conservative 16; Mismatches 36; Indels 0; Gaps 0;

QY 1 MCAPAIILGFLLLLPFGTRCDIQWTSFSSLSASLGQVSLTCRASQDIGINLHWLQEP 60
DB 3 MRVPAQLGLLLLRVRRCDIQWTSFSSLSASVGDRTITCRAGHNTNPLSLWQKP 62
QY 61 DGTIRKLIYATSSLGSGVSKRSGSDYSLTISSESEDFVAYYCLOQYASSPYTFGG 120
DB 63 GKAPLLIYAVNLQVGPSPSGSGAEFTLTISLQPEDFATYICQNNYNSFTFGG 122
QY 121 GTKLEIK 127
DB 123 GTKVDNK 129
```

```
RESULT 15
KV5S_MOUSE STANDARD; PRT; 108 AA.
AC P01652;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region J606.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N.; Slankard J.; Paul L.; Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR; A92811; KVM506.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11810 MW; 8DB4DD31076F2AFB CRC64;

Query Match 49.6%; Score 367; DB 1; Length 108;
Best Local Similarity 65.7%; Pred. No. 1.2e-29;
Matches 71; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 21 DIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQEPDGTIKRLIYATSSLGSGVK 80
DB 1 DVQMIQSPSSLSASLGDIVITMCASQGSITNLNFWQKPGKAPKLLIYGASNLDEGVPS 60
QY 81 RFGSGRSGSDYSLTISSESEDFVAYYCLOQYASSPYTFGGTKLEIKR 128
DB 61 RFGSGRYGTDFTLTISSEDEDMATYFCIQHSYLYPTFGGTKLEIKR 108

Search completed: August 30, 2003, 22:04:34
Job time : 10.2181 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2003, 21:05:00 ; Search time 34.547 Seconds
(without alignments)
1083.094 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 740

Sequence: 1 MGAQAIIIGLFLLLFPGRTRC.....IKRADAAPTSTIFFPSSKLG 149

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	642	86.8	127	11	Q925S9	Q925S9 mus musculus
2	513	69.3	234	11	Q8R062	Q8R062 mus musculus
3	506	68.4	234	11	Q91WF8	Q91WF8 mus musculus
4	492	66.5	233	11	Q91WS9	Q91WS9 mus musculus
5	450	60.8	234	11	Q8VCP0	Q8VCP0 mus musculus
6	433	58.5	214	11	Q9RIA5	Q9RIA5 mus musculus
7	416	56.2	234	4	Q8NEK1	Q8NEK1 homo sapien
8	391.5	52.9	239	11	Q8K0F8	Q8K0F8 mus musculus
9	382.5	51.7	235	11	Q91W12	Q91W12 mus musculus
10	380	51.4	107	11	Q9UL84	Q9UL84 mus musculus
11	374	50.5	238	11	Q99M37	Q99M37 mus musculus
12	371.5	50.2	239	4	Q8TCD0	Q8TCD0 homo sapien
13	370	50.0	238	11	Q8VCI6	Q8VCI6 mus musculus
14	363.5	49.1	134	11	Q8VDD0	Q8VDD0 mus musculus
15	360.5	48.7	114	11	Q8K1F1	Q8K1F1 mus musculus
16	360	48.6	108	4	Q9UL70	Q9UL70 homo sapien

17	359.5	48.6	107	4	Q96SA9	Q96sa9 homo sapien
18	357.5	48.3	112	11	Q8K1F3	Q8k1f3 mus musculus
19	357	48.2	108	4	Q9UL77	Q9ul77 homo sapien
20	356.5	48.2	239	11	Q8VC55	Q8vc55 mus musculus
21	352.5	47.6	239	4	Q8NEK0	Q8nek0 homo sapien
22	346	46.8	234	11	Q8R028	Q8r028 mus musculus
23	342.5	46.3	112	11	Q8K1F2	Q8k1f2 mus musculus
24	341.5	46.1	112	11	Q8K1F0	Q8k1f0 mus musculus
25	339	45.8	108	11	Q8VIJ0	Q8viJ0 mus musculus
26	338	45.7	116	4	Q96PF6	Q96pf6 homo sapien
27	337.5	45.6	107	4	Q9UL81	Q9ul81 homo sapien
28	336	45.4	108	4	Q9UL79	Q9ul79 homo sapien
29	334	44.5	298	11	Q9QYF0	Q9qyf0 mus musculus
30	334	44.3	109	11	Q920E6	Q920e6 mus musculus
31	317.5	42.9	109	4	Q9UL78	Q9ul78 homo sapien
32	316	42.7	108	4	Q9UL83	Q9ul83 homo sapien
33	315.5	42.6	109	4	Q9UL85	Q9ul85 homo sapien
34	310	41.9	111	11	Q920E9	Q920e9 mus musculus
35	299.5	40.5	109	4	Q9UL86	Q9ul86 homo sapien
36	296.5	40.1	106	5	Q9UL40	Q9ul40 schistosoma
37	295	39.9	97	11	Q9JL76	Q9j176 mus musculus
38	294.5	39.8	241	11	Q921A6	Q921a6 mus musculus
39	293	39.6	101	11	Q9JL78	Q9j178 mus musculus
40	275	37.2	114	4	Q9UL80	Q9ul80 homo sapien
41	273	36.9	236	4	Q8NEJ1	Q8nej1 homo sapien
42	270.5	36.6	237	4	Q8WUK4	Q8wuk4 homo sapien
43	269	36.4	103	11	Q9JL80	Q9j180 mus musculus
44	268.5	36.3	237	4	Q8WTU6	Q8wtu6 homo sapien
45	267	36.1	107	11	Q9ER29	Q9er29 mus musculus

ALIGNMENTS

RESULT 1

ID	Q925S9	PRELIMINARY;	PRT;	127 AA.
AC	Q925S9;			
DT	01-DEC-2001 (TReMBLrel. 19, Created)			
DT	01-DEC-2001 (TReMBLrel. 19, Last sequence update)			
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)			
DE	Immunoglobulin light chain (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c;			
RX	MEDLINE=99306687; PubMed=10380019;			
RA	Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,			
RA	Foon K.A., Chatterjee S.K.;			
RT	"Construction and characterization of a chimeric fusion protein			
RT	associated antigen and the cytokine GM-CSF.";			
RL	Hybridoma 18:193-202(1999).			
DR	EMBL; AF124721; AAK55120.1; -			
DR	InterPro: IPR007110; Ig-like.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS00835; IG_LIKE; 1.			
FT	NON_TER 127 127			
SQ	SEQUENCE 127 AA; 13794 MW; 13F61BEBB981FA5 CRC64;			

Query Match 86.8%; Score 642; DB 11; Length 127;

Best Local Similarity 99.2%; Pred. No. 8.5e-60;

Matches 126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGAQAIIIGLFLLLFPGRTRC.....IKRADAAPTSTIFFPSSKLG 60

DB 1 MRAQAIIIGLFLLLFPGRTRC.....IKRADAAPTSTIFFPSSKLG 60


```

DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031498; AAH31498.1; -
DR InterPro; IPR002198; ADH_Short.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;

Query Match 52.9%; Score 391.5; DB 11; Length 239;
Best Local Similarity 55.4%; Pred. No. 4.7e-33;
Matches 82; Conservative 20; Mismatches 41; Indels 5; Gaps 1;

QY 1 MGAPAIQLGLLLFPFG--TRCDIQMTQSPSSLSASLGQVSLTCRASQDI-----GNLHW 55
DB 1 MMSPAQLFLLLVLSIQINGDVVMTQPTFLSVITIGPASISKSSQSLFYTNKMYLSW 60

QY 56 LQPEPDGTLKRLIYATSSLSGSGVSKRFSRSGDYSLTISSEDFVAYYCLOYASSP 115
DB 61 LLQPCQSPKRLISLVSLDGGVDPDRFSGSGGTDTFLKISRVEADGLGVYICLQSTHP 120

QY 116 YTFGGGTLKLEIKRADAAPTIVSIFPPSSK 143
DB 121 YTFGGGTLKLEIKRADAAPTIVSIFPPSS 148

RESULT 9
Q91W12 PRELIMINARY; PRT; 235 AA.
ID Q91W12
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Unknown (Protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00409; Ig; 2.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 51.7%; Score 382.5; DB 11; Length 235;
Best Local Similarity 55.9%; Pred. No. 4e-32;
Matches 81; Conservative 22; Mismatches 39; Indels 3; Gaps 2;

```

```

QY 1 MGAPAIQLGLLLFPFG--TRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQ 58
DB 1 MDFQVQIFSLTISASVILSRQIVLTQSPAINSPGERVTMTCSASSVS-HMHVQQ 59

QY 59 EPDGTIKRLIYATSSLSGSGVSKRFSRSGDYSLTISSEDFVAYYCLOYASSPPTF 118
DB 60 KSGTSPKRWIYDTFKLTSGVDPDRFSGSGGTYSLTISNWEADVATYYCCQWSRNPPTF 119

QY 119 GGGTKLEIKRADAAPTIVSIFPPSSK 143
DB 120 GVGTKLEIKRADAAPTIVSIFPPSS 144

RESULT 10
Q9JL84 PRELIMINARY; PRT; 107 AA.
ID Q9JL84
AC Q9JL84;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-myoisin immunoglobulin light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206022; AAF69320.1; -
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11648 MW; ACF9B1253ACAL1E5D CRC64;

Query Match 51.4%; Score 380; DB 11; Length 107;
Best Local Similarity 71.0%; Pred. No. 2.6e-32;
Matches 76; Conservative 5; Mismatches 26; Indels 0; Gaps 0;

QY 21 DIQMTQSPSSLSASLGQVSLTCRASQDIGINLHWLQEPDGTIKRLIYATSSLSGSPVK 80
DB 1 DIQMTQSTSLASLGDVRVXXCSASQGISNXXXWFQKPKDGTGTVKLLIYTTSLXSGVPS 60

QY 81 RFSGSRSGDYSLTISSEDFVAYYCLOYASSPPTFGGTTLEIK 127
DB 61 RFSGSGGXDYSLTISNLEPDATATYCCQISKFPPTFGGTTLEIK 107

RESULT 11
Q99M37 PRELIMINARY; PRT; 238 AA.
ID Q99M37
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```


DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14525 MW; CDF8E2236E2D0CF CRC64;

Query Match 49.1%; Score 363.5; DB 11; Length 134;
Best Local Similarity 57.8%; Pred. No. 1.9e-30;
Matches 78; Conservative 17; Mismatches 37; Indels 3; Gaps 2;
Qy 1 MGAPAIQLGFLLLFPG--TRCDIQMTQSPSSLSASLGQRVSLTCRASODIGINLHWLQ 58
Db 1 MDFQVQIFSFLLISASVILSRGQIVLTQSPAINSPGKVTMTCSASSISY-MHWYQ 59
Qy 59 EPDGTIKRLIYATSSLGSGVSKPREFSGSGSDYSLTISSEDFVAYYCLOYASSPYTF 118
Db 60 KPGTSPKRWIYDTSKLASGVPAFSGSGSGTSYSLTISSEDAEADATYCHQRSSYPWTF 119
Qy 119 GGGTKLEIKRADAAP 133
Db 120 GGGTKLEIKRADAAP 134

RESULT 15
Q8K1F1 PRELIMINARY; PRT; 114 AA.
AC O8K1F1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=Hyperimmunized spleen;
RA Zhou X.-X., Taguchi H., Plaque S., Karle S., Nishiyama Y., Paul S.;
RT "Innate proteolytic antibodies: Failed D-VIPase response to the D-
RT entantioner of VIP and identification of L-VIPase VL domains."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516284; AAM64202.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR07110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 114
SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3EEFD1 CRC64;

Query Match 49.7%; Score 360.5; DB 11; Length 114;
Best Local Similarity 63.2%; Pred. No. 3.2e-30;
Matches 72; Conservative 16; Mismatches 25; Indels 1; Gaps 1;
Qy 21 DIQMTQSPSSLSASLGQRVSLTCRASODIGIN-LHWLQRPDGTIKRLIYATSSLGSGVP 79
Db 1 DIVLTQSPAINSPGKVTMTCSASSVSSYLHWYQKSGASPKLWIYSTNLSGVP 60
Qy 80 KRFGSGSGSDYSLTISSEDFVAYYCLOYASSPYTFGGGTKLEIKRADAAP 133
Db 61 ARFGSGSGSYSLTISSEDAEADATYCCQYHSYPTFGGTKLEIKRADAAP 114

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2003, 18:46:00 ; Search time 2089.42 Seconds
(without alignments)
9026.108 Million cell updates/sec

Title: US-08-836-455-3

Perfect score: 461

Sequence: 1 ATGAATGACAGCTGGTCTT.....CTGGTCCCTGGAAGCTTGGG 461

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:**

1: gb_ba:**

2: gb_htg:**

3: gb_in:**

4: gb_ov:**

5: gb_pat:**

6: gb_ph:**

7: gb_pl:**

8: gb_pr:**

9: gb_ro:**

10: gb_sts:**

11: gb_sy:**

12: gb_un:**

13: gb_vl:**

14: gb_vl:**

15: em_ba:**

16: em_fun:**

17: em_hum:**

18: em_in:**

19: em_mu:**

20: em_om:**

21: em_or:**

22: em_ov:**

23: em_pat:**

24: em_ph:**

25: em_pl:**

26: em_ro:**

27: em_sts:**

28: em_un:**

29: em_vl:**

30: em_htg_hum:**

31: em_htg_inv:**

32: em_htg_other:**

33: em_htg_mus:**

34: em_htg_pln:**

35: em_htg_rod:**

36: em_htg_man:**

37: em_htg_vrt:**

38: em_sy:**

39: em_htgo_hum:**

40: em_htgo_mus:**

41: em_htgo_other:**

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	461	100.0	461	6	AR164506	AR164506 Sequence
2	461	100.0	461	6	BD085738	BD085738 Methods O
3	407	88.3	411	10	AF124720	AF124720 Mus muscu
4	96	20.8	294	10	AF303872	AF303872 Mus muscu
5	84	18.2	471	10	AB050080	AB050080 Mus muscu
6	83	18.0	735	12	SC0250760	AJ250760 Mus muscu
7	77	16.7	902	12	XU049832	U49832 Synthetic s
8	76	16.5	458	6	AR083801	AR083801 Sequence
9	76	16.5	458	6	AR198720	AR198720 Sequence
10	76	16.5	458	6	AR275320	AR275320 Sequence
11	66	14.3	484	10	MUSIGH4C11	M54977 Mus musculu
12	66	14.3	490	10	MUSIG4C11A	M24785 Mouse anti-
13	61	13.2	453	10	MMU24114	U24114 Mus musculu
14	60	13.0	279	10	MMIGGCVRG	225453 M.musculus
15	60	13.0	282	10	MMIGGCVRB	225443 M.musculus
16	60	13.0	285	10	MMIGGCVRG	225445 M.musculus
17	60	13.0	290	10	MMIGGCVRG	225451 M.musculus
18	60	13.0	294	10	AF303873	AF303873 Mus muscu
19	60	13.0	302	10	MMIGGCVRG	225457 M.musculus
20	60	13.0	303	10	MMIGGCVRD	225447 M.musculus
21	60	13.0	305	10	MMIGGCVRG	225449 M.musculus
22	60	13.0	306	10	AY171955	AY171955 Mus muscu
23	60	13.0	321	10	AY171952	AY171952 Mus muscu
24	60	13.0	352	10	MMMD50C	273339 M.musculus
25	60	13.0	355	10	MMMD47C	273342 M.musculus
26	60	13.0	356	10	AY247151	AY247151 Mus muscu
27	60	13.0	358	10	MMMD01C	273357 M.musculus
28	60	13.0	358	10	MMMD52C	273338 M.musculus
29	60	13.0	360	10	AY229957	AY229957 Mus muscu
30	60	13.0	360	12	AF277091	AF277091 Synthetic
31	60	13.0	387	10	AY058907	AY058907 Mus muscu
32	60	13.0	457	10	AY178830	AY178830 Mus muscu
33	60	13.0	765	6	AX057984	AX057984 Sequence
34	60	13.0	765	6	AX057985	AX057985 Sequence
35	60	13.0	959	10	AF025445	AF025445 Mus muscu
36	60	13.0	1239	6	AX057945	AX057945 Sequence
37	60	13.0	1280	6	AX057947	AX057947 Sequence
38	59	12.8	336	10	AB090857	AB090857 Mus muscu
39	59	12.8	360	6	I73511	I73511 Sequence 14
40	59	12.8	360	10	AB058183	AB058183 Mus muscu
41	59	12.8	360	10	AB058198	AB058198 Mus muscu
42	59	12.8	363	10	AB057826	AB057826 Mus muscu
43	59	12.8	363	10	AB057827	AB057827 Mus muscu
44	59	12.8	363	10	AB090858	AB090858 Mus muscu
45	59	12.8	368	10	MMEAD24	X97535 M.musculus

ALIGNMENTS

RESULT 1
AR164506

LOCUS

DEFINITION

AR164506

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AR164506 AR164506 461 bp DNA linear PAT 17-OCT-2001
Sequence 3 from patent US 6274143,
AR164506
AR164506.1 GI:16237556

Unknown.

Unclassified.

1 (bases 1 to 461)

Chatterjee, M. and Foon, K. A.

Methods of delaying development of HMFG-associated tumors using

anti-idiotypic antibody 11b10

Patent: US 6274143-A 3 14-AUG-2001;


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FEATURES             source            Location/Qualifiers
     1..471
     /organism="Mus musculus"
     /mol_type="mrna"
     /strain="BALB/c"
     /db_xref="taxon:10090"
     /cell_line="hybridoma 9H8"
     1..471
     /gene="VH9H8"
     11..>469
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     /codon_start=1
     /product="anti-A/u antibody"
     /protein_id="BAB87192.1"
     /db_xref="GI:19909936"
     /translation="MGWTVGLILLITTVGHSQAYLQSGAELVRSGASVKMSCKRAS
GYNFTSYNMHWKOTPGQGLEWICYIFLNAGTNYNOKFKGKATLTADTSSSTAYMQLS
SLRSEDSAVFCARGEYGNFWFAYWGQGLTVTSNAKTTAQPVPYPLAPGSL"
BASE COUNT          114 a 126 c 121 g 110 t
ORIGIN

Query Match          18.2%; Score 84; DB 10; Length 471;
Best Local Similarity 100.0%; Pred. No. 6.4e-37;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GCAGACATCTCTCCAGCACAGCCTACATGCAGATCAGCAGCCTGACATCTGAAGACTCT 330
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Db 278 GCAGACATCTCTCCAGCACAGCCTACATGCAGATCAGCAGCCTGACATCTGAAGACTCT 337

Qy 331 CGGCTCTATTCTCTGCAAGAGG 354
      |||||||||||||||||||||||||||
Db 338 CGGCTCTATTCTCTGCAAGAGG 361

RESULT 6
SC0250760
LOCUS              735 bp  mRNA  linear  SYN 11-MAY-2000
DEFINITION         Mus musculus synthetic construct for anti-guinea pig C5 ScFv
                    antibody, clone E10.
VERSION            AJ250760
KEYWORDS           antibody; heavy chain; immunoglobulin superfamily; light chain;
                    ScFv; variable region.
SOURCE             synthetic construct
ORGANISM           artificial sequences.
REFERENCE          1
AUTHORS            Link,C., Hawlisch,H., Meyer zu Vilsendorf,A., Gylernuez,S., Nagel,E.
                    and Koehl,J.
TITLE              Selection of phage-displayed anti-guinea pig C5 or C5a antibodies
                    and their application in xenotransplantation
JOURNAL            Mol. Immunol. 38, 1235-1247 (1999)
AUTHORS            Link,C.
TITLE              Direct Submission
JOURNAL            Submitted (01-NOV-1999) Link C., Medizinische Mikrobiologie,
                    Medizinische Hochschule Hannover, Carl-Neuberg-Str. 1, 30625
                    Hannover, GERMANY
FEATURES           Location/Qualifiers
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     /db_xref="taxon:32630"
     /clone="E10"
     /focus
     1..366
     /organism="Mus musculus"
     /mol_type="mrna"
     /db_xref="taxon:10090"
     412..735
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     /mol_type="mrna"
     /db_xref="taxon:10090"

FEATURES           source            Location/Qualifiers
     1..>735
     /note="synthetic"
     /codon_start=1
     /product="anti-guinea pig C5 ScFv antibody"
     /protein_id="CAB60133.1"
     /db_xref="GI:6272273"
     /translation="EVOLQQSGAELVRSGASVKMSCKASGYTFARYNVHWKOTPGQG
LEWIGTYPRDGTNTNOKFKGKATLTADTSSSTAYMQLSSTSEDSAVFCFTRSRDA
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KASQNYCTNVAYTQKPGQSPKALIVSASVRSYSGVPDRFTGSGGDTFTLTISNQSE
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V_region           1..366
                    /product="immunoglobulin heavy chain variable region"
misc_feature       367..411
                    /note="(Gly4Ser)3 linker sequence"
V_region           412..735
                    /product="immunoglobulin light chain variable region"
BASE COUNT          194 a 170 c 206 g 165 t
ORIGIN

Query Match          18.0%; Score 83; DB 12; Length 735;
Best Local Similarity 100.0%; Pred. No. 2.4e-36;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 263 CATTGACTGCAGACATCTCTCCAGCACAGCCTACATGCAGATCAGCAGCCTGACATCTG 322
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 206 CATTGACTGCAGACATCTCTCCAGCACAGCCTACATGCAGATCAGCAGCCTGACATCTG 265

Qy 323 AAGACTCTGGGCTATTCTGT 345
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Db 266 AAGACTCTGGGCTATTCTGT 288

RESULT 7
XXU49832
LOCUS              902 bp  mRNA  linear  SYN 24-MAR-1996
DEFINITION         Synthetic single chain Fv antibody against potato virus V coat
                    protein, mRNA, partial cds.
VERSION            U49832
KEYWORDS           U49832.1 GI:1236090
SOURCE             synthetic construct
ORGANISM           synthetic construct
                    artificial sequences.
REFERENCE          1 (bases 1 to 902)
AUTHORS            Chen,Z.C., Cockburn,W., Torrance,L., Barker,H. and Whitelam,G.C.
TITLE              Cytoplasmic accumulation of a soluble functional scFv protein to a
                    plant virus expressed as a thiorodoxin fusion in Escherichia coli
JOURNAL            Unpublished
REFERENCE          2 (bases 1 to 902)
AUTHORS            Chen,Z.C., Cockburn,W., Torrance,L., Barker,H. and Whitelam,G.C.
TITLE              Direct Submission
JOURNAL            Submitted (23-FEB-1996) Z C. Chen, Botany, Univ. of Leicester,
                    University Road, Leicester LE1 7RH, UK
FEATURES           Location/Qualifiers
     1..902
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     /db_xref="taxon:32630"
     /note="PCR synthesized gene from mouse hybridoma cell line
                    SCR 40"
     <1..885
     /codon_start=1
     /product="single chain Fv antibody"
     /protein_id="AA92722.1"
     /db_xref="GI:1236091"
     /translation="SRPMADVQIIQTASLSASVGETVTTCRASEHIYSILAWYQOK
QKSPQLLVYSAKTLAEKVPGRFSGSGGFQSLKINSIQLPEDFGSYCQHHDYTPRT
FGGKTKLEIRADAAPTVSIFFPSSPGGGGGGGGGSDIVMTQSKFMSTSVGDRVSVTC
SVKMSCKASGYTFSTNMHWKOTPGQLEWIGIYIPNGGTIYNQFKGKATLTADT
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FEATURES           source            Location/Qualifiers
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     412..735
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BASE COUNT      223 a      239 c      234 g      206 t
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Query Match      16.7%; Score 77; DB 12; Length 902;
Best Local Similarity 99.2%; Pred. No. 7.2e-33;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 77 CTGGGCGCTGAGCTGTGGGCTCTGGGCGCTCAGTGAAGATGCTCTGCAAGGCTTCTGGCT 136
    |||||
Db 452 CTGGGCGCTGAGCTGTGGGCTCTGGGCGCTCAGTGAAGATGCTCTGCAAGGCTTCTGGCT 511
    |||||

QY 137 ACACATTGACCACTTACATATGCACTGGTGAACACACACACCTGCAGAGGCCCTGGGAAT 196
    |||||
Db 512 ACACATTTACCACTTACATATGCACTGGTGAACACACACACCTGCAGAGGCCCTGGGAAT 571
    |||||

QY 197 GGATTGGA 204
    |||||
Db 572 GGATTGGA 579

RESULT 8
AR083801
LOCUS      AR083801      458 bp      DNA      linear      PAT 01-SEP-2000
DEFINITION Sequence 3 from patent US 5977316.
ACCESSION  AR083801
VERSION     AR083801.1 GI:10010572
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 458)
AUTHORS     Chatterjee,M., Foon,K.A. and Chatterjee,S.K.
TITLE       Monoclonal antibody 1A7 and related polypeptides
JOURNAL     Patent: US 5977316-A 3 02-NOV-1999;
FEATURES    Location/Qualifiers
            source
            1..458
            /organism="unknown"

BASE COUNT   106 a      131 c      114 g      107 t
ORIGIN

Query Match      16.5%; Score 76; DB 6; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.9e-32;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 TGCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAACGACACC 425
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Db 363 TGCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAACGACACC 422
    |||||

QY 426 CCCACCCGCTCTATCCA 441
    |||||
Db 423 CCCACCCGCTCTATCCA 438

RESULT 9
AR198720
LOCUS      AR198720      458 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 3 from patent US 6355244.
ACCESSION  AR198720
VERSION     AR198720.1 GI:20248794
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 458)
AUTHORS     Foon,K.A. and Chatterjee,M.
TITLE       Methods and compositions for the treatment of psoriasis
JOURNAL     Patent: US 6355244-A 3 12-MAR-2002;
FEATURES    Location/Qualifiers
            source
            1..458
            /organism="unknown"

BASE COUNT   106 a      131 c      114 g      107 t
ORIGIN

LEGAGSGOPELAPEDPED"

Query Match      16.7%; Score 77; DB 12; Length 902;
Best Local Similarity 99.2%; Pred. No. 7.2e-33;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 77 CTGGGCGCTGAGCTGTGGGCTCTGGGCGCTCAGTGAAGATGCTCTGCAAGGCTTCTGGCT 136
    |||||
Db 452 CTGGGCGCTGAGCTGTGGGCTCTGGGCGCTCAGTGAAGATGCTCTGCAAGGCTTCTGGCT 511
    |||||

QY 137 ACACATTGACCACTTACATATGCACTGGTGAACACACACACCTGCAGAGGCCCTGGGAAT 196
    |||||
Db 512 ACACATTTACCACTTACATATGCACTGGTGAACACACACACCTGCAGAGGCCCTGGGAAT 571
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QY 197 GGATTGGA 204
    |||||
Db 572 GGATTGGA 579

RESULT 8
AR083801
LOCUS      AR083801      458 bp      DNA      linear      PAT 01-SEP-2000
DEFINITION Sequence 3 from patent US 5977316.
ACCESSION  AR083801
VERSION     AR083801.1 GI:10010572
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 458)
AUTHORS     Chatterjee,M., Foon,K.A. and Chatterjee,S.K.
TITLE       Monoclonal antibody 1A7 and related polypeptides
JOURNAL     Patent: US 5977316-A 3 02-NOV-1999;
FEATURES    Location/Qualifiers
            source
            1..458
            /organism="unknown"

BASE COUNT   106 a      131 c      114 g      107 t
ORIGIN

Query Match      16.5%; Score 76; DB 6; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.9e-32;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 TGCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAACGACACC 425
    |||||
Db 363 TGCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAACGACACC 422
    |||||

QY 426 CCCACCCGCTCTATCCA 441
    |||||
Db 423 CCCACCCGCTCTATCCA 438

RESULT 9
AR198720
LOCUS      AR198720      458 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 3 from patent US 6355244.
ACCESSION  AR198720
VERSION     AR198720.1 GI:20248794
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 458)
AUTHORS     Foon,K.A. and Chatterjee,M.
TITLE       Methods and compositions for the treatment of psoriasis
JOURNAL     Patent: US 6355244-A 3 12-MAR-2002;
FEATURES    Location/Qualifiers
            source
            1..458
            /organism="unknown"

BASE COUNT   106 a      131 c      114 g      107 t
ORIGIN

LEGAGSGOPELAPEDPED"

Query Match      16.5%; Score 76; DB 6; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.9e-32;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 TGCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAACGACACC 425
    |||||
Db 363 TGCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAACGACACC 422
    |||||

QY 426 CCCACCCGCTCTATCCA 441
    |||||
Db 423 CCCACCCGCTCTATCCA 438

RESULT 11
MUSIGH4C11
LOCUS      MUSIGH4C11      484 bp      mRNA      linear      ROD 12-JUN-2000
DEFINITION Mus musculus immunoglobulin heavy chain precursor (IGH) mRNA,
            partial cds.
ACCESSION  M54977
VERSION     M54977.1 GI:194528
KEYWORDS    C-region; V-region; immunoglobulin heavy chain.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 484)
REFERENCE   1 (bases 1 to 484)
AUTHORS     Sood,A.K., Cheng,H.L. and Kohler,H.
TITLE       An efficient and general method for sequencing immunoglobulin mRNAs
JOURNAL     J. Immunol. Methods 95 (2), 227-235 (1986)
MEDLINE     87084812
PUBMED      2432131
COMMENT     Original source text: Mouse anti-idiotypic hybridoma cell line
            4C11, cDNA to mRNA.
            Location/Qualifiers
            source
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            /organism="Mus musculus"
            /mol_type="mRNA"
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GYFTDITHHWKQSGKSLGWIGGDPNDFTFYNEKFKATLTVDKSSITAYMEL
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37. .93
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/product="immunoglobulin heavy chain"
445. .>484
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Best Local Similarity 100.0%; Pred. No. 1.9e-26;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 GGTGCTGTGACTACTGGGCTCAAGGAACCTCAGTCACCGCTCCTCAGCAAAAGACA 423
|||||
Db 397 GGTGCTGTGACTACTGGGCTCAAGGAACCTCAGTCACCGCTCCTCAGCAAAAGACA 456

QY 424 CCCCCA 429
|||||
Db 457 CCCCCA 462

RESULT 12
MUSIG4C11A 490 bp mRNA linear ROD 27-APR-1993
LOCUS Mouse anti-idiotypic immunoglobulin heavy chain variable, constant,
DEFINITION and complementarity determining regions 1-3 (4C11) mRNA.
ACCESSION M24785
VERSION M24785.1 GI:194133
KEYWORDS C-region; V-region; anti-idiotypic antibody; complementarity
determining region; immunoglobulin heavy chain.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 490)
AUTHORS Cheng, H.L., Sood, A.K., Ward, R.E., Kieber-Emmons, T. and Kohler, H.
TITLE Structural basis of stimulatory anti-idiotypic antibodies
JOURNAL Mol. Immunol. 25 (1), 33-40 (1988)
MEDLINE 86142863
PUBMED 3125424
COMMENT Original source text: Mus musculus (strain BALB/c; sub_species
domesticus) cDNA to mRNA.
FEATURES
source Location/Qualifiers
1. .490
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gene 1. .490
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gene 184. .198
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BASE COUNT 120 a 134 c 116 g 120 t
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Best Local Similarity 100.0%; Pred. No. 1.9e-26;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 GGTGCTGTGACTACTGGGCTCAAGGAACCTCAGTCACCGCTCCTCAGCAAAAGACA 423
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Db 397 GGTGCTGTGACTACTGGGCTCAAGGAACCTCAGTCACCGCTCCTCAGCAAAAGACA 456

QY 424 CCCCCA 429
|||||
Db 457 CCCCCA 462

RESULT 13
MMU24114 453 bp mRNA linear ROD 20-APR-1995
LOCUS Mus musculus immunoglobulin F9.13.7 heavy chain mRNA, partial cds.
DEFINITION U24114
ACCESSION U24114
VERSION U24114.1 GI:777410
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 453)
AUTHORS Lescar, J., Pellegri, M., Souchon, H., Tello, D., Poljak, R.J.,
Peterson, N.C., Greene, M.I. and Alzari, P.M.
TITLE Crystal structure of a cross-reaction complex between Fab F9.13.7
and Guinea-fowl lysozyme
JOURNAL J. Biol. Chem. (1995) In press
REFERENCE 2 (bases 1 to 453)
AUTHORS Peterson, N.C.
TITLE Direct Substitution
JOURNAL Submitted (03-APR-1995) Norman C. Peterson, Pathology and
Laboratory Medicine, University of Pennsylvania School of Medicine,
252 John Morgan Bldg., 36th St. and Hamilton Walk, Philadelphia, PA
19104, USA
FEATURES
source Location/Qualifiers
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/cell_type="lymphocyte/hybridoma"
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64. .81
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Best Local Similarity 100.0%; Pred. No. 1.5e-23;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 369 TCTGGACTACTGGGCTCAAGGACCTCAGTCACCGTCTCTCAGCCAAAGCAGCACCC 428
Db 300 TCTGGACTACTGGGCTCAAGGACCTCAGTCACCGTCTCTCAGCCAAAGCAGCACCC 359

Qy 429 A 429
Db 360 A 360

RESULT 14
MMIGGCVRG      279 bp mRNA linear ROD 13-OCT-1993
LOCUS
DEFINITION      M.musculus immunoglobulin gamma heavy chain (DBA/1) gene, v region.
ACCESSION      Z25453
VERSION      Z25453.1 GI:407822
KEYWORDS      heavy chain; IgG gene; immunoglobulin; variable region.
SOURCE      Mus musculus
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 279)
AUTHORS      Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE      Variable region gene selection of immunoglobulin G expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL      Eur. J. Immunol. (1993) In press
REFERENCE      2 (bases 1 to 279)
AUTHORS      Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE      Variable region gene selection of immunoglobulin G-expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL      Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE      94009207
PUBMED      7691608
REFERENCE      3 (bases 1 to 279)
AUTHORS      Mo,J.A.
TITLE      Direct Submission
JOURNAL      Submitted (02-AUG-1993) John A Mo, Department of Medical and
Physiological, Department of, Medical and Physiological Chemistry,
Husargatan 3, Uppsala, 75123, Sweden
FEATURES      Location/Qualifiers
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gene
CDS
V_region
BASE COUNT      76 a 66 c 77 g 60 t
ORIGIN
Query Match      13.0%; Score 60; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 6.1e-23;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 ACCAGTTACAATATGCCTGGTAAAGCAGACACCTGGACAGGCGCTGGAATGGATTGGA 204
Db 67 ACCAGTTACAATATGCCTGGTAAAGCAGACACCTGGACAGGCGCTGGAATGGATTGGA 126

RESULT 15
MMIGGCVRB      282 bp mRNA linear ROD 13-OCT-1993
LOCUS
DEFINITION      M.musculus immunoglobulin gamma heavy chain (DBA/1) gene, v region.
ACCESSION      Z25443
VERSION      Z25443.1 GI:407812
KEYWORDS      heavy chain; IgG gene; immunoglobulin; variable region.
SOURCE      Mus musculus
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 282)
AUTHORS      Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE      Variable region gene selection of immunoglobulin G expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL      Eur. J. Immunol. (1993) In press
REFERENCE      2 (bases 1 to 282)
AUTHORS      Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE      Variable region gene selection of immunoglobulin G-expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL      Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE      94009207
PUBMED      7691608
REFERENCE      3 (bases 1 to 282)
AUTHORS      Mo,J.A.
TITLE      Direct Submission
JOURNAL      Submitted (02-AUG-1993) John A Mo, Department of Medical and
Physiological, Department of, Medical and Physiological Chemistry,
Husargatan 3, Uppsala, 75123, Sweden
FEATURES      Location/Qualifiers
1..282
/organism="Mus musculus"
/mol_type="mRNA"
/strain="DBA/1"
/db_xref="taxon:10090"
/chromosome="12"
/cell_line="C11CB20 hybridoma"
/cell_type="B cell hybridoma"
/tissue_type="lymph node"
/dev_stage="adult"
1..282
/gene="IgG"
<1..>282
/gene="IgG"
/codon_start=1
/product="immunoglobulin gamma heavy chain"
/protein_id="CAA80930.1"
/db_xref="GI:407813"
/translation="GAELVPGASVKMSCKASGYFTSYNNHWWKOTPGQGLEWIGAI
YPNGDTSYNQKFKGKATLTADKSSSTAYMQLSLTSEDSAVYYCARGEA"
gene
CDS
V_region
BASE COUNT      74 a 68 c 80 g 60 t
ORIGIN
Query Match      13.0%; Score 60; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 6.1e-23;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 ACCAGTTACAATATGCCTGGTAAAGCAGACACCTGGACAGGCGCTGGAATGGATTGGA 204
Db 67 ACCAGTTACAATATGCCTGGTAAAGCAGACACCTGGACAGGCGCTGGAATGGATTGGA 126

```

Search completed: August 30, 2003, 21:04:56
Job time : 2091.42 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2003, 17:38:10 ; Search time 201.688 Seconds
(without alignments)
6170.144 Million cell updates/sec

Title: US-08-836-455-3
Perfect score: 461
Sequence: 1 ATGGAATGACAGCTGGTCTT.....CTGCTCCCTGGAAGCTTGGG 461

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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25:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	461	18	AAT85150 Murine monoclonal
2	461	100.0	461	20	AAV83773 Antibody 11D10 hea
3	461	100.0	461	25	AA151274 Mouse 11D10 antibo
4	76	16.5	458	17	AA131333 Anti-idiotype mono
5	76	16.5	458	20	AA131366 Mab 1A7 heavy chai
6	76	16.5	458	20	AA189553 Heavy chain variab
7	76	16.5	458	20	AA160630 Monoclonal antibod
8	67	14.5	861	16	AAQ81500 sfv anti-rev seque

9	67	14.5	861	18	AAT45347	Single chain sfv a
10	60	13.0	765	22	AAC86590	DNA encoding a fus
11	60	13.0	765	22	AAC86591	DNA encoding a fus
12	60	13.0	1239	22	AAC88563	DNA encoding a fus
13	60	13.0	1280	22	AAC88564	Anti-CD20 single c
14	60	13.0	1925	21	AA15019	DNA encoding a CD-
15	59	12.8	360	18	AAT96345	cDNA for Ig Heavy
16	59	12.8	420	22	AAF81910	Anti-CA125 bifunct
17	59	12.8	447	20	AA57786	Anti-HCV Ser/Thr p
18	59	12.8	458	10	AA91146	2H7 Vh sequence
19	59	12.8	459	20	AAV82357	Mouse antibody 2H7
20	59	12.8	459	22	AAH22070	2H7 heavy chain va
21	59	12.8	470	16	AAQ99892	Mouse VLA-4 antibo
22	59	12.8	470	18	AAT74760	Alpha-4 integrin m
23	59	12.8	477	18	AAT70806	Mouse anti-idiotyp
24	59	12.8	486	18	AAT59339	MH1 monoclonal ant
25	59	12.8	491	18	AAT70868	2H7 heavy chain va
26	59	12.8	491	19	AAV18557	Mouse 2H7 antibody
27	59	12.8	491	19	AAV03926	Mouse 2H7 antibody
28	59	12.8	491	19	AAV18593	Mouse 2H7 antibody
29	59	12.8	518	18	AAT36316	2H7 antibody heavy
30	59	12.8	520	18	AAT51042	Coding sequence fo
31	59	12.8	588	14	AAQ43385	H-chain V-region o
32	59	12.8	626	25	ACC44926	TSH receptor antib
33	59	12.8	626	25	ACC44927	TSH receptor antib
34	59	12.8	736	25	ABX16571	Mouse DNA encoding
35	59	12.8	1347	11	AAQ05708	Heavy chain of ant
36	59	12.8	1347	14	AAQ51534	Sequence encoding
37	59	12.8	1347	17	AAT23056	Murine anti-BGH MA
38	59	12.8	1347	17	AAT13733	Anti-BGH monoclon
39	59	12.8	1528	5	AA40024	Combined cDNA inse
40	59	12.8	1528	5	AA40025	mRNA encoding gamm
41	59	12.8	1553	16	AAQ79930	Anti-tobacco mosai
42	59	12.8	1797	17	AAT15733	3B1 single chain a
43	59	12.8	1848	18	AAT96346	Chimeric gene cont
44	59	12.8	3343	11	AAQ04655	Plasmid p10169 enc
45	57	12.4	399	16	AAQ90425	DNA encoding anti-

ALIGNMENTS

RESULT 1	AAT85150	AAT85150 standard; cDNA; 461 BP.
ID	AAT85150	
XX	XX	
AC	AAT85150:	
XX	XX	
DT	25-MAR-2003 (updated)	
DT	04-JAN-1998 (first entry)	
XX	XX	
DE	Murine monoclonal anti-idiotype antibody 11D10 VH cDNA.	
XX	XX	
KW	Monoclonal antibody 11D10; anti-idiotype antibody; mucin;	
KW	human milk fat globule; HMF; tumour; breast cancer; vaccine; ss.	
XX	XX	
OS	Mus musculus.	
XX	XX	
FH	Key	Location/Qualifiers
FT	sig_peptide	1..57
FT	mat_peptide	/*tag= a
FT	FT	58..461
FT	FT	/*tag= b
XX	XX	
PN	WO9722699-A2.	
XX	XX	
PD	26-JUN-1997.	
XX	XX	
PF	19-DEC-1996;	96WO-US20757.
XX	XX	
PR	20-DEC-1995;	95US-0575762.
PR	26-JAN-1996;	96US-0591965.
PR	13-DEC-1996;	96US-0766350.

XX 17-JAN-1995; 95US-0372676.
 PR 16-JAN-1996; 96US-0591196.
 PR 17-JAN-1995; 95US-0372676.
 PR 16-JAN-1996; 96US-0591196.
 XX (KENT) UNIV KENTUCKY.
 PA

XX Chatterjee M, Chatterjee SK, Foon KA;
 PI

XX WPI: 1996-354530/35.
 DR P-PSDB; AAW03200.
 DR

XX Monoclonal antibody 1A7 and related polynucleotide(s) and
 PT polypeptide(s) - useful to treat or palliate a GD2-associated
 PT disease, e.g. melanoma and glioma
 PT

XX Claim 11; Fig 2; 141pp; English.
 PS

XX The present sequence encodes the murine anti-idiotypic monoclonal
 CC antibody (MAB) 1A7 variable heavy chain. MAB 1A7 was raised against
 CC the anti-ganglioside 2 (GD2) MAB 14G2a, which binds an unique
 CC epitope of GD2. As the glycosphingolipid GD2 is expressed at high
 CC density by human neuroectodermal tumours, e.g. malignant melanoma,
 CC neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma,
 CC of the lung, MAB 1A7, or its cDNA can be used in a vaccine to treat
 CC or palliate such diseases. They can also be used to reduce the
 CC risk of recurrence of a clinically detectable tumour, and detect an
 CC anti-GD2 Ab bound to a tumour cell.
 CC MAB 1A7 overcomes immune tolerance and induces an immune response
 CC against GD2, which comprises anti-GD2 Ab (humoral response) and
 CC GD2-specific cells (cellular response). It can be used to purify
 CC anti-1A7 (Ab3), anti-GD2 (Ab1') or 14G2a (Ab1), detect anti-1A7 or
 CC anti-GD2 in a sample or measure the level of cellular anti-1A7 or
 CC anti-GD2 activity.
 CC The cDNA can be used in expression systems for 1A7 prodn., and in
 CC the prepn. of probes and primers to respectively assay for 1A7
 CC cDNA, and amplify desired polynucleotides for use in gene therapy.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX

XX Sequence 458 BP; 106 A; 131 C; 114 G; 107 T; 0 other;
 SQ

Query Match 16.5%; Score 76; DB 17; Length 458;
 Best Local Similarity 100.0%; Pred. No. 3.2e-25;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 TGCCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAGACAC 425
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 363 TGCCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAGACAC 422

QY 426 CCCACCGTCTATCCA 441
 ||||||||||||||||
 DB 423 CCCACCGTCTATCCA 438

RESULT 5
 AAZ31366
 ID AAZ31366 standard; cDNA: 458 BP.
 XX
 AC AAZ31366;
 XX

DE 07-FEB-2000 (first entry)
 XX

XX MAB 1A7 heavy chain variable region encoding cDNA.
 DE

XX Monoclonal antibody; MAB; 1A7; GD2; immune response; melanoma;
 KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
 KW tumor-associated antigen; ss.
 XX

OS Synthetic.
 OS Mus sp.
 XX

XX US5977316-A.
 PN

XX 02-NOV-1999.
 XX PD
 XX 16-JAN-1996; 96US-0591196.
 XX PF
 XX 17-JAN-1995; 95US-0372676.
 XX PR
 XX (KENT) UNIV KENTUCKY.
 XX PA

XX Foon KA, Chatterjee SK, Chatterjee M;
 XX PI

XX WPI: 1999-619711/53.
 DR P-PSDB; AAY49210.
 DR

XX Monoclonal antibody 1A7 which elicits an anti-GD2 immunological
 PT response, useful for the development of products for the detection and
 PT treatment of cancers
 PT

XX Disclosure; Fig 2; 74pp; English.
 PS

XX The invention provides a monoclonal antibody (MAB) designated 1A7, which
 CC elicits an anti-GD2 (tumor-associated antigen) immunological response in
 CC humans. MAB 1A7 has defined light and heavy chain variable region
 CC sequences. The MAB 1A7 and polypeptides can be used for eliciting an
 CC anti-GD2 immune response. The polypeptides can also be used for detecting
 CC or purifying anti-GD2 antibody. The products can be used for treating GD2
 CC -associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue
 CC carcinoma, and small cell carcinoma. They can be used for palliating the
 CC disease or for reducing the risk of recurrence. The present sequence
 CC represents the cDNA encoding the heavy chain variable region of MAB 1A7.
 XX

XX Sequence 458 BP; 106 A; 131 C; 114 G; 107 T; 0 other;
 SQ

Query Match 16.5%; Score 76; DB 20; Length 458;
 Best Local Similarity 100.0%; Pred. No. 3.2e-25;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 TGCCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAGACAC 425
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 363 TGCCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAGACAC 422

QY 426 CCCACCGTCTATCCA 441
 ||||||||||||||||
 DB 423 CCCACCGTCTATCCA 438

RESULT 6
 AAX89553

ID AAX89553 standard; cDNA: 458 BP.
 XX

AC AAX89553;
 XX

DT 06-OCT-1999 (first entry)
 XX

XX Heavy chain variable region of MAB 1A7.
 DE

XX heavy chain variable region; antibody 1A7; T cell response; melanoma;
 KW ganglioside GD2; CDR; complementarity determining region; carcinoma; ss.
 KW

OS Mus musculus.
 OS

XX Key Location/Qualifiers
 FH CDS 1..456
 FT

FT /*tag= a
 FT /product= "Vh chain MAB 1A7
 FT /note= "No stop codon given"

FT sig_peptide 1..57
 FT /*tag= b

FT mat_peptide 58..456
 FT /*tag= c

XX US5935821-A.
 XX

PD 10-AUG-1999.
 XX
 PF 21-NOV-1996; 9605-0752844.
 XX
 PR 21-NOV-1996; 9605-0752844.
 PR 17-JAN-1995; 9505-0372676.
 PR 16-JAN-1996; 9605-0591196.
 XX
 PA (KENT) UNIV KENTUCKY.
 XX
 XX Chatterjee M, Chatterjee SK, Foon KA;
 PI WPI; 1999-457600/38.
 XX P-PSDB; AAY28469.
 DR
 XX
 XX Anti-GD2 immunological peptides useful for the treatment of tumours
 PT especially melanomas and small cell carcinomas
 XX
 XX Claim 7; Fig 2; 84pp; English.
 PS
 CC The sequence is the variable heavy chain region of monoclonal
 CC anti-idiotypic antibody 1A7. The polypeptide encoded by this sequence has
 CC three CDRs (complementarity determining regions). When administered to
 CC an individual the 1A7 antibody induces an immune response against
 CC ganglioside GD2. The light chain variable region of the 1A7 antibody
 CC (AAY28468) is also capable of eliciting an anti GD2 response in mammals.
 CC Both the heavy and light chain variable regions of the 1A7 antibody
 CC produce anti-GD2 T cell and antibody responses. The peptides and
 CC antibodies may be useful for the modulation of ganglioside GD2, and
 CC particularly for the treatment of GD2-associated tumours (e.g. melanoma,
 CC neuroblastoma, glioma, soft tissue sarcoma, and small cell carcinoma
 CC (including small cell lung cancer)).
 XX
 XX Sequence 458 BP; 106 A; 131 C; 114 G; 107 T; 0 other;
 SQ
 Query Match 16.5%; Score 76; DB 20; Length 458;
 Best Local Similarity 100.0%; Pred. No. 3.2e-25;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 366 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAACGACACC 425
 DB 363 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAACGACACC 422
 QY 426 CCCACCCGCTATCCA 441
 DB 423 CCCACCCGCTATCCA 438
 RESULT 7
 AAX60630
 ID AAX60630 standard; cDNA; 458 BP.
 XX
 AC AAX60630;
 XX
 DT 03-AUG-1999 (first entry)
 XX
 DE Monoclonal antibody 1A7 heavy chain variable region encoding cDNA.
 XX
 DE Psoriasis; immunological response; anti-idiotypic antibody; glutamate;
 KW chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis;
 KW monoclonal antibody; 1A7; ss.
 XX
 OS Unidentified.
 OS
 XX WO9925380-A2.
 PN
 XX 27-MAY-1999.
 PD
 XX 17-NOV-1998; 98WO-0524607.
 PF
 XX 16-NOV-1998; 98US-0192838.
 PR
 PR 17-NOV-1997; 97US-0065774.
 XX

PA (KENT) UNIV KENTUCKY RES FOUND.
 XX Chatterjee M, Foon KA;
 PI WPI; 1999-347407/29.
 DR P-PSDB; AAY21546.
 XX
 XX Treatment of psoriasis
 PT
 XX
 PS Disclosure; Fig 3; 48pp; English.
 XX
 CC The invention provides a method of treating of psoriasis by administering
 CC an antigen which has similar immunogenic properties to an antigen
 CC expressed on cells of psoriatic tissue so that an immunological response
 CC is elicited in the individual. The antigen stimulates the generation of
 CC anti-idiotypic antibodies that neutralize the aberrant immune response
 CC causing the psoriasis. The method is used to treat psoriasis, especially
 CC chronic plaque, glutamate, pustular, plaque-type psoriasis or psoriatic
 CC arthritis. The compositions allow the individual's own immune system to
 CC act against psoriatic tissue. The present sequence represents a cDNA
 CC encoding the heavy chain variable region of monoclonal antibody 1A7.
 XX
 SQ Sequence 458 BP; 106 A; 132 C; 113 G; 107 T; 0 other;
 Query Match 16.5%; Score 76; DB 20; Length 458;
 Best Local Similarity 100.0%; Pred. No. 3.2e-25;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 366 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAACGACACC 425
 DB 363 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAACGACACC 422
 QY 426 CCCACCCGCTATCCA 441
 DB 423 CCCACCCGCTATCCA 438
 RESULT 8
 AAQ81500
 ID AAQ81500 standard; cDNA; 861 BP.
 XX
 AC AAQ81500;
 XX
 DT 25-MAR-2003 (updated)
 DT 30-AUG-1995 (first entry)
 XX
 DE SFV anti-rev sequence.
 XX
 KW HIV-1; human immunodeficiency virus type 1; AIDS; Rev protein;
 KW intracellular immunization; gene therapy; single chain antibody; Fv;
 KW SFV; antibody engineering; resistance; cell immunity; HeLa; ss.
 XX
 OS Synthetic.
 OS
 XX WO9503832-A1.
 PN
 XX 09-FEB-1995.
 PD
 XX 28-JUL-1994; 94WO-US08448.
 PF
 XX 30-JUL-1993; 93US-0099870.
 PR
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA
 XX Duan L, Pomerantz R;
 PI WPI; 1995-082039/11.
 DR
 XX Method for conducting gene therapy - comprises using recombinant
 PT gene encoding antibody binding antigen associated with a disease;
 PT useful for providing cell immunity.
 XX
 PS Example 4; Page 23; 62pp; English.

XX The sequence given in AA081500 encodes an sfv anti-rev antibody
CC consisting of the variable domains of the heavy and light chains
CC of a mouse MAB against HIV-1 IIIB rev. The sfv specifically
CC binds a highly conserved Rev domain. HeLa T4 cells expressing the
CC sfv were resistant to all HIV-1 clinical isolates tested.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 861 BP; 199 A; 234 C; 230 G; 198 T; 0 other;
Query Match 14.5%; Score 67; DB 16; Length 861;
Best Local Similarity 100.0%; Pred. No. 4.4e-21;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 374 ACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCAAAACGACACCCGCCG 433
|||||
Db 792 ACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCAAAACGACACCCGCCG 851
|||||

QY 434 TCTATCC 440
|||||
Db 852 TCTATCC 858

RESULT 9
AAT45347
ID AAT45347 standard; cDNA; 861 BP.
XX AC AAT45347;
XX
DT 08-AUG-1997 (first entry)
XX
XX Single chain sfv anti-rev antibody encoding cDNA.
XX
XX Gene therapy; antibody; immunisation; human immunodeficiency virus;
KW HIV; human T-cell leukaemia virus; ss.
XX
XX Mus musculus.
XX
XX WO9637234-A1.
XX
XX 28-NOV-1996.
XX
XX 23-MAY-1996; 96WO-US07393.
XX
XX 23-MAY-1995; 95US-0447610.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Duan L, Pomerantz RJ;
XX
XX WPI; 1997-020948/02.
XX

PT Improved gene therapy using recombinant gene coding for an antibody
PT - for intracellular immunisation against pathogens recognised by the
PT antibody, esp. human immunodeficiency virus HIV-1
XX
XX Example 4; Page 54; 213pp; English.
XX

XX The present sequence encodes a single chain sfv anti-rev antibody
CC constructed using variable domains of the heavy and light chains of a
CC murine monoclonal antibody against (HIV-1IIIB) rev (the parent
CC antibody). This is incorporated into a viral vector where
CC expression of the anti-rev gene causes inhibition of the rev function
CC and so affects replication of the other virus (HIV). Rev is one of the
CC essential regulatory proteins of HIV, it binds to rev responsive element
CC (RRE) and promotes the nuclear export, stabilisation and utilisation of
CC the viral mRNA's containing RRE. A novel gene therapy method has been
CC produced, where a recombinant (rev) gene is introduced into the cells of
CC a mammal. The method is improved by using a rec gene encoding an
CC antibody (Ab) that is selectively specific for an intracellular (IC)
CC antigen associated with a disease. The method is used to prevent or
CC halt the progress of a disease by IC immunisation. Specifically, the Ab
CC can be used to inhibit the replication of a virus, such as human T-cell

CC Is useful for expressing of streptavidin fusion proteins. In particular,
CC these are useful as tools for medical diagnostics and therapeutic
CC purposes, e.g. for detecting the presence or absence of, or treating, a
CC target site within a mammalian host.

SQ Sequence 765 BP; 169 A; 201 C; 230 G; 165 T; 0 other;

Query Match 13.0%; Score 60; DB 22; Length 765;

Best Local Similarity 100.0%; Pred. No. 7.5e-18;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 ACCAGTTACAATATGCACTGGTAAAGCAGACACCTGGAGCCCTGGAATGGATTGGA 204

Db 88 ACCAGTTACAATATGCACTGGTAAAGCAGACACCTGGAGCCCTGGAATGGATTGGA 147

RESULT 11

AAC86591

ID AAC86591 standard; DNA; 765 BP.

XX AC AAC86591;

XX AC AAC86591;

XX AC AAC86591;

DT 02-APR-2001 (first entry)

XX AC AAC86591;

DE DNA encoding a fusion of a single chain antibody and streptavidin.

XX AC AAC86591;

XX AC AAC86591;

XX AC AAC86591;

XX AC AAC86591;

XX AC AAC86591;

XX AC AAC86591;

XX AC AAC86591;

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XX AC AAC86591;

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XX AC AAC86591;

XX AC AAC86591;

XX AC AAC86591;

XX AC AAC86591;

XX AC AAC86591;

Query Match 13.0%; Score 60; DB 22; Length 1239;
 Best Local Similarity 100.0%; Pred. No. 7.2e-18;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTTACAAATATGCACTGGGTAAGACACACACCTGGACAGGCGCTGGGAATGGATTGGA 204
 |||||
 Db 469 ACCAGTTACAAATATGCACTGGGTAAGACACACACCTGGACAGGCGCTGGGAATGGATTGGA 528
 |||||

RESULT 13

AAC86564

ID AAC86564 standard; DNA; 1280 BP.

XX AAC86564;

AC 02-APR-2001 (first entry)

DT 02-APR-2001 (first entry)

DE Anti-CD20 single chain antibody/streptavidin fusion protein cassette.

XX Streptavidin; tumour cell; cancer; adenocarcinoma;

KW hematological malignancy; ss.

KW Synthetic.

OS Streptomyces avidinii.

OS Homo sapiens.

XX Key

OS Location/Qualifiers

XX 3..1274

FT CDS

FT /*tag= a

FT /product= "anti-CD20 scFv and streptavidin fusion"

FT

XX WO200075333-A1.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000WO-US15595.

XX 07-JUN-1999; 99US-0137900.

PR 03-DEC-1999; 99US-0168976.

XX (NEOR-) NEORX CORP.

XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;

PI WPI; 2001-091213/10.

XX P-PSDB; AAB30695.

DR New vector constructs for expressing genomic streptavidin fusion

PT proteins which are useful for targeting tumour cells associated with

PT cancer, e.g. adenocarcinomas

XX Example 2; Fig 11C; 100pp; English.

XX The present sequence encodes a fusion of an anti-CD20 single chain

CC antibody (B9E9) streptavidin. The fusion protein is expressed using

CC vectors of the invention. The specification describes vector constructs

CC for expressing streptavidin fusion proteins. The vector comprises a

CC nucleic acid encoding streptavidin or its functional variant operatively

CC linked to a promoter, and a cloning site for insertion of a second

CC nucleic acid sequence encoding a polypeptide to be fused with

CC streptavidin, interposed between the promoter and the first nucleic

CC acid sequence. Alternatively, the vector construct comprises a nucleic

CC acid, operatively linked to a promoter, encoding a polypeptide to be

CC fused with streptavidin, and a cloning site for insertion of a second

CC nucleic acid encoding at least 129 amino acids of streptavidin or its

CC functional variant. The fusion proteins are useful for targeting tumour

CC cells, particularly tumour cells associated with cancer,

CC e.g. adenocarcinomas or hematological malignancies. The vector construct

CC is useful for expressing of streptavidin fusion proteins. In particular,

CC these are useful as tools for medical diagnostics and therapeutic

CC purposes, e.g. for detecting the presence or absence of, or treating, a

CC target site within a mammalian host.

XX

SQ Sequence 1280 BP; 267 A; 397 C; 388 G; 228 T; 0 other;

Query Match 13.0%; Score 60; DB 22; Length 1280;

Best Local Similarity 100.0%; Pred. No. 7.2e-18;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTTACAAATATGCACTGGGTAAGACACACACCTGGACAGGCGCTGGGAATGGATTGGA 204

|||||

Db 96 ACCAGTTACAAATATGCACTGGGTAAGACACACACCTGGACAGGCGCTGGGAATGGATTGGA 155

|||||

RESULT 14

AAAI5019

ID AAAI5019 standard; DNA; 1925 BP.

XX AAAI5019;

AC 21-AUG-2000 (first entry)

DT 21-AUG-2000 (first entry)

DE DNA encoding a CD-20 specific chimeric receptor.

XX CD20-specific receptor; CD-20 specific redirected T cell; leukemia;

KW CD20+ malignancy; non-Hodgkin's lymphoma; mysoablative chemotherapy;

OS stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis; ss.

XX Synthetic.

OS Mus sp.

XX Key

XX Location/Qualifiers

FT CDS

FT 27..1928

FT /*tag= a

FT

XX WO200023573-A2.

XX 27-APR-2000.

XX 20-OCT-1999; 99WO-US24484.

XX 20-OCT-1998; 98US-0105014.

XX (CITY) CITY OF HOPE.

XX Raubitschek A, Jensen MC, Wu AM;

PI WPI; 2000-339676/29.

DR P-PSDB; AAY84965.

XX Genetically engineered CD20-specific redirected T cells useful for

PT treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+

PT acute or chronic leukemia, and autoimmune disease

XX Example 1; Page 50-53; 58pp; English.

XX The present sequence encodes a synthetic CD20-specific chimeric

CC receptor. The specification describes CD-20 specific redirected T cells

CC which express and bear on the cell surface membrane a CD20-chimeric

CC receptor comprising an intracellular signalling domain, a transmembrane

CC domain and an extracellular domain, the extracellular domain comprising

CC a CD20-specific receptor. The genetically engineered CD20-specific

CC redirected T cells are useful for treating a CD20+ malignancy, such

CC as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, in a

CC human patient having previously undergone myeloablative chemotherapy and

CC stem cell rescue. The genetically engineered CD20-specific redirected

CC T cells are also useful for abrogating an untoward B cell function, such

CC as autoimmune disease (lupus or rheumatoid arthritis) in a patient.

XX Sequence 1925 BP; 471 A; 554 C; 541 G; 359 T; 0 other;

SQ

Query Match 13.0%; Score 60; DB 21; Length 1925;

Best Local Similarity 100.0%; Pred. No. 7.1e-18;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTTACAAATATGCACTGGGTAAGACACACACCTGGACAGGCGCTGGGAATGGATTGGA 204

Job time : 203.688 secs

Db 546 ACCAGTTACATATGCTAGCTGGTAAAGCAGACACCTGGAGGGCCCTGGAATGGATTGGA 605
|||||

RESULT 15

AAT96345
ID AAT96345 standard; cDNA; 360 BP.
XX
XX AAT96345;
XX
XX
DT 08-APR-1998 (first entry)
XX
DE cDNA for Ig heavy chain variable region of anti-asparaginase MAb.
XX

XX Immunoglobulin; Ig; heavy chain; variable region; murine;
KW asparaginase II; monoclonal antibody; MAb;
KW recombinant chimeric polypeptide; ss.
XX
XX
OS Mus sp.

XX US5686579-A.
XX
XX 11-NOV-1997.
XX
XX 23-MAY-1995; 95US-0447422.
XX
XX 22-JUN-1993; 93US-0081410.
PR 21-JUN-1988; 88US-0205748.
PR 31-AUG-1992; 92US-0938505.
PR 23-MAY-1995; 95US-0447422.
XX
XX (HYBR-) HYBRISSENS LTD.

XX Ramjeesingh M, Rothstein A, Shami EY;
XX
XX WPI; 1997-558200/51.
XX

PT Self-protecting chimeric polypeptide comprising biologically active
PT sequence and single-chain antibody sequence - has resistance to e.g.
PT disrupting temperature, presence of proteolytic enzymes, etc.
XX
XX Example 2; Columns 27-28; 29pp; English.

XX The present sequence is the cDNA for the immunoglobulin (Ig) heavy
CC chain variable region of a murine anti-asparaginase II monoclonal
CC antibody (MAB). The cDNA was used in the preparation of a novel
CC recombinant chimeric polypeptide, comprising a 1st region
CC comprising a biologically active domain and another domain
CC containing an epitope, linked via a polypeptide to a 2nd region
CC including a single chain antibody (SCA) having the light and heavy
CC chains of an antibody variable region which specifically binds the
CC epitope in the 1st region. The chimeric polypeptide assumes a
CC conformation in which the SCA is bound to the epitope of the 1st
CC region and protects its biological activity from deactivation by
CC denaturing temperatures or pH conditions, proteolytic enzymes,
CC oxidising agents or alcohol. The regions of the chimeric
CC polypeptide interact to form a structure analogous to an
CC antibody-antigen complex. A L-asparaginase-SCA fusion protein of
CC the above type has better trypsin resistance than free
CC L-asparaginase.

XX Sequence 360 BP; 85 A; 101 C; 95 G; 79 T; 0 other;

Query Match 12.8%; Score 59; DB 18; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.3e-17;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCCAGCCAAACGACACCCCA 429
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DB 270 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCCAGCCAAACGACACCCCA 328

Search completed: August 30, 2003, 19:57:04

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Result No.	Query	Score	Query			ID	Description
			Match	Length	DB		
1	461	100.0	461	9	US-09-861-294-3	Sequence 3, Appli	
2	461	100.0	461	12	US-10-367-506-3	Sequence 3, Appli	
3	76	16.5	458	10	US-09-990-205-3	Sequence 3, Appli	
4	76	16.5	458	14	US-10-153-401-3	Sequence 3, Appli	
5	60	13.0	765	12	US-10-244-821-44	Sequence 44, Appli	
6	60	13.0	765	12	US-10-244-821-44	Sequence 44, Appli	
7	60	13.0	765	14	US-10-013-173-44	Sequence 44, Appli	
8	60	13.0	765	14	US-10-013-173-44	Sequence 44, Appli	
9	60	13.0	765	14	US-10-013-173-44	Sequence 44, Appli	
10	60	13.0	765	14	US-10-150-762-44	Sequence 45, Appli	
11	60	13.0	765	12	US-10-150-762-45	Sequence 45, Appli	
12	60	13.0	1239	14	US-10-244-821-5	Sequence 5, Appli	
13	60	13.0	1239	14	US-10-013-173-5	Sequence 5, Appli	
14	60	13.0	1280	12	US-10-150-762-5	Sequence 5, Appli	
15	60	13.0	1280	14	US/10/244	Sequence 7, Appli	
16	60	13.0	1280	14	US/10/013	Sequence 7, Appli	
17	60	13.0	1280	14	US/10/150	Sequence 7, Appli	

QY 61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGGGCTCAGTGAAGATGCC 120
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Db 61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGGGCTCAGTGAAGATGCC 120
|||||
QY 121 TGAAGGCTTCTGGCTACACATTGACCACTTACAATATGACCTGGGTAAGCAGACACCT 180
|||||
Db 121 TGAAGGCTTCTGGCTACACATTGACCACTTACAATATGACCTGGGTAAGCAGACACCT 180
|||||
QY 181 GGACAGGCTTGAATGGATTGGAATATATTTTCTGGAATGGTGATCTTACTACAAT 240
|||||
Db 181 GGACAGGCTTGAATGGATTGGAATATATTTTCTGGAATGGTGATCTTACTACAAT 240
|||||
QY 241 CAGAAGTTTAAAGGCAAGGCTCATTGACTGCAGACACATCTCCAGCAGACCTACATG 300
|||||
Db 241 CAGAAGTTTAAAGGCAAGGCTCATTGACTGCAGACACATCTCCAGCAGACCTACATG 300
|||||
QY 301 CAGATCAGCAGCTGACATCTGAGACTCTGCGGTCTATTTCTGCAAGGGAAGCTGG 360
|||||
Db 301 CAGATCAGCAGCTGACATCTGAGACTCTGCGGTCTATTTCTGCAAGGGAAGCTGG 360
|||||
QY 361 GAGGCTCTGAGCTACTGGGCTCAAGGAACCTCAGTCAACCTCTCCTCAGCCAAAACG 420
|||||
Db 361 GAGGCTCTGAGCTACTGGGCTCAAGGAACCTCAGTCAACCTCTCCTCAGCCAAAACG 420
|||||
QY 421 ACACCCCCACCGCTATCCACTGGTCCCTGGAGCTTTGGG 461
|||||
Db 421 ACACCCCCACCGCTATCCACTGGTCCCTGGAGCTTTGGG 461
|||||

RESULT 2

US-10-367-506-3
; Sequence 3, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(461)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(57)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (58)...(461)

Query Match 100.0%; Score 461; DB 12; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.9e-236;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATGACAGTGGGCTTTCTTCTCCTCTGTCATAAATACTACAGGTGCCACTCCAG 60
|||||
Db 1 ATGGAATGACAGTGGGCTTTCTTCTCCTCTGTCATAAATACTACAGGTGCCACTCCAG 60
|||||
QY 61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGGGCTCAGTGAAGATGCC 120
|||||

Db 61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGGGCTCAGTGAAGATGCC 120
|||||
QY 121 TGAAGGCTTCTGGCTACACATTGACCACTTACAATATGACCTGGGTAAGCAGACACCT 180
|||||
Db 121 TGAAGGCTTCTGGCTACACATTGACCACTTACAATATGACCTGGGTAAGCAGACACCT 180
|||||
QY 181 GGACAGGCTTGAATGGATTGGAATATATTTTCTGGAATGGTGATCTTACTACAAT 240
|||||
Db 181 GGACAGGCTTGAATGGATTGGAATATATTTTCTGGAATGGTGATCTTACTACAAT 240
|||||
QY 241 CAGAAGTTTAAAGGCAAGGCTCATTGACTGCAGACACATCTCCAGCAGACCTACATG 300
|||||
Db 241 CAGAAGTTTAAAGGCAAGGCTCATTGACTGCAGACACATCTCCAGCAGACCTACATG 300
|||||
QY 301 CAGATCAGCAGCTGACATCTGAGACTCTGCGGTCTATTTCTGCAAGGGAAGCTGG 360
|||||
Db 301 CAGATCAGCAGCTGACATCTGAGACTCTGCGGTCTATTTCTGCAAGGGAAGCTGG 360
|||||
QY 361 GAGGCTCTGAGCTACTGGGCTCAAGGAACCTCAGTCAACCTCTCCTCAGCCAAAACG 420
|||||
Db 361 GAGGCTCTGAGCTACTGGGCTCAAGGAACCTCAGTCAACCTCTCCTCAGCCAAAACG 420
|||||
QY 421 ACACCCCCACCGCTATCCACTGGTCCCTGGAGCTTTGGG 461
|||||
Db 421 ACACCCCCACCGCTATCCACTGGTCCCTGGAGCTTTGGG 461
|||||

RESULT 3

US-09-990-205-3
; Sequence 3, Application US/09990205
; Patent No. US20020150572A1
; GENERAL INFORMATION:
; APPLICANT: FOON, Kenneth A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000501
; CURRENT APPLICATION NUMBER: US/09/990,205
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: U.S. 09/192,838
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/065,774
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Mus Musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(456)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(456)

US-09-990-205-3
Query Match 16.5%; Score 76; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 TGCTCTGGACTACTGGGCTCAAGGAACCTCAGTCAACCTCCTCAGCCAAAACGACACC 425
|||||
Db 363 TGCTCTGGACTACTGGGCTCAAGGAACCTCAGTCAACCTCCTCAGCCAAAACGACACC 422
|||||
QY 426 CCCACCGCTCTATCCA 441
|||||
Db 423 CCCACCGCTCTATCCA 438
|||||

RESULT 4

US-10-153-401-3
; Sequence 3, Application US/10153401
; Publication No. US20030114398A1

```
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; Foon, Kenneth A.
; Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,401
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/293,533
; FILING DATE: 1999-04-15
; APPLICATION NUMBER: US 08/372,676
; FILING DATE: 1995-01-17
; APPLICATION NUMBER: US 08/591,196
; FILING DATE: 1996-01-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine M. Polizzi
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 304142000202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..456
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-153-401-3
Query Match 16.5%; Score 76; DB 14; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 366 TGCCTCGGACTACTGGGGTCAAGGACCTCAGTCACCGTCTCTCTCAGCCAAACGACACC 425
DB 363 TGCCTCGGACTACTGGGGTCAAGGACCTCAGTCACCGTCTCTCTCAGCCAAACGACACC 422
QY 426 CCCACCCGCTATCCA 441
DB 423 CCCACCCGCTATCCA 438
RESULT 5
US-10-244-821-44
; Sequence 44, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
```

```
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
; US-10-244-821-44
Query Match 13.0%; Score 60; DB 12; Length 765;
Best Local Similarity 100.0%; Pred. No. 8.8e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 ACCAGTTACAATATGCACCTGGGTAAAGCAGACACCTGGAGCGCCTGGATGGATGGA 204
DB 88 ACCAGTTACAATATGCACCTGGGTAAAGCAGACACCTGGAGCGCCTGGATGGATGGA 147
RESULT 6
US-10-244-821-45
; Sequence 45, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C2B8 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
; US-10-244-821-45
Query Match 13.0%; Score 60; DB 12; Length 765;
Best Local Similarity 100.0%; Pred. No. 8.8e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 ACCAGTTACAATATGCACCTGGGTAAAGCAGACACCTGGAGCGCCTGGATGGATGGA 204
DB 88 ACCAGTTACAATATGCACCTGGGTAAAGCAGACACCTGGAGCGCCTGGATGGATGGA 147
RESULT 7
US-10-013-173-44
; Sequence 44, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
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; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013.173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-013-173-44

Query Match 13.0%; Score 60; DB 14; Length 765;
Best Local Similarity 100.0%; Pred. No. 8.8e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTTACAATATGCACCTGGGTAAGACACACACCTGGAGCGCCTGGGAATGGATTGGA 204
|||||
DB 88 ACCAGTTACAATATGCACCTGGGTAAGACACACACCTGGAGCGCCTGGGAATGGATTGGA 147
|||||

RESULT 8
US-10-013-173-45
; Sequence 45, Application US/10013173
; Publication No. US2003009577A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013.173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C2B8 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-013-173-45

Query Match 13.0%; Score 60; DB 14; Length 765;
Best Local Similarity 100.0%; Pred. No. 8.8e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTTACAATATGCACCTGGGTAAGACACACACCTGGAGCGCCTGGGAATGGATTGGA 204
|||||
DB 88 ACCAGTTACAATATGCACCTGGGTAAGACACACACCTGGAGCGCCTGGGAATGGATTGGA 147
|||||

RESULT 9
US-10-150-762-44
; Sequence 44, Application US/10150762
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.

; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150.762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-150-762-44

Query Match 13.0%; Score 60; DB 14; Length 765;
Best Local Similarity 100.0%; Pred. No. 8.8e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTTACAATATGCACCTGGGTAAGACACACACCTGGAGCGCCTGGGAATGGATTGGA 204
|||||
DB 88 ACCAGTTACAATATGCACCTGGGTAAGACACACACCTGGAGCGCCTGGGAATGGATTGGA 147
|||||

RESULT 10
US-10-150-762-45
; Sequence 45, Application US/10150762
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150.762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C2B8 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-150-762-45

Query Match 13.0%; Score 60; DB 14; Length 765;
Best Local Similarity 100.0%; Pred. No. 8.8e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTTACAATATGCACCTGGGTAAGACACACACCTGGAGCGCCTGGGAATGGATTGGA 204
|||||
DB 88 ACCAGTTACAATATGCACCTGGGTAAGACACACACCTGGAGCGCCTGGGAATGGATTGGA 147
|||||

RESULT 11
US-10-244-821-5
; Sequence 5, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:

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; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion
US-10-244-821-5

Query Match      13.0%; Score 60; DB 12; Length 1239;
Best Local Similarity 100.0%; Pred. No. 8.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTTACAATATGCACTGGGTAAGCAGACACCTGGACAGGCGCTGGAATGGATTGGA 204
      |||||||
Db 469 ACCAGTTACAATATGCACTGGGTAAGCAGACACCTGGACAGGCGCTGGAATGGATTGGA 528

RESULT 12
US-10-013-173-5
; Sequence 5, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013.173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion
US-10-013-173-5

Query Match      13.0%; Score 60; DB 14; Length 1239;
Best Local Similarity 100.0%; Pred. No. 8.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTTACAATATGCACTGGGTAAGCAGACACCTGGACAGGCGCTGGAATGGATTGGA 204
      |||||||
Db 469 ACCAGTTACAATATGCACTGGGTAAGCAGACACCTGGACAGGCGCTGGAATGGATTGGA 528

RESULT 13
US-10-150-762-5
; Sequence 5, Application US/10150762
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
```

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; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150.762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion
US-10-150-762-5

Query Match      13.0%; Score 60; DB 14; Length 1239;
Best Local Similarity 100.0%; Pred. No. 8.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTTACAATATGCACTGGGTAAGCAGACACCTGGACAGGCGCTGGAATGGATTGGA 204
      |||||||
Db 469 ACCAGTTACAATATGCACTGGGTAAGCAGACACCTGGACAGGCGCTGGAATGGATTGGA 528

RESULT 14
US/10/244
; Sequence 7, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1280
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion constr
US/10/244,821-7

Query Match      13.0%; Score 60; DB 12; Length 1280;
Best Local Similarity 100.0%; Pred. No. 8.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTTACAATATGCACTGGGTAAGCAGACACCTGGACAGGCGCTGGAATGGATTGGA 204
      |||||||
Db 96 ACCAGTTACAATATGCACTGGGTAAGCAGACACCTGGACAGGCGCTGGAATGGATTGGA 155

RESULT 15
US/10/013
; Sequence 7, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
```

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; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1280
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion construct
US/10/013,173-7

Query Match      13.0%; Score 60; DB 14; Length 1280;
Best Local Similarity 100.0%; Pred. No. 8.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      145 ACCAGTTACAATATGCACCTGGGTAAGCAGACACACCTGGAGGGCCTGGGAATGGATTGGA 204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96 ACCAGTTACAATATGCACCTGGGTAAGCAGACACACCTGGAGGGCCTGGGAATGGATTGGA 155

Search completed: August 30, 2003, 22:02:42
Job time : 168.244 secs
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	Best Local Similarity	100.0%;	Pred. No.	2.6e-14;	Mismatches	49;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	371	TGGACTACTGGGTC	CAAGAACCTCAGTCCACCGTCTCTCTCAGCCAAAC	419										
Db	399	TGGACTACTGGGTC	CAAGAACCTCAGTCCACCGTCTCTCTCAGCCAAAC	447										
RESULT 3														
LOCUS	BF137216													
DEFINITION	601784466F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4012360 5'; mRNA sequence.													
ACCESSION	BF137216													
VERSION	BF137216.1													
KEYWORDS	EST.													
SOURCE	Mus musculus (house mouse)													
ORGANISM	Mus musculus													
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.													
AUTHORS	1 (bases 1 to 802)													
TITLE	NIH-MGC http://mgc.nci.nih.gov/.													
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)													
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D. Email: cgabbs-re@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9253 row: c column: 17 High quality sequence stop: 697.													
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	/organism="Mus musculus"													
	/mol_type="mRNA"													
	/strain="CZECH II"													
	/db_xref="taxon:10090"													
	/clone="IMAGE:4012360"													
	/tissue_type="tumor, metastatic to mammary"													
	/lab_host="DH10B"													
	/clone_lib="NCI_CGAP_Lu30"													
	/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; transgenic model WNT-1, expression driven by MTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"													
BASE COUNT	191 a	217 c	211 g	183 t										
ORIGIN														
Query Match														
Best Local Similarity	10.6%;													
Mismatches	Score 49;													
DB 10;	Length 802;													
Matches	49;													
Conservative	0;													
Mismatches	0;													
Indels	0;													
Gaps	0;													
QY	371	TGGACTACTGGGTC	CAAGAACCTCAGTCCACCGTCTCTCTCAGCCAAAC	419										
Db	399	TGGACTACTGGGTC	CAAGAACCTCAGTCCACCGTCTCTCTCAGCCAAAC	447										
RESULT 4														
LOCUS	BI455668													
DEFINITION	603173862F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5253279 5'; mRNA sequence.													
ACCESSION	BI455668													
VERSION	BI455668.1													
KEYWORDS	EST.													
SOURCE	Mus musculus (house mouse)													
ORGANISM	Mus musculus													
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.													

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 861)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11639 row: 1 column: 16
High quality sequence stop: 780.

FEATURES
source

1. .861

Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5253279"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: Sali;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 205 a 239 c 211 g 206 t
ORIGIN

Query Match 10.68; Score 49; DB 12; Length 861;

Best Local Similarity 100.0%; Pred. No. 2.9e-14;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 371 TGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAAC 419
|||||

Db 441 TGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAAC 489

RESULT 5
B1151077
LOCUS
DEFINITION 602917012F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5067314 5',
883 bp mRNA linear EST 05-JUL-2001
mRNA sequence.

B1151077

B1151077.1 GI:14611078

VERSION

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 883)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM1181 row: h column: 03

High quality sequence stop: 719.

Location/Qualifiers

1. .883

FEATURES

source

/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5067314"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin.
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu29"

/note="Organ: lung; Vector: pCMV-SPORT6; Site.1: Sali;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 211 a 268 c 217 g 187 t
ORIGIN

Query Match 10.68; Score 49; DB 12; Length 883;

Best Local Similarity 100.0%; Pred. No. 2.9e-14;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 371 TGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAAC 419

|||||

Db 255 TGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCCAAAC 303

RESULT 6

B142302

LOCUS

DEFINITION 601791844F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4022459 5',
1012 bp mRNA linear EST 24-OCT-2000
mRNA sequence.

B142302

B142302.1 GI:10981252

VERSION

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1012)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence stop: 711.

Location/Qualifiers

1. .1012

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CZECH II"

/db_xref="taxon:10090"

/clone="IMAGE:4022459"

/tissue_type="tumor, metastatic to mammary"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Lu30"

/note="Organ: lung; Vector: pCMV-SPORT6; Site.1: NotI;

Site.2: Sali; transgenic model WNT-1, expression driven by

MTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo

dt. Library constructed by Life Technologies.

Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 273 a 271 c 267 g 201 t

ORIGIN

Query Match 10.68; Score 49; DB 10; Length 1012;

Best Local Similarity 100.0%; Pred. No. 3e-14;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES

source

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QY 371 TGGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCTCTCAGCCAAAC 419
|||||
Db 411 TGGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCTCTCAGCCAAAC 459

RESULT 7
BF136279 601780989F1 NCI_CGAP_Lu30 718 bp mRNA linear EST 24-OCT-2000
LOCUS 601780989F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009197 5',
DEFINITION mRNA sequence.
ACCESSION BF136279
VERSION BF136279.1 GI:10975319
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 718)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9244 row: 0 column: 22
High quality sequence stop: 671.
Location/Qualifiers
1. 718
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:4009197"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 173 a 196 c 181 g 168 t
ORIGIN
Query Match 10.4%; Score 48; DB 10; Length 718;
Best Local Similarity 100.0%; Pred. No. 8.9e-14;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 TGGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCTCTCAGCCAAAC 418
|||||
Db 410 TGGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCTCTCAGCCAAAC 457

RESULT 8
BF143948 601786493F1 NCI_CGAP_Lu30 862 bp mRNA linear EST 24-OCT-2000
LOCUS 601786493F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014430 5',
DEFINITION mRNA sequence.
ACCESSION BF143948
VERSION BF143948.1 GI:10982988
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 862)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9258 row: 1 column: 23
High quality sequence stop: 671.
Location/Qualifiers
1. 862
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:4014430"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 213 a 236 c 236 g 176 t 1 others
ORIGIN
Query Match 10.4%; Score 48; DB 10; Length 862;
Best Local Similarity 100.0%; Pred. No. 9.5e-14;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCTCTCAGCCAAAC 419
|||||
Db 411 GGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCTCTCAGCCAAAC 458

RESULT 9
BF583109 602098016F1 NCI_CGAP_Co24 913 bp mRNA linear EST 12-DEC-2000
LOCUS 602098016F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4218099 5',
DEFINITION mRNA sequence.
ACCESSION BF583109
VERSION BF583109.1 GI:11656827
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 913)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9797 row: p column: 04
High quality sequence stop: 656.
Location/Qualifiers
1. 913
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"

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/db_xref="taxon:10090"
/clone="IMAGE:4218099"
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/clone_lib="NCI_CGAP_Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      183 a      261 c      250 g      219 t
ORIGIN
Query Match      10.2%; Score 47; DB 10; Length 913;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 366 TGCTCGGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCCTCAG 412
|||||
Db 383 TGCTCGGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCCTCAG 429
|||||

RESULT 10
B0929209
LOCUS      B0929209      933 bp      mRNA      linear      EST 20-AUG-2002
DEFINITION AGENCOURT_8953380 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6477383 5', mRNA sequence.
B0929209
ACCESSION B0929209
VERSION   B0929209
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 933)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM14019 row: d column: 24
High quality sequence stop: 546.
FEATURES             source
Location/Qualifiers
1..933
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6477383"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      223 a      261 c      236 g      211 t      2 others
ORIGIN
Query Match      10.2%; Score 47; DB 13; Length 933;
Best Local Similarity 100.0%; Pred. No. 3.3e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 366 TGCTCGGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCCTCAG 412
|||||
Db 368 TGCTCGGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCCTCAG 414
|||||

RESULT 11

```

BY703373

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY703373 991 bp mRNA linear EST 16-DEC-2002
 cDNA clone 0610041A01 5', mRNA sequence.

BY703373.1 GI:27114480

Mus musculus (house mouse)
 EST.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 991)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Saito, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H.

, Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,

Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A.,

Gojkenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S.,

Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani

, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest

, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.

, Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J.,

Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M.,

King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons

, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki

, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G.,

Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D.,

Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring

, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C. A., Setou

, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale

, R. D., Tomlita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,

Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa

, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,

Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura

, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.

, Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii

, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shiba

, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander

, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

CONTACT: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suenho-cho, Tsukuba, Ibaraki, 305-8565, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda

, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, E., Imotani, K.,

Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno

, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K.,

Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H.,

Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y.,

Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct

Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
source Location/Qualifiers
1. 991
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="0610041A01"
/sex="male"
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/lab_host="SOLR"
/note="lib="RIKEN full-length enriched, adult male kidney"
/note="Site:1: XhoI; Site:2: SstI; cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cdna was primed with a primer [5'
GAGAGAGCGCGCCGCACTCGAGTTTCTTTTCTTTT 3'], cdna was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cdna was prepared with the primer adapter of sequence [5'
GAGAGAGAGATCCAGAGCTCAATTAATTAATTAACCCCCCCCC 3'].
cdna was cleaved with XhoI and SstI."
BASE COUNT 231 a 289 c 238 g 232 t 1 others
ORIGIN
Query Match 10.28; Score 47; DB 14; Length 991;
Best Local Similarity 100.0%; Pred. No. 3.3e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 305 TCAGCAGCCTGACATCTGAGACTCTCGGCTCTATTTCTGTGCAAGA 351
|||||
DB 186 TCAGCAGCCTGACATCTGAGACTCTCGGCTCTATTTCTGTGCAAGA 232
|||||
RESULT 12
LOCUS AK002875 1384 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus adult male kidney cdna, RIKEN full-length enriched library, clone:0610041A01 product:immunoglobulin heavy chain 6 (heavy chain of IgM), full insert sequence.
ACCESSION AK002875
VERSION AK002875.1 GI:12833178
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cdna libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cdna libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

TITLE

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Yamamoto,R., Matsumoto,H., Sakauchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Kiyosawa,H., Kondo,S., Yamana,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,Y., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staib,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,P., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
Functional annotation of a full-length mouse cdna collection
Nature 409 (6821), 685-690 (2001)
21085660
MEDLINE 11217851
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1384)
ADACHI,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:<http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cdna was primed with a primer [5' GAGAGAGCGCGCCGCACTCGAGTTTCTTTTCTTTT 3'], cdna was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cdna went through one round of normalization to Rot = 5.0. Second strand cdna was prepared with the primer adapter of sequence[5' GAGAGAGAGATCCAGAGCTCAATTAATTAATTAACCCCCCCCC 3']. cdna was

COMMENT

cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:

FEATURES

Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="MGI:1907162"
/db_xref="taxon:10090"
/clone="0610041A01"
/sex="male"
/tissue_type="kidney"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
53. .1333
/note="unnamed protein product: Immunoglobulin heavy chain
6 (heavy chain of IgM) (MGI:96448, GB|AK008342,
evidence: BLASTN, 100%, match=137)
putative"
/codon_start=1
/protein_id="BAB22422.1"
/db_xref="GI:12833179"
/db_xref="MGI:96486"
/translation="MGFSRIFLLSVTTGNGDTSYNQKFKGKATLVDKSSSTAYWQ
LSSITSDSAVYFCARDSDYGPYAMDYWGQSTVTSSEARNPTIYPLTPRALSSD
PVIITGLIHDFPSTGMVTKGSKDITVTFPPALASGGYTMSSQLTLPALVECE
GSKVCSQHDNSAVQELDKVCGPPCPPCPPCHPSLSLORPALEDLLIGSDASL
TCTLNGLRNPEGAVTWPSTGDKAVOKKAVONSCGCVSYSVLPGCAERNNSGASK
CTVHPSPSDILTGIAKITVTFPPQVHLPLPPSEELALNELVSLTCLVRAFNPKVL
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/note="putative"
1360. .1365
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/note="putative"

CDS

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polyA_site
BASE COUNT 321 a 413 c 342 g 308 t
ORIGIN
Query Match 10.2%; Score 47; DB 11; Length 1384;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 305 TCACAGCCTGACATCTGAGACTCTGGGTCATTCTGTGCAAGA 351
|||||
Db 186 TCACAGCCTGACATCTGAGACTCTGGGTCATTCTGTGCAAGA 232
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RESULT 13
LOCUS BF016722 406 bp mRNA linear EST 29-DEC-2000
DEFINITION uy34h12.y1 NCI-CCAP Lu30 Mus musculus cDNA clone IMAGE:3661511 5',
similar to SW:HV02.MOUSE P01746 IG HEAVY CHAIN V REGION 93G7
PRECURSOR. ., mRNA sequence.
ACCESSION BF016722.1 GI:10748054
VERSION BF016722.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 406)
REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

FEATURES

Location/Qualifiers
Seq primer: -40RP from Gibco.
1. .406
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:3661511"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI-CCAP Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site1: NotI;
Site2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 109 a 102 c 98 g 97 t
ORIGIN
Query Match 9.3%; Score 43; DB 10; Length 406;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 98 CTGGGGCTCAGTCAAGATGCTCTGCAAGGCTTCTGGCTACAC 140
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Db 133 CTGGGGCTCAGTCAAGATGCTCTGCAAGGCTTCTGGCTACAC 175
|||||

RESULT 14
LOCUS CA579143 429 bp mRNA linear EST 19-NOV-2002
DEFINITION K0733D01-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
cDNA Library (Long) Mus musculus cDNA clone NIA:K0733D01
IMAGE:30076740 5', mRNA sequence.
ACCESSION CA579143.1 GI:25127534
VERSION CA579143
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 429)
REFERENCE Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,
Alba, K., Taub, D., Longo, D.L., Keller, J., and Ko, M.S.H.,
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)
Unpublished
JOURNAL Other ESTs: K0733D01-3
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6920, USA
Email: cdnaelgusn.grc.nia.nih.gov
Plate: K0733 row: D column: 01
Seq primer: M13 Reverse
High quality sequence stop: 429
POLYA-No.

FEATURES

Location/Qualifiers
1. .429
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/mol_type="mRNA"
/strain="C57BL/6Ncr"
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/db_xref="taxon:10090"
/clone="NIA:K0733D01 IMAGE:30076740"
/tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)"
/dev_stage="Age approx.10 weeks old"
/lab_host="DH10B"

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(Lin-/c-Kit-/Sca-1-) cDNA library (Long)"
/notes="vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001)). [PMID: 11544199]]. Total RNAs were
obtained from Drs. Dennis Taub, Dan Longo (National
Institute on Aging, USA), Jonathan Keller (National Cancer
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) primer [Invitrogen:
5'-pGACTAGTCTAGTCGCGAGCGCGCCCTTTT-3'] from
0.9 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Loe-linker L1-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.1 kb. The library was constructed
by Yulan Piao (NIA)."
BASE COUNT      104 a 112 c 108 g 105 t
ORIGIN

```

```

Query Match      9.1%; Score 42; DB 14; Length 429;
Best Local Similarity 100.0%; Pred. No. le-10;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 TGGACTACTGGGTCAGGACCTCAGTCACCGTCTCCTCAG 412
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Db 353 TGGACTACTGGGTCAGGACCTCAGTCACCGTCTCCTCAG 394

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```

RESULT 15
CA580198
LOCUS
DEFINITION
IMAGE:30078168 5', mRNA sequence.
CA580198.1 GI:25128589
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 451)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,
Alba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)
Unpublished
Other_ESTS: K0748C01-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0748 row: C column: 01
Seq primer: M13 Reverse
High quality sequence stop: 451
POLYA-No. Location/Qualifiers
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/organism="Mus musculus"
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FEATURES
source

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/db_xref="taxon:10090"
/clone="NTA:K0748C01 IMAGE:30078168"
/tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-
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/dev_stage="Age approx. 10 weeks old"
/lab_host="DH10B"
/clone_lib="NTA Mouse Hematopoietic Stem Cell.
(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"
/notes="vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001)). [PMID: 11544199]]. Total RNAs were
obtained from Drs. Dennis Taub, Dan Longo (National
Institute on Aging, USA), Jonathan Keller (National Cancer
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) primer [Invitrogen:
5'-pGACTAGTCTAGTCGCGAGCGCGCCCTTTT-3'] from
0.9 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Loe-linker L1-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.1 kb. The library was constructed
by Yulan Piao (NIA)."
BASE COUNT      99 a 129 c 104 g 119 t
ORIGIN
Query Match      9.1%; Score 42; DB 14; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 TGGACTACTGGGTCAGGACCTCAGTCACCGTCTCCTCAG 412
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Db 363 TGGACTACTGGGTCAGGACCTCAGTCACCGTCTCCTCAG 404

Search completed: August 30, 2003, 21:57:09
Job time : 1606.24 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2003, 13:43:39 ; Search time 2088.91 Seconds
(without alignments)
9028.331 Million cell updates/sec

Title: US-08-836-455-3
Perfect score: 461
Sequence: 1 ATGGAATGCAGCTGGTCTT.....CTGGTCCCTGGAAGCTTGGG 461

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
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- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_man:*
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- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	461	100.0	461	6	AR164506	AR164506 Sequence
2	461	100.0	461	6	BD085738	BD085738 Methods O
3	409.4	88.8	411	10	AF124720	AF124720 Mus muscu
4	355.2	77.0	471	10	AB050080	AB050080 Mus muscu
5	353.6	76.7	457	10	AY178830	AY178830 Mus muscu
6	337.8	73.3	1542	10	BC002121	BC002121 Mus muscu
7	328.2	71.2	483	10	MMU39899	U39899 Mus muscu
8	327.2	71.0	409	6	BD092129	BD092129 Diagnosti
9	325	70.5	1544	10	MUSIGB1H1	D14625 Mus musculu
10	324.6	70.4	453	6	ARI09947	ARI09947 Sequence
11	323	70.1	525	10	MUSIGHALPA	M28834 Mus musculu
12	323	70.1	540	6	A13735	A13735 variable re
13	322	69.8	458	6	I05921	I05921 Sequence 37
14	322	69.8	458	6	I08811	I08811 Sequence 12
15	322	69.8	458	6	I09199	I09199 Sequence 38
16	322	69.8	458	10	MUSIGHXW	M17953 Mouse Ig re
17	321.6	69.8	450	10	AY178829	AY178829 Mus muscu
18	320.6	69.5	1553	6	E08434	E08434 cDNA encodi
19	320.2	69.5	902	12	XX049832	U49832 Synthetic s
20	320	69.4	1683	6	E35543	E35543 Transgenic
21	318.6	69.1	473	10	AB050071	AB050071 Mus muscu
22	314.8	68.3	494	6	BD021876	BD021876 Humanized
23	313.4	68.0	451	10	MMLB4IHEV	X65773 M.musculus
24	311.6	67.6	1568	6	E33134	E33134 Humanized a
25	311.6	67.6	1570	6	A22261	A22261 M.musculus
26	311.6	67.6	1570	6	A77138	A77138 Sequence 6
27	311	67.5	489	10	MMU39900	U39900 Mus musculu
28	310.8	67.4	1526	10	MMU555822	AJ555622 Mus muscu
29	310.6	67.4	1573	10	BC018280	BC018280 Mus muscu
30	310.2	67.3	1581	6	A78881	A78881 Sequence 1
31	310.2	67.3	1581	10	MMIGHC2AA	X70423 M.musculus
32	310	67.2	1570	6	AR029102	AR029102 Sequence
33	308.6	66.9	1564	10	BC019489	BC019489 Mus muscu
34	308.2	66.9	588	6	A23165	A23165 Artificial
35	308.2	66.9	588	10	MUSIGGVZ	L02346 Mus musculu
36	308	66.8	490	10	MUSIG4C11A	M24785 Mouse anti-
37	308	66.8	1558	10	AF466769	AF466769 Mus muscu
38	307	66.6	484	10	MUSIGH4C11	M54977 Mus musculu
39	306.8	66.6	520	10	MMU416332	A7416332 Mus muscu
40	306.6	66.5	2154	10	BC018315	BC018315 Mus muscu
41	306.4	66.5	1500	10	MMWAMST2	X79907 M.musculus
42	304.4	66.0	1572	6	A44967	A44967 Sequence 23
43	304.4	66.0	1572	6	I64458	I64458 Sequence 23
44	303.2	65.8	1547	10	BC028249	BC028249 Mus muscu
45	303	65.7	747	10	MMU012555	AJ012555 Mus muscu

ALIGNMENTS

RESULT 1						
AR164506						
LOCUS	AR164506	461 bp	DNA	linear	PAT 17-OCT-2001	
DEFINITION	Sequence 3 from patent US 6274143.					
ACCESSION	AR164506					
VERSION	AR164506.1	GI:16237556				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 461)					
AUTHORS	Chatterjee,M. and Foon,K.A.					
TITLE	Methods of delaying development of HMFG-associated tumors using anti-idiotypic antibody 11D10					
JOURNAL	Patent: US 6274143-A 3 14-AUG-2001;					

[illegible]

421	ACACCCCCCACCCTGATCCATCCCTGGCCCTCCCTGGAGCTGGG	461
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Db		
RESULT 3		
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LOCUS	411 bp mRNA	linear ROD 22-MAY-2001
DEFINITION	Mus musculus immunoglobulin heavy chain mRNA,	partial cds.
ACCESSION	AF124720	
VERSION	AF124720.1	GI:14164544
KEYWORDS		
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Mus musculus	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE	1 (bases 1 to 411)	
	Tripathi,P.K., Qin,H., Bhattacharya-Chatterjee,M., Ceriani,R.L., Foon,K.A. and Chatterjee,S.K.	
	Construction and characterization of a chimeric fusion protein consisting of an anti-idiotypic antibody mimicking a breast cancer-associated antigen and the cytokine GM-CSF	
	Hybridoma 18 (2), 193-202 (1995)	
JOURNAL	99306687	
MEDLINE	10380019	
REFERENCE	2 (bases 1 to 411)	
AUTHORS	Chatterjee,S.K. and Tripathi,P.K.	
TITLE	Direct Submission	
JOURNAL	Submitted (29-JAN-1999) Internal Medicine, University of Kentucky,	
FEATURES	800 Rose Street, Lexington, KY 40536, USA	
	Location/Qualifiers	

JOURNAL	Published Only in Database (2002)
REFERENCE	3 (bases 1 to 471)
AUTHORS	Kitagawa,Y.
TITLE	Direct Submission
JOURNAL	Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural University, Biotechnology Institute; Minami 2-2, Ogata, Akita 010-0444, Japan (E-mail:kitagawa@agri.akita-pu.ac.jp, URL:www.akita-u.ac.jp/, Tel:81-185-45-2026(ex.400), Fax:81-185-45-2678)
FEATURES	Location/Qualifiers
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CDS	1..471 /gene="VH9H8" 11..>469 /codon_start=1 /product="anti-A/U antibody" /protein_id="BAB87192.1" /db_xref="GI:19909936"
translation	"MGWTGVFLILLSTTGVHSQAYLQQSGAELVRSGAVKMSCKRAS GYTFYSNMHWVKPTGGGLEWGNIFPNAGDTYINQFKGKATLTADTSSTAYMOI SLTSDSAVFYFCARGNWPWFAYWGQGLTVWSAAKTTAQPVPLAPGSL"
BASE COUNT	114 a 126 c 121 g 110 t
ORIGIN	
Query Match	77.0%; Score 355.2; DB 10; Length 471;
Best Local Similarity	88.4%; Pred. No. 3.6e-110;
Matches	410; Conservative 0; Mismatches 48; Indels 6; Gaps 2;
QY	1 ATGGAATCAGCTGGGTCTTTCTTCCTCTCTCTCAATAACTACAGTGTCCTCCAC 60
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QY	61 GCTTATCTACAGCAGCTCGGGCTGAGCTGGTGAGGTCTGGGGCTCAGTGAAGATGCC 120
Db	
QY	121 TGCAGAGCTTCGGCTACACATTGACCAGTTACAATATGCACCTGGGTAAAGCAGACCT 180
Db	
QY	181 GCACAGGCGCTGGAATGGATTGGAAATATTTTCTCGAATGTGTACTTACTACAAT 240
Db	
QY	241 CAGAAGTTTAAGGGCAAGCGCTCATTTGACTCGACACATCTCTCCAGCACAGCTACATG 300
Db	
QY	301 CAGATCAGCAGCCTGACATCTGAAGACTCTCGGTCTATTCTGTGCAAGAGGGAAC-- 358
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QY	359 -GGGAGGTGCTCTGGACTACTGGGTCAAGAACCTCAGTCACCGTCTCTCTCAGCCAAA 417
Db	
QY	418 ACACAGCCCCACCGCTCTATCCACTGCTCCCTGGAAGCTTGGG 461
Db	
QY	428 ACAACAGCCCACCGCTTATCCCTTGCCCTGGAAGCTTGGG 471
Db	
RESULT 5	
AB050080	AY178830 457 bp mRNA linear ROD 15-JAN-2003
LOCUS	Mus musculus clone 13G10 antiporphyrin immunoglobulin G heavy chain
DEFINITION	variable region mRNA, partial cds.
ACCESION	AY178830

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Query Match	88.8%; Score 409.4; DB 10; Length 411;
Best Local Similarity	99.8%; Pred. No. 8.5e-129;
Matches	410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY	181 GGACAGGCGCTGGAATGGATTGGAATATTTTCTCGAATGTGTACTTACTACAAT 240
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QY	301 CAGATCAGCAGCCTGACATCTGAAGACTCTCGGTCTATTCTGTGCAAGAGGGAAC 360
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QY	361 GAGGCTGCTCGACTACTGCGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411
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AB050080	AB050080 471 bp mRNA linear ROD 02-APR-2002
LOCUS	Mus musculus VH9H8 mRNA for anti-A/U antibody, partial cds.
DEFINITION	antibody
ACCESSION	AB050080
VERSION	AB050080.1 GI:19909935
KEYWORDS	
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 Kitagawa,Y. and Okuhara,E. The separation of three antibody populations from anti-poly(A).poly(U) antibodies elicited in mice or rabbits and antigenic features of poly(A).poly(U) Mol. Immunol. 19 (2), 257-266 (1982) 82245325 PUBMED 6178956
JOURNAL	Kitagawa,Y.
MEDLINE	anti-dsrNA (A/U) Ab VH region VH9H8
PUBMED	
AUTHORS	
TITLE	

[illegible]

DEFINITION
Diagnostic and therapeutic agents for the diseases related
monocytes and macrophages.

ACCESSION
BD092129

VERSION
BD092129.1 GI:22637740

KEYWORDS
WO 0079275-A/3

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 409)

AUTHORS
Shitara,K. and Shibuya,M.

TITLE
Diagnostic and therapeutic agents for the diseases related
monocytes and macrophages

JOURNAL
PATENT: WO 0079275-A 3 28-DEC-2000;
KYOWA HAKKO KOGYO CO LTD, KENYA SHITARA, MASABUMI SHIBUYA

COMMENT
OS Mus musculus (mouse)
PN WO 0079275-A/3
PD 28-DEC-2000
PF 16-JUN-2000 WO 2000JP003957
PP 17-JUN-1999 JP 99P 171709
PI KENYA SHITARA, MASABUMI SHIBUYA
PC G01N35/53, A61K45/00, A61K39/395//C12N15/06, C12N15/12, C07K16/28
CC

FT Key Location/Qualifiers
CDS (1)..(408).

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Best Local Similarity 88.8%; Pred. NO. 1.5e-100;
Matches 366; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

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DB 1 ATGGGATTCAGCAGGATCTTTCTTCTCTCTCTGCTACATTAACAGGTGTCTCCACTCCAG 60
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QY 61 GCTATCTACAGCAGCTGGGCTGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
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DB 61 GCTTTCTACAGCAGCTGGGCTGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
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QY 121 TGCAGGCTTCTGGCTACACATTCAGCTGACATATGCAATATGCAATATGCAATATGCAATATGCA 180
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DB 121 TGCAGGCTTCTGGCTACACATTCAGCTGACATATGCAATATGCAATATGCAATATGCAATATGCA 180
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DB 181 AGACAGGCTTCTGGCTACACATTCAGCTGACATATGCAATATGCAATATGCAATATGCAATATGCA 240
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QY 241 CAGAAGTTAAGGCAAGCCTCATGCTGACATGACATATGCAATATGCAATATGCAATATGCAATATGCA 300
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DB 241 CAGAAGTTAAGGCAAGCCTCATGCTGACATGACATATGCAATATGCAATATGCAATATGCAATATGCA 300
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DB 301 CAGCTCCGAGCCTGACATCTGAACATCTGGGCTATTTCTGGAATGGTGTGATCTACTACAAT 360
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QY 361 GAGGCTGCTCTGGCTACTTGGGCTCAAGGACCTCAGTCACGCTCTCTCTCAG 412
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DB 358 GACTATTACTTTGACTACTGGGGCAAGCACCACCTCTCAGCTCTCTCTCAG 409
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RESULT 9
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LOCUS Mus musculus mRNA for immunoglobulin gamma-3 heavy chain precursor,
complete cds.
DI14625
ACCESSION DI14625.1 GI:286089
VERSION

DEFINITION
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1544)

AUTHORS
Takahashi,S., Itoh,J., Nose,M., Ono,M., Yamamoto,T. and Kyogoku,M.

TITLE
Cloning and cDNA sequence analysis of nephritogenic monoclonal
antibodies derived from an MRL/lpr lupus mouse

JOURNAL
Mol. Immunol. 30 (2), 177-182 (1993)

MEDLINE
93156722

PUBMED
8429833

REFERENCE
2
Ono,M., Yamamoto,T., Kyogoku,M. and Nose,M.
Sequence analysis of the germ-line VH gene corresponding to a
nephritogenic antibody in MRL/lpr lupus mice
Clin. Exp. Immunol. 100 (2), 284-290 (1995)

JOURNAL
MEDLINE 95262286

PUBMED
7743668

REFERENCE
3 (bases 1 to 1544)

AUTHORS
Nose,M.

TITLE
Direct Submission

JOURNAL
Submitted (10-MAR-1993) Masato Nose, Tohoku University School of
Medicine, Dept. of Pathology; 2-1 Seiry-cho Aoba-ku, Sendai,
Miyagi 980, Japan (E-mail:d22181@ccu.co.tohoku.ac.jp,
Tel:81-22-273-9042, Fax:81-22-234-1986)

FEATURES
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33..1445
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90..1442

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90..452
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C_region
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1446..1544

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1514..1519

BASE COUNT
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Best Local Similarity 83.0%; Pred. NO. 1.1e-99;
Matches 386; Conservative 0; Mismatches 70; Indels 9; Gaps 1;

QY 1 ATGGGAATGCAGCTGGGTCTTTCTTCTCTCTCTGCTACATTAACAGGTGTCTCCACTCCAG 60
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DB 33 ATGGAATGCAGCTGGGTCTTTCTTCTCTCTCTGCTACATTAACAGGTGTCTCCACTCCAG 92
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Db      49  ATGGAAGGCACTGGATCTTCTCTCTGTTTTCAGTTACTGAGGTTGCCACTCCAG 108
QY      61  GCTTATCTACAGCAGTCTGGGCTGAGCTGTGTGAGGCTCTGGGCTCAGTGAAGATGCC 120
Db      109  GTCCAGCTTACAGCAGTCTGGGCTGAACTGGCAAAACCTGGGCTCAGTGAAGATGCC 168
QY      121  TGCAGGCTTCTGGCTACACATTCACCAATGACCAATGACCAATGACCAATGACCAATGACCAAT 180
Db      169  TGCAGGCTTCTGGCTACACCTTTACTGCTTACTGCTTACTGCTTACTGCTTACTGCTTACTGCTT 228
QY      181  GCAGAGGCTTGGATGATGGAATATTTTCTGGAATGTTGATGATGATGATGATGATGATGATGAT 240
Db      229  GCAGAGGCTTGGATGATGGAATATTTTCTGGAATGTTGATGATGATGATGATGATGATGATGAT 288
QY      241  CAGAAGTTTAAGGCAAGGCTCATTTGACTGCAGACACATCTCCAGCACAGCCCTACATG 300
Db      289  CAGAATTTCAAGGCAAGGCTCATTTGACTGCAGACACATCTCCAGCACAGCCCTACATG 348
QY      301  CAGATCAGCAGCTGACATCTGAAGACTCTGGGCTGATGCTGATGCTGATGCTGATGCTGATGCT 354
Db      349  CAATGAGCAGCTGACATCTGAGGACTCTGAGTCTTATTTGTTACAAAGAGCTACTAT 408
QY      355  AACTGGGAGGCTGCTGACTACTGGGCTCAAGGAACCTCAGTCACCGCTCTCTCAGCC 414
Db      409  AACTAGAGGGCTGATGACTACTGGGCTCAAGGAACCTCAGTCACCGCTCTCTCAGCC 468
QY      415  AAAAGCAGACCCCAAGGCTCTATCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 451
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RESULT 12

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LOCUS      A13735                      540 bp    DNA          linear    PAT 03-JAN-1994
DEFINITION variable region of a monoclonal antibody which cross reacts with 19
known Pseudomonas aeruginosa serotypes.

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ACCESSION A13735

VERSION A13735.1 GI:491743

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 540)

AUTHORS Domdey,H., Margel,M. and von Specht,B.U.

TITLE Monoclonal antibodies to Pseudomonas aeruginosa, their production

and use

JOURNAL Patent: EP 0338395-A 3 25-OCT-1989;

BEHRINGWERKE Aktiengesellschaft

FEATURES Location/Qualifiers

source

1..540

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BASE COUNT 145 a 144 c 130 g 121 t

ORIGIN

Query Match

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Matches 381; Conservative 0; Mismatches 70; Indels 6; Gaps 1;

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Db 64 ATGGAAGGCACTGGATCTTCTCTCTGTTTTCAGTTACTGAGGTTGCCACTCCAG 123

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QY      301  CAGATCAGCAGCTGACATCTGAAGACTCTGGGCTGATGCTGATGCTGATGCTGATGCTGATGCT 354
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RESULT 13

I05921

LOCUS I05921

DEFINITION Sequence 37 from Patent EP 0274394.

ACCESSION I05921

VERSION I05921.1 GI:590876

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 458)

AUTHORS Robinson,R.R., Liu,A.Y., Hellstrom,K.E., Hellstrom,I. and

Ledbetter,J.A.

TITLE Chimeric antibody with specificity to human B cell surface antigen

JOURNAL Patent: EP 0274394-A2 37 13-JUL-1988;

FEATURES Location/Qualifiers

source

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BASE COUNT 113 a 120 c 112 g 113 t

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Db 99 GCTTATCTACAGCAGTCTGGGCTGAGCTGTGTGAGGCTCTGGGCTCAGTGAAGATGCC 158

QY 121 TGCAGGCTTCTGGCTACACATTCACCAATGACCAATGACCAATGACCAATGACCAATGACCAAT 180

Db 159 TGCAGGCTTCTGGCTACACATTCACCAATGACCAATGACCAATGACCAATGACCAATGACCAAT 218

QY 181 GCAGAGGCTTGGATGATGGAATATTTTCTGGAATGTTGATGATGATGATGATGATGATGATGAT 240

Db 219 AGACAGGCTTGGATGATGGAATATTTTCTGGAATGTTGATGATGATGATGATGATGATGATGAT 278

QY 241 CAGAAGTTTAAGGCAAGGCTCATTTGACTGCAGACACATCTCCAGCACAGCCCTACATG 300

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2003, 16:05:49 ; Search time 202.202 Seconds
(without alignments)
6154.444 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	461	100.0	461	25	AAL51274 Mouse 11D10 antibo
4	327.2	71.0	409	21	AAZ87715 Anti-human VEGF re
5	327.2	71.0	409	22	AAF70192 Anti-human Flt-1 m
6	326.6	70.8	736	25	ABX16571 Mouse DNA encoding
7	323	70.1	540	10	AAN91645 Heavy chain of mon
8	322	69.8	458	10	AAN91146 2H7 Vh sequence.

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10	322	69.8	459	22	AAT22070	2H7 heavy chain va
11	322	69.8	491	18	AAH70868	2H7 heavy chain va
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13	322	69.8	491	19	AAV03926	Mouse 2H7 antibody
14	322	69.8	491	19	AAV18593	Mouse 2H7 antibody
15	322	69.8	518	18	AAT36316	2H7 antibody heavy
16	322	69.8	520	18	AAT51042	Coding sequence fo
17	320.6	69.5	1553	16	AAQ79930	Anti-tobacco mosai
18	320	69.4	1683	20	AAQ61084	Mouse immunoglobul
19	314.8	68.3	494	19	AAV20085	Consensus DNA sequ
20	311.6	67.6	1570	12	AAQ12637	Monoclonal antibody
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23	308.6	66.9	420	22	AAH81910	Anti-CA125 bifunct
24	308.2	66.9	588	14	AAQ43985	H-chain V-region o
25	308.2	66.9	1392	18	AAQ62936	3F4 (Chimeric) hum
26	308.2	66.9	1395	18	AAQ62935	Murine anti-porcine
27	308.2	66.9	3400	18	AAQ62937	3F4 human G2/G4 ch
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31	304.4	66.0	1582	16	AAQ94037	Mab 55.1 heavy cha
32	299.8	65.0	440	19	AAV22074	DNA encoding the h
33	299	64.9	458	12	AAQ15164	VH186 region of an
34	297.4	64.5	1773	18	AAH88869	H chain subunit of
35	297.4	64.5	1773	19	AAH66735	Anti-human Fas mon
36	297.4	64.5	1773	21	AAH78202	Anti-human Fas ant
37	297.2	64.5	1083	24	AAQ45753	Human CH2 domain d
38	297.2	64.5	1083	25	ABZ24017	Antibody C2B8 CH2
39	297.2	64.5	1413	21	AAA63531	DNA encoding a dlm
40	297.2	64.5	1413	24	AAQ45752	Human C2B8 antibody
41	297.2	64.5	1413	25	ABZ24016	Antibody C2B8 heav
42	297.2	64.5	9208	15	AAQ65629	Vector contg. TCAR
43	297.2	64.5	9209	25	ABX94203	TCAR8 expression v
44	297.2	64.5	19001	19	AAV61793	Traget plasmid Mol
45	297	64.4	10844	14	AAQ43848	Plasmid PAH4808.

ALIGNMENTS

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ID AAT85150 standard; cDNA; 461 BP.

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XX	AC	AAT85150;			
XX	DT	25-MAR-2003 (updated)			
XX	DT	04-JAN-1998 (first entry)			
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XX	DE	Monoclonal antibody 11D10; anti-idiotyp antibody; mucin;			
XX	KW	human milk fat globule; HMF; tumour; breast cancer; vaccine; ss.			
XX	XX	Mus musculus.			
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XX	XX	Key			
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XX	XX	mat_peptide	58..461		
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XX	XX	26-JUN-1997.			
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 361 GAGGGTGCTCTGGACTACTGGGCTCAAGGAACCTCAGTCACCGTCTCTCCCTCAGCCAAAGG 420
 QY 421 ACACCCCAACCGTCTATCCACTGTCCTCGTGGAGCTTGGG 461
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RESULT 3

AAL51274

ID AAL51274 standard; cDNA; 461 BP.

XX

AC AAL51274;

XX

DT 20-MAR-2003 (first entry)

XX

DE Mouse 11D10 antibody heavy chain variable region coding sequence.

XX

KW Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; HMFG;
 KW carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour;
 KW CEA-associated tumour; anti-idiotypic antibody.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT CDS

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FT /*tag- a

FT /partial

FT /product= "Mouse 11D10 anti-idiotypic antibody heavy chain

FT variable region"

FT /note= "No stop codon is given"

FT sig_peptide

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FT /*tag- b

FT mat_peptide

FT 58..459

FT /*tag- c

FT

XX

PN WO200292012-A2.

XX

PD 21-NOV-2002.

XX

PF 17-MAY-2002; 2002WO-US15840.

XX

PR 17-MAY-2001; 2001US-0861294.

XX

PA (KENT) UNIV KENTUCKY RES FOUND.

XX

PI Chatterjee M, Foon KA;

XX

XX WPI; 2003-129216/12.

DR

DR P-PSDB; AAO16293.

XX

XX Use of anti-idiotypic antibodies for human milk fat globules (HMFG) - or

PT carcinoembryonic antigen (CEA)-associated tumor for delaying the

PT development of, or treating a HMFG- or CEA-associated tumor (e.g.

PT breast tumor) in humans

XX

XX Disclosure; Fig 2; 98pp; English.

PS

XX

CC present DNA sequence encodes the heavy chain variable region of the mouse
 CC 11D10 anti-idiotypic antibody.

XX
 SQ Sequence 461 BP; 112 A; 121 C; 119 G; 109 T; 0 other;

Query Match 100.0%; Score 461; DB 25; Length 461;

Best Local Similarity 100.0%; Pred. No. 1e-117;

Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 ATGGAATCAGCTGGGTCTTTCTCTCTCTCTCAATACTACAGTGTCCACTGCCAG 60

QY 61 GCTTATCTACAGCAGTCTGGGGCTGAGTGTGGTCTGGGGCTCAGTGAAGATGTC 120

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

61 GCTTATCTACAGCAGTCTGGGGCTGAGTGTGGTCTGGGGCTCAGTGAAGATGTC 120

QY 121 TGCAGGCTTCTGGCTACACATTGACCAATTGACCAATTGACCAATTGACCAATTGACCA 180

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

121 TGCAGGCTTCTGGCTACACATTGACCAATTGACCAATTGACCAATTGACCAATTGACCA 180

QY 181 GGACAGGCTTGAATGGATTGGAAATATTTTCTGGAAATGGTATCTTACTACAAT 240

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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QY 241 CAGAAATTTAAGGCAAGGCTCATTTGACTGCAGACACATCTCTCCAGCAGCAGCCTACATG 300

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

241 CAGAAATTTAAGGCAAGGCTCATTTGACTGCAGACACATCTCTCCAGCAGCAGCCTACATG 300

QY 301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGGAAGTGG 360

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGGAAGTGG 360

QY 361 GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCCAGCAGCA 420

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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QY 421 ACACCCCAACCGTCTATCCACTGTCCTCGTGGAGCTTGGG 461

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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RESULT 4

AAL51274

ID AAL51274 standard; DNA; 409 BP.

XX

AC AAL51274;

XX

DT 08-MAY-2000 (first entry)

XX

DE Anti-human VEGF receptor Flt-1 antibody related sequence #3.

XX

KW Antibody; human; vascular endothelial growth factor; VEGF receptor;

KW Flt-1; neovascularisation; cell proliferation; metastasis; tumour;

KW rheumatoid arthritis; retinopathy; psoriasis; ss.

XX

OS Mus musculus.

XX

PN WO9960025-A1.

XX

PD 25-NOV-1999.

XX

PF 20-MAY-1999; 99WO-JP02661.

XX

PR 20-MAY-1998; 98JP-0139000.

XX

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX

XX Shitara K, Ito M, Kawada Y, Nakamura K;

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XX WPI; 2000-072431/06.

DR

DR P-PSDB; AAY77593.

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GenCore version 5.1.6
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6267.222 Million cell updates/sec

Title: US-08-836-455-3

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Maximum Match 100%

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SUMMARIES

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11	297.2	64.5	18986 13	US-10-109-853-2
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13	295.2	64.0	482 9	US-09-881-823-19
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ALIGNMENTS

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; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE OF INVENTION: TUMORS BEARING HMEF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861.294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(461)
; NAME/KEY: sig_peptide
; LOCATION: (1)...(57)
; NAME/KEY: mat_peptide
; LOCATION: (58)...(461)
US-09-861-294-3

Query Match 100.0%; Score 461; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 5.4e-142;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAATGCAGCTGGTCTTCTCTCTCTGTCATAACTACAGCTGTCCTCCAG 60

Db 1 ATGGAATGCAGCTGGTCTTCTCTCTCTGTCATAACTACAGCTGTCCTCCAG 60

61	QY	GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGGAGTCTGGGGCCTCAGTGAAGATGTCC	120
61	Db		120
121	QY	TGCAAGGCTTCTGGCTACACATTCACACAGTACAAATATGCATGGGTAAAGCAGACACCT	180
121	Db		180
181	QY	GGCAGGGCCTGGAATGGATTGGAATATTTTCTCGAAATGGTGATCTACTTACTACAAT	240
181	Db		240
241	QY	CAGAAGTTTAAGGGCAGGCCCTCAATTGACTGCAGACACATCTCTCCAGCAGCGCTTACATG	300
241	Db		300
301	QY	CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGGAACCTGG	360
301	Db		360
361	QY	GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAAGC	420
361	Db		420
421	QY	ACACCCCAACCGCTCTATCCACTGGTCCCTCGGAAGCTTTGGG	461
421	Db		461

RESULT 2
US-10-367-506-3
; Sequence 3, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMGF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506

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, FILE REFERENCE: 304142000620
, CURRENT APPLICATION NUMBER: US/10/367,506
, CURRENT FILING DATE: 2003-02-13
, PRIOR APPLICATION NUMBER: US/09/861,294
, PRIOR FILING DATE: 2001-05-17
, PRIOR APPLICATION NUMBER: 60/049,540
, PRIOR FILING DATE: 1997-06-13
, PRIOR APPLICATION NUMBER: 09/096,244
, PRIOR FILING DATE: 1998-06-11
, NUMBER OF SEQ ID NOS: 38
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 3
, LENGTH: 461

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;
; TYPE: DNA
; ORGANISM: Mus musculus
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(461)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(57)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (58)...(461)
US-10-367-506-3

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Query Match	100.0%	Score 461;	DB 12;	Length 461;
Best Local Similarity	100.0%;	Pred. NO. 5.4e-142;		
Matches 461;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	ATGGAATGCAGCTGGGGCTTTCTCTCTCTCTGTGTCATATACTACAGGTGTCCATCCCGAG	60
Db	1	ATGGAATGCAGCTGGGGCTTTCTCTCTCTGTGTCATATACTACAGGTGTCCATCCCGAG	60
Qy	61	GCATTATCTACAGCAGTCTGGGGGCTTGAGCTGTGTGAGGCTCTGGGGGCTCAGTGAAGATGTCC	120

Db	61	GCATTATCTAGCAGAGCTCTGGGGCTGAGCTGGTGGAGTCTGGGGCTCAGTGAAGATGCC	120
Qy	121	TGCAAGGCTTCTTGCTACACATTGACCAGTTACAATATGCAATGGGTAAAGCAGACACCT	180
Db	121	TGCAAGGCTTCTTGCTACACATTGACCAGTTACAATATGCAATGGGTAAAGCAGACACCT	180
Qy	181	GGCAGGGCCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATCTACTTACACAT	240
Db	181	GGCAGGGCCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATCTACTTACACAT	240
Qy	241	CAGAAGTTTAAAGGCAAGGCCCTCAATTGACTGCAGACACATCCTCCAGCAGACGCTTACATG	300
Db	241	CAGAAGTTTAAAGGCAAGGCCCTCAATTGACTGCAGACACATCCTCCAGCAGACGCTTACATG	300
Qy	301	CAGATCAGCAGCCTGACATCTGAAGACTCTGGGTCTATTCTGTGCAAGAGGGGAACATGG	360
Db	301	CAGATCAGCAGCCTGACATCTGAAGACTCTGGGTCTATTCTGTGCAAGAGGGGAACATGG	360
Qy	361	GAGGGTCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACG	420
Db	361	GAGGGTCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACG	420
Qy	421	ACACCCCAACCCGCTCTATCCACTGGTCCCTGGAAGCTTGGG	461
Db	421	ACACCCCAACCCGCTCTATCCACTGGTCCCTGGAAGCTTGGG	461

RESULT 3
US-10-160-232-7
; Sequence 7, Application US/10160232
; Publication NO. US20030088075A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASAHUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/10/160,232

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CURRENT FILING DATE: 2002-08-04
PRIORITY APPLICATION NUMBER: US/09/453,718
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 09/315,051
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/119,014
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: PCT/J997/04259
PRIOR FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7

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; LENGTH: 409
; TYPE: DNA
; ORGANISM: A
; FEATURE:
; OTHER INFO:
; FEATURE:
; NAME/KEY: C
; LOCATION: (
; FEATURE:
; NAME/KEY: s
; LOCATION: (
; FEATURE:
; NAME/KEY: m
; LOCATION: (
US-10-160-232-7

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Query Match	71.0%	Score	327.2;	DB 14;	Length	409;			
Best Local Similarity	88.8%	Pred. NO.	8.6e-98;						
Matches	366;	Conservative	0;	Mismatches	43;	Indels	3;	Gaps	1;

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;
; FEATURE:
;
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

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RESULT 11
US-10-109-853-2
; Sequence 2, Application US/10109853
; Publication No. US20020192820A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; BARNETT, Richard Spence
; MCLACHLAN, Karen Retta
; TITLE OF INVENTION: SPECIFIC METHOD FOR INTEGRATING GENES AT
; SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
; RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,853
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,715
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/819,866

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RESULT 12
US/10-216-484-8
; Sequence 8, Application US/10216484
; Publication NO. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, NO. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126C1P/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US/09/583
; PRIOR FILING DATE: 1998-04-01

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FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,520
FILING DATE: 03-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 911:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 911:
US-10-040-739-911

Query Match 63.3%; Score 292; DB 13; Length 478;
Best Local Similarity 82.2%; Pred. No. 4e-86;
Matches 350; Conservative 0; Mismatches 70; Indels 6; Gaps 1;
QY 1 ATGGAATGAGCTGGGCTCTTCTTCCTCCTGTCATTAACATACAGGTGTCACCTCCAG 60
DB 47 ATGGATGAGCTATATCATCTCTTTTGGTAGCAACAGCTACAGGTGTCACCTCCAG 106
QY 61 GCTTATCTACAGCTCTGGGCTGAGCTGGTGGGCTCTGAGGTGTCAGTGAAGATGTC 120
DB 107 GTCCAACTGCAGCGCTGGGCTGAGCTGGTGGTAAAGCTGGGCTCTCAGTGAAGTGTCC 166
QY 121 TGCAAGGCTCTGCTACACATTTGACAGTATGCAATATGCAATATGCAATGCTGGGCTAAAGCAGACACCT 180
DB 167 TGCAAGGCTCTGCTACATTTTACCAGCTACTGATGCTGCTGGTGAAGCAGAGGCT 226
QY 181 GGACAGGCTGGATGATGGAATATTTTCTGGAATGGAATGGAATGGAATGGAATGGAAT 240
DB 227 GGCAAGGCTTTGAGTGGATGGAATGATTCCTTAATAGTGGTAGTACTAACTACAAAT 286
QY 241 CAGAAAGTTTAAAGGCAAGGCTTATTGCTGAGCAGACATCTCCAGCAGACGCTACATG 300
DB 287 GGAAGTTCAAGCAGAGCGCCACACTGACTGTAGACAATCTCCAGCAGACGCTACATG 346
QY 301 CAGATCAGAGCTGACATCTGAGACTCTGGGCTCTATTTCTGTGCAAGAGGGA----- 355
DB 347 CAACCTCAGAGCTGACATCTGAGGCTCTGGGCTCTATTTCTGTGCAAGGAGGCTCA 406
QY 356 -ACTGGGAGGCTGCTGGACTGAGGCTCAAGGAACCTCAGTCAAGGCTCTCCTCAGCC 414
DB 407 GGCTACGACTATGCTATGACTTACTGGGCTCAAGGAACCTCAGTCAAGGCTCTCCTCAGCC 466
QY 415 AAAACG 420
DB 467 AAAACG 472

RESULT 15

US-09-903-327A-5
Sequence 5, Application US/09903327A
Patent No. US20020164333A1
GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
APPLICANT: Li, Erquan
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: GENE DELIVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1314
TYPE: DNA
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: (0)....(1314)
OTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein
OTHER INFORMATION: bifunctional antibody
US-09-903-327A-5

Query Match 63.2%; Score 291.4; DB 10; Length 1314;
Best Local Similarity 79.9%; Pred. No. 9.6e-86;
Matches 362; Conservative 0; Mismatches 76; Indels 15; Gaps 1;
QY 1 ATGGAATGAGCTGGGCTCTTCTTCCTCCTGTCATTAACATACAGGTGTCACCTCCAG 60
DB 1 ATGGATGAGCTGGATCTTCTTCCTCCTGTCAGAACTGCAAGCGCTCCACTCTGAG 60
QY 61 GCTTATCTACAGCTCTGGGCTGAGCTGGTGGGCTCTGAGGTGTCAGTGAAGATGTC 120
DB 61 GTCCAGCTTTCAGCAGTCAGGACCTGAGCTGGTGAACCTGGGCTCTCAGTGAAGATGTC 120
QY 121 TGCAAGGCTCTGCTACACATTTGACAGTATGCAATATGCAATATGCAATGCTGGGCTAAAGCAGACACCT 180
DB 121 TGCAAGGCTCTGCTACACATTTGACAGTATGCAATATGCAATGCTGGGCTAAAGCAGACACCT 180
QY 181 GGACAGGCTGGATGGAATGGAATATTTTCTGGAATGGAATGGAATGGAATGGAAT 240
DB 181 GGAAGAGGCTTTGAGTGGATGGAATATTTTCTTACAAAGGCTGGTACTGGCTACAAC 240
QY 241 CAGAAAGTTTAAAGGCAAGGCTCTTACTGCTGAGCAGACATCTCCAGCAGCAGCTACATG 300
DB 241 CAGAAAGTTTCAAGCAGCAAGGCTGATGCAACAGCAGTCTCTCCAAACAGCAGCTACATG 300
QY 301 CAGATCAGAGCTGACATCTGAGACTCTGAGGCTCTATTTCTGTGCAAGAGGGAAGCTGG 360
DB 301 GAGCTCCGAGGCTGACATCTGATGCTCTGAGCTCTATTTACTGTGCAAGAGGGA----- 355
QY 361 GAGGCTGCTCTGAGCTACTGGGCTCAAGGAACCTCAGTCAAGGCTCTCCTCAGCAGCAACG 420
DB 356 -----TTGCTTACTGGGCTCAAGGAGCTCTGGTCACTGCTCTCTGAGCAGCAACG 405
QY 421 ACACCCCAACCGCTCTATCCACTGGTCCCTGGA 453
DB 406 ACACCCCAATCTGCTATCCACTGGGCTCCCTGGA 438

Search completed: August 30, 2003, 19:50:22
Job time: 170.759 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2003, 16:08:05 ; Search time 1603.21 Seconds
(without alignments)
6988.707 Million cell updates/sec

Title: us-08-836-455-3

Perfect score: 461

Sequence: 1 ATGGATGACGTGGTCTT.....CTGGTCCCTGGAAGCTGGG 461

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	337.8	73.3	739	10	BE284158 601099428
2	326.8	70.9	892	10	BG518664 602578528
3	326.6	70.8	637	14	BY724721 BY724721
4	320.8	69.6	941	10	BF138189 601781314

5	320.2	69.5	667	14	BY724790
6	319.6	69.3	1576	11	AK007918 Mus muscu
7	316.6	68.7	767	10	BF165456 601777347
8	316.4	68.6	794	12	BI150371 602915205
9	315.6	68.5	745	12	BG871607 602790090
10	311.2	67.5	546	14	CA576594
11	310.6	67.4	771	10	BF140551 601787584
12	309.6	67.2	529	14	CA576389 6044412
13	308.6	66.9	616	10	BF136295 601781413
14	308.6	66.9	748	10	BF136397 601783927
15	306.6	66.5	700	10	BF540088 602050325
16	305	66.2	644	10	BE281961 601099538
17	305	66.2	793	10	BF136093
18	303	66.2	891	10	BF138460 601782916
19	303	65.7	955	13	BQ947728 AGENCOURT
20	302.6	65.6	469	14	CA574907 K0622H02
21	301.6	65.4	690	12	BG968682 602836513
22	301.6	65.4	724	12	BG962137 602826902
23	299.8	65.0	604	10	BF140035 601791175
24	298.4	64.7	538	14	CA578968 K0731A04
25	297.4	64.5	540	14	CA579750 K0741H07
26	296.8	64.4	724	10	BF168514 601775412
27	296.8	64.4	847	10	BF165486 601777393
28	296.2	64.3	507	10	BF015548 uy23a08.y
29	295.8	64.2	519	14	CA580087 K0746G01
30	295.2	64.0	769	10	BF168856 601775314
31	293.6	63.7	819	12	BG966397 602832896
32	293	63.6	477	14	CA570382 K0505G11
33	292.8	63.5	640	13	BQ109114 imageqc_6
34	292.6	63.5	485	14	CA578116 K0718G11
35	292.4	63.4	475	14	CA578534 K0725B11
36	292.2	63.4	911	10	BE286958 601092470
37	292	63.3	429	14	CA579143 K0733D01
38	292	63.3	1003	14	CB236612 AGENCOURT
39	291.4	63.2	529	14	CA577954 K0716F08
40	290.8	63.1	896	13	BUS24012 AGENCOURT
41	290.6	63.0	508	14	CA577080 K0704C12
42	290.6	63.0	538	14	CA580316 K0749H01
43	290.4	63.0	598	12	BI104341 602889919
44	290	62.9	1012	10	BF579009 602096127
45	289.6	62.8	672	10	BF580337 602097080

ALIGNMENTS

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LOCUS 601099428F1 NCI_CGAP_Lu29 Mus musculus cdna clone IMAGE:3491766 5',
DEFINITION mRNA sequence.
ACCESSION BE284158
VERSION BE284158.1 GI:9160900
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 739)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8536 row: h column: 07
High quality sequence stop: 535.

[illegible]


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KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM

REFERENCE
1 (bases 1 to 941)
TITLE      NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL
COMMENT    Unpublished
           Contact: Robert Strausberg, Ph.D.
           Email: cga@phs-femail.nih.gov
           Tissue Procurement: Gilbert Smith, Ph.D.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           National Institutes of Health, Mammalian Gene Collection (MGC)
           Cloned through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LAM9245 row: k column: 04
           High quality sequence stop: 637.
           Location/Qualifiers
             1. 941
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               /mol_type="mRNA"
               /strain="CZECH II"
               /db_xref="taxon:10090"
               /clone="IMAGE:4009467"
               /tissue_type="tumor, metastatic to mammary"
               /lab_host="DH10B"
               /clone_lib="NCI CGAP Lu30"
               /notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
               Site_2: SalI; transgenic model WNT-1, expression driven by
               MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
               dT. Library constructed by Life Technologies.
               Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT      232 a 266 c 248 g 195 t
ORIGIN

Query Match      69.6%; Score 320.8; DB 10; Length 941;
Best Local Similarity 84.2%; Pred. No. 1.4e-80;
Matches 377; Conservative 0; Mismatches 62; Indels 9; Gaps 1;

Qy 13 TGGTCTTTCTCTTCCTCCCTGTCATTAATACAGTGTCTCCAGCTTATCTACAG 72
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Db 20 TGTATCTTTCTCTTCCTCCCTGTCATTAATACAGTGTCTCCAGCTTATCTACAG 79

Qy 73 CAGTCTGGGCTGAGCTGTGAGCTGTGGGCTCAGTGAAGATGCTCTCAAGGCTTCT 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 CAGTCTGGGCTGAGCTGTGAGCTGTGGGCTCAGTGAAGATGCTCTCAAGGCTTCT 139

Qy 133 GCCTACACATGACAGTTCATATGCTGGTGAAGCAGACACCTGGACAGGCGCTG 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 140 GGCTACGATTCAGTACTCTCTGGATGAAGTGGTGAAGCAGGCGCTGGAAAGGCTT 199

Qy 193 GAATGGATTGGAATATTTTCTCGAAATGGTGATCTTACTACATCAGAGTTTAAAG 252
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 200 GAGTGGATTGGACGATTATCTTGGAGATGGAGATGACTACATGGAATTCAG 259

Qy 253 GGCAAGGCCCTATTGACTGCAGACACATCTCCAGCAGCAGCTACATCAGCAGC 312
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 260 GGCAAGGCCACACTGACTGCAGACACATCTCCAGCAGCAGCTACATCAGCAGC 319

Qy 313 CTGACATCTGAAGACTCTGGGCTCTATTTCTGTGCAAGAGGAGTGGGAGG----- 365
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 320 CTGACATCTGAGGACTCTGGGCTCTACTTCTGTCAAGAGTAACTACTATGCTTCTAC 379

Qy 366 --TGCCTGACTACTGGGCTCAAGGAACTCAGTCAACCTCTCCTCAGCAACACACA 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 380 AATGCTATGACTACTGGGCTCAAGGAACTCAGTCAACCTCTCCTCAGCAACACACA 439

Qy 424 CCCCACCCCTCTATCCACTGGTCCCTG 451
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 440 GCCCATCGTCTATCCACTGGGCCCCG 467

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RESULT 5
BY724790
LOCUS
DEFINITION
MUSCULUS CDNA clone A530085L22 5', mRNA sequence.
BY724790
BY724790.1 GI:27137917
EST.
Mus musculus (house mouse)

REFERENCE
1 (bases 1 to 667)
AUTHORS

CONTACT: Robert Strausberg, Ph.D.
Email: cga@phs-femail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
National Institutes of Health, Mammalian Gene Collection (MGC)
Cloned through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9245 row: k column: 04
High quality sequence stop: 637.
Location/Qualifiers
1. 941
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Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT
232 a 266 c 248 g 195 t

ORIGIN

Query Match
Best Local Similarity
Matches 377; Conservative 0; Mismatches 62; Indels 9; Gaps 1;

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Db 20 TGTATCTTTCTCTTCCTCCCTGTCATTAATACAGTGTCTCCAGCTTATCTACAG 79

Qy 73 CAGTCTGGGCTGAGCTGTGAGCTGTGGGCTCAGTGAAGATGCTCTCAAGGCTTCT 132
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Db 80 CAGTCTGGGCTGAGCTGTGAGCTGTGGGCTCAGTGAAGATGCTCTCAAGGCTTCT 139

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Db 440 GCCCATCGTCTATCCACTGGGCCCCG 467

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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/

ADACHI, J., AIZAWA, K., AKIMURA, T., ARAKAWA, T., CARNINCI, P., FUKUDA
S., HASHIZUME, W., HAYASHIDA, K., HIROZANE, T., HORI, F., IMOTANI, K.,
ISHII, Y., ITOH, M., KAGAWA, I., KAWAI, J., KOJIMA, Y., KONDO, S., KONNO
H., KOYA, S., MIYAZAKI, A., MURATA, M., NAKAMURA, K., NOMURA, K.,
NUMAZAKI, R., OHNO, M., OHSETO, N., SAITO, R., SAKAZUME, N., SANO, H.,
SASAKI, D., SATO, K., SHIBATA, K., SHIRAKI, T., TAGAMI, M., TAKEDA, Y.,
WAKI, K., WAHAKI, A., MURAMATSU, M. and HAYASHIZAKI, Y. Direct
Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system -384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a

BY724790 667 bp mRNA linear EST 17-DEC-2002
BY724790 RIKEN full-length enriched, adult male aorta and vein Mus
musculus cDNA clone A530085L22 5', mRNA sequence.

BY724790
BY724790.1 GI:27137917
EST.
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 667)
AUTHORS

CONTACT: Robert Strausberg, Ph.D.
Email: cga@phs-femail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
National Institutes of Health, Mammalian Gene Collection (MGC)
Cloned through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9245 row: k column: 04
High quality sequence stop: 637.
Location/Qualifiers
1. 941
/organism="Mus musculus"
/mol_type="mRNA"
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Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT
232 a 266 c 248 g 195 t

ORIGIN

Query Match
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Matches 377; Conservative 0; Mismatches 62; Indels 9; Gaps 1;

Qy 13 TGGTCTTTCTCTTCCTCCCTGTCATTAATACAGTGTCTCCAGCTTATCTACAG 72
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 20 TGTATCTTTCTCTTCCTCCCTGTCATTAATACAGTGTCTCCAGCTTATCTACAG 79

Qy 73 CAGTCTGGGCTGAGCTGTGAGCTGTGGGCTCAGTGAAGATGCTCTCAAGGCTTCT 132
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Qy 313 CTGACATCTGAAGACTCTGGGCTCTATTTCTGTGCAAGAGGAGTGGGAGG----- 365
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Qy 424 CCCCACCCCTCTATCCACTGGTCCCTG 451
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Db 440 GCCCATCGTCTATCCACTGGGCCCCG 467

CONTACT: Yoshihide Hayashizaki
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URL: http://genome.gsc.riken.go.jp/

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prepare full-length cDNA libraries for rapid discovery of new
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a


```
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Qy 361 GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACG 420
Db 391 CGATGGTACTTCGATGTCTGGGGCGCAGGACCCACGTCACCGTCTCCTCAGAGAGTCAG 450
Qy 421 ACACCCCCACCGCTCTATCCACTGGTCCC 449
Db 451 TCCTTCCCAAATGTCTTTCCCGCTCGTCTC 479
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Search completed: August 30, 2003, 19:44:51
Job time : 1608.21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2003, 22:04:11 ; Search time 26.1846 Seconds
(without alignments)
927.461 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 153
Sequence: 1 MECSWVFLLSITGVHSQ.....TVSSAKTPPPVPIVPGSL 153

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

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Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153	100.0	153	18	AAW27120 Murine monoclonal
2	153	100.0	153	20	AAW87594 Antibody 11D10 hea
3	153	100.0	153	24	AAO16293 Mouse 11D10 antibo
4	31	20.3	152	20	AAI49210 MAb 1A7 heavy chai
5	31	20.3	152	20	AAI28469 Heavy chain variab
6	31	20.3	152	20	AAI21546 Monoclonal antibod
7	27	17.6	122	20	AAI21816 Anti-STX1 heavy ch
8	27	17.6	122	17	AAW03200 Anti-idiotype mono
9	21	13.7	279	23	AAW80224 Gamma-glutamyl tra

10	13.1	20	412	22	AAW30694	A fusion of anti-C
11	13.1	20	423	22	AAW30695	A fusion of anti-C
12	20	13.1	633	21	AAV84965	Amino acid sequenc
13	19	12.4	124	15	AAW60565	Anti-carcinomaembryo
14	19	12.4	124	15	AAW60566	Anti-carcinomaembryo
15	19	12.4	124	20	AAI39528	Murine COL1 VH cha
16	19	12.4	124	23	ABB83941	Mouse monoclonal a
17	19	12.4	124	23	AAU76632	Murine Col-1(CEA a
18	19	12.4	124	24	ABG75594	Mouse COL-1 variab
19	19	12.4	130	14	AAW33308	Mae13 heavy chain.
20	19	12.4	130	21	AAV70791	Murine anti-PAB-42
21	19	12.4	130	21	AAV85196	Heavy chain amino
22	19	12.4	133	16	AAW74960	Anti-idiotype anti
23	19	12.4	134	14	AAW33345	Sequence of the va
24	19	12.4	134	17	AAW09273	Monoclonal antibod
25	19	12.4	135	16	AAW74961	Anti-idiotype anti
26	19	12.4	140	8	AAW70627	Sequence encoded b
27	19	12.4	140	10	AAW94780	2 H7 VH gene. Syn
28	19	12.4	140	18	AAW10588	2H7 antibody heavy
29	19	12.4	140	18	AAW16343	2H7 heavy chain va
30	19	12.4	140	18	AAW10242	Heavy chain variab
31	19	12.4	140	19	AAW41070	Mouse 2H7 antibody
32	19	12.4	140	19	AAW47513	Mouse 2H7 antibody
33	19	12.4	140	19	AAW47520	Mouse 2H7 antibody
34	19	12.4	140	20	AAW89540	Mouse antibody 2H7
35	19	12.4	140	22	AAW98092	2H7 heavy chain va
36	19	12.4	140	22	AAW74791	Anti-CA125 bifunct
37	19	12.4	143	21	AAW43867	Heavy chain (VH) g
38	19	12.4	149	20	AAV14355	Anti-HCV Ser/Thr p
39	19	12.4	158	18	AAW19577	Mouse anti-idiotyp
40	19	12.4	158	18	AAW19579	Mouse anti-idiotyp
41	19	12.4	159	18	AAW19575	Mouse anti-idiotyp
42	19	12.4	162	16	AAW01752	MH1 monoclonal ant
43	19	12.4	170	16	AAW77306	Mouse monoclonal a
44	19	12.4	209	24	ABP96771	TSH receptor antib
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ALIGNMENTS

RESULT 1
AAW27120
ID AAW27120 standard; Protein; 153 AA.
XX AC AAW27120;
XX DT 25-MAR-2003 (updated)
DT 04-JAN-1998 (first entry)
XX Murine monoclonal anti-idiotype antibody 11D10 VH region.
DE Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
KW human mlk fat globule; HMF6; tumour; breast cancer; vaccine.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
FT Peptide /label= Sig_peptide
FT Protein /label= Mat_protein
FT Region /label= FR1
FT /note= "framework region 1"
FT Region /label= CDRL
FT /note= "complementarity determining region 1"
FT Region /label= FR2
FT /note= "framework region 2"
FT Region /label= CDR2

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FT Region /note= "complementarity determining region 2"
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FT /note= "complementarity determining region 3"
FT 127..137
FT /label= FR1
FT /note= "framework region 4"
FT 138..153
FT /label= Constant
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XX W09722699-A2.
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XX 26-JUN-1997.
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XX 19-DEC-1996; 96WO-US20757.
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XX 20-DEC-1995; 95US-0575762.
XX 26-JAN-1996; 96US-0591965.
XX 13-DEC-1996; 96US-0766350.
XX
XX (KENT ) UNIV KENTUCKY.
XX
XX Chatterjee M, Chatterjee SK, Foon KA;
XX WPI; 1997-341690/31.
XX N-PSDB; AAT85150.
XX
XX Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
XX against human milk fat globule disease associated tumours,
XX especially breast cancer
XX
XX Claim 10; Page 94-95; 130pp; English.
XX
XX This polypeptide sequence comprises the heavy chain variable region
XX (VH) of monoclonal anti-idiotypic antibody 11D10 produced by
XX hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
XX naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotypic
XX response. It elicits an immune response against a specific epitope
XX of a high mol.wt. mucin of human milk fat globule (HMFG). It
XX induces an immunological response to HMFG in mice, rabbits, monkeys
XX and patients with advanced HMFG-associated tumours. Pharmaceutical
XX compositions and vaccines comprising 11D10, 11D10 polypeptides
XX and/or 11D10 polynucleotides (see also AAT85149-50) are claimed.
XX Also claimed are diagnostic kits and methods of using 11D10, 11D10
XX polypeptides and/or 11D10 polynucleotides, including methods of
XX treating HMFG-associated tumours. 11D10 is also used in a claimed
XX method of palliating HMFG-associated disease and in claimed kits to
XX detect or quantify anti-HMFG antibody.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 153 AA;
XX
XX Query Match 100.0%; Score 153; DB 18; Length 153;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-130;
XX Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MEGSWFLFLSLTTGVHSGAYLQSGAELVRSGASVKMSKASGYTLTSTNNHWVKQTP 60
Db 1 MEGSWFLFLSLTTGVHSGAYLQSGAELVRSGASVKMSKASGYTLTSTNNHWVKQTP 60
QY 61 GQGLEWIGNIFPGNGDTYYNQRKFKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNW 120
Db 61 GQGLEWIGNIFPGNGDTYYNQRKFKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNW 120
QY 121 EGALDWGQGTSTVSSAKTTPPPVPLVPGSL 153
Db 121 EGALDWGQGTSTVSSAKTTPPPVPLVPGSL 153

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RESULT 2

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AAW87594
ID AAW87594 standard; Protein; 153 AA.
XX
XX AAW87594;
XX
XX 16-MAR-1999 (first entry)
XX
XX Antibody 11D10 heavy chain variable region.
XX
XX Murine; mouse; antibody; heavy chain; variable region; anti-idiotypic;
XX human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX /note= "signal peptide"
XX Protein 20..153
XX /note= "mature protein"
XX Region 20..49
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XX Domain 50..54
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XX Region 55..68
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XX Domain 69..85
XX /label= CDR2
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XX /note= "complementarity determining region 3"
XX Region 127..137
XX /label= framework_4
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XX W09856419-A1.
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XX 17-DEC-1998.
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XX 12-JUN-1998; 98WO-US12250.
XX
XX 11-JUN-1998; 98US-0096244.
XX 13-JUN-1997; 97US-0049540.
XX
XX (KENT ) UNIV KENTUCKY RES FOUND.
XX
XX Chatterjee M, Foon KA;
XX WPI; 1999-060029/05.
XX N-PSDB; AAV83773.
XX
XX Delaying development of, or treating, HMFG-associated tumours -
XX using anti-idiotypic antibody 11D10 raised against antibodies to
XX human milk fat globule protein
XX
XX Disclosure; Fig 2; 54pp; English.
XX
XX This sequence represents the heavy chain variable region of the murine
XX antibody 11D10. This anti-idiotypic antibody is used to delay the
XX development of, or treat, a human milk fat globule (HMFG) associated
XX tumour in an individual having low tumour burden. The antibody 11D10
XX is used to prevent the recurrence of HMFG-associated tumours e.g.
XX ovarian, non-small cell lung and pancreatic carcinoma, especially for
XX treating breast tumours.
XX
XX Sequence 153 AA;
XX
XX Query Match 100.0%; Score 153; DB 20; Length 153;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-130;
XX Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MECSWVFLFLSITTCVHSQAYLQSGAELVRSGASVKMSCKASGYTLTSYNNHWVKQTP 60
 Db 1 MECSWVFLFLSITTCVHSQAYLQSGAELVRSGASVKMSCKASGYTLTSYNNHWVKQTP 60
 QY 61 GQGLEWIGNIFPGNGDTYYNQKFKGASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
 Db 61 GQGLEWIGNIFPGNGDTYYNQKFKGASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
 QY 121 EGALDYWGQGTSTVTVSSAKTTPPPVPLVPGSL 153
 Db 121 EGALDYWGQGTSTVTVSSAKTTPPPVPLVPGSL 153

RESULT 3
 AAO16293
 ID AAO16293 standard; Protein; 153 AA.
 XX
 AC AAO16293;
 DT 20-MAR-2003 (first entry)
 XX
 DE Mouse 11D10 antibody heavy chain variable region.
 XX
 KW Mouse; murine; vaccine; tumour; human milk fat globules; HMFG;
 KW carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour;
 KW CEA-associated tumour; anti-idiotypic antibody.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal_peptide
 FT Protein 20..153
 FT /note= "Mature murine 11D10 antibody heavy chain variable
 region"
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 PN WO200292012-A2.
 XX
 PD 21-NOV-2002.
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 PF 17-MAY-2002; 2002WO-US15840.
 XX
 PR 17-MAY-2001; 2001US-0861294.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 PI Chatterjee M, Foon KA;
 DR WPI; 2003-129216/12.
 DR N-PSDB; AAL51274.
 XX
 PT Use of anti-idiotypic antibodies for human milk fat globules (HMFG) - or
 PT carcinoembryonic antigen (CEA)-associated tumor for delaying the
 PT development of, or treating a HMFG- or CEA-associated tumor (e.g.
 PT breast tumor) in humans
 XX
 PS Claim 2; Fig 2; 98pp; English.
 CC The invention comprises a method for delaying the development of, or
 CC treating a tumour that is associated with human milk fat globules (HMFG)
 CC or carcinoembryonic antigen (CEA). The method of the invention involves
 CC administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an
 CC anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for
 CC delaying the development, of or treating HMFG/CEA-associated tumours. The
 CC present amino acid sequence represents the heavy chain variable region of
 CC the mouse 11D10 anti-idiotypic antibody.
 XX
 SQ Sequence 153 AA;
 Query Match 100.0%; Score 153; DB 24; Length 153;
 Best Local Similarity 100.0%; Pred. No. 1.8e-130;
 Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECSWVFLFLSITTCVHSQAYLQSGAELVRSGASVKMSCKASGYTLTSYNNHWVKQTP 60
 Db 1 MECSWVFLFLSITTCVHSQAYLQSGAELVRSGASVKMSCKASGYTLTSYNNHWVKQTP 60
 QY 61 GQGLEWIGNIFPGNGDTYYNQKFKGASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
 Db 61 GQGLEWIGNIFPGNGDTYYNQKFKGASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
 QY 121 EGALDYWGQGTSTVTVSSAKTTPPPVPLVPGSL 153
 Db 121 EGALDYWGQGTSTVTVSSAKTTPPPVPLVPGSL 153

RESULT 4
 AAY49210
 ID AAY49210 standard; Protein; 152 AA.
 XX
 AC AAY49210;
 DT 07-FEB-2000 (first entry)
 XX
 DE MAb 1A7 heavy chain variable region.
 XX
 KW Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma;
 KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
 KW tumor-associated antigen.
 OS Synthetic.
 OS Mus sp.
 XX
 PN US5977316-A.
 XX
 PD 02-NOV-1999.
 XX
 PE 16-JAN-1996; 96US-0591196.
 XX
 PR 17-JAN-1995; 95US-0372676.
 XX
 PA (KENT) UNIV KENTUCKY.
 XX
 PI Foon KA, Chatterjee SK, Chatterjee M;
 XX
 XX WPI; 1999-619711/53.
 DR N-PSDB; AAZ31366.
 DR
 XX
 PT Monoclonal antibody 1A7 which elicits an anti-GD2 immunological
 PT response, useful for the development of products for the detection and
 PT treatment of cancers
 XX
 PS Claim 1; Fig 2; 74pp; English.
 CC The invention provides a monoclonal antibody (MAb) designated 1A7, which
 CC elicits an anti-GD2 (tumor-associated antigen) immunological response in
 CC humans. MAb 1A7 has defined light and heavy chain variable region
 CC sequences. The MAb 1A7 and polypeptides can be used for eliciting an
 CC anti-GD2 immune response. The polypeptides can also be used for detecting
 CC or purifying anti-GD2 antibody. The products can be used for treating GD2
 CC -associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue
 CC carcinoma, and small cell carcinoma. They can be used for palliating the
 CC disease or for reducing the risk of recurrence. The present sequence
 CC represents the heavy chain variable region of MAb 1A7.
 XX
 SQ Sequence 152 AA;
 Query Match 20.3%; Score 31; DB 20; Length 152;
 Best Local Similarity 100.0%; Pred. No. 3.9e-20;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 ALDYWGQGTSTVTVSSAKTTPPPVPLVPGSL 153
 Db 122 ALDYWGQGTSTVTVSSAKTTPPPVPLVPGSL 152

RESULT 5

AA28469
ID AAY28469 standard; Protein; 152 AA.
XX AC AAY28469;
XX DT 06-OCT-1999 (first entry)
XX DE Heavy chain variable region of MAb 1A7.
XX KW Heavy chain variable region; antibody 1A7; T cell response; carcinoma;
XX KW ganglioside GD2; CDR; complementarity determining region; melanoma.
XX OS Mus musculus.

Key Location/Qualifiers
FT Peptide 1..19
FT /label= "Signal peptide"
FT Protein 20..152
FT /label= "Mature peptide"
FT Region 20..49
FT /label= "Framework 1"
FT Domain 50..54
FT /label= "CDR 1"
FT /note= "Complementarity determining region 1"
FT Region 55..65
FT /label= "Framework 2"
FT Domain 69..84
FT /label= "CDR 2"
FT /note= "Complementarity determining region 2"
FT Region 85..116
FT /label= "Framework 3"
FT Domain 117..125
FT /label= "CDR 3"
FT /note= "Complementarity determining region 3"
FT Region 126..136
FT /label= "Framework 4"
FT Region 137..152
FT /label= "Constant region"

US5935821-A.

10-AUG-1999.

21-NOV-1996; 96US-0752844.

21-NOV-1996; 96US-0752844.

17-JAN-1995; 95US-0372676.

16-JAN-1996; 96US-0591196.

(KENT) UNIV KENTUCKY.

Chatterjee M, Chatterjee SK, Foon KA;

WPI; 1999-457600/38.

N-PSDB; AAX89553.

Anti-GD2 immunological peptides useful for the treatment of tumours especially melanomas and small cell carcinomas

Claim 1; Fig 2; 84pp; English.

This polypeptide is the variable heavy chain region of monoclonal anti-idiotypic antibody 1A7. The polypeptide has three CDRs (complementarity determining regions) and four frame work regions. When administered to an individual the 1A7 antibody induces an immune response against ganglioside GD2. The light chain variable region of the 1A7 antibody (AAY28468) is also capable of eliciting an anti GD2 response in mammals. Both the heavy and light chain variable regions of the 1A7 antibody produce anti-GD2 T cell and antibody responses. The peptides and antibodies may be useful for the modulation of ganglioside GD2, and particularly for the treatment of GD2-associated tumours e.g. melanoma, neuroblastoma, glioma, soft tissue sarcoma, and small cell carcinoma

CC (including small cell lung cancer).

XX Sequence 152 AA;

Query Match 20.3%; Score 31; DB 20; Length 152;
Best Local Similarity 100.0%; Pred. No. 3.9e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 ALDYGQGTSTVTSSAKTTPPPVPLVPGSL 153

|||||

Db 122 ALDYGQGTSTVTSSAKTTPPPVPLVPGSL 152

|||||

RESULT 6

AA21546

ID AAY21546 standard; Protein; 152 AA.

XX AC AAY21546;

XX DT 03-AUG-1999 (first entry)

XX DE Monoclonal antibody 1A7 heavy chain variable region.

XX KW Psoriasis; immunological response; anti-idiotypic antibody; glutamate;

XX KW chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis;

XX KW monoclonal antibody; 1A7.

XX OS Unidentified.

XX PN WO9925380-A2.

XX PD 27-MAY-1999.

XX PF 17-NOV-1998; 98WO-US24607.

XX PR 16-NOV-1998; 98US-0192838.

XX PR 17-NOV-1997; 97US-0065774.

XX PA (KENT) UNIV KENTUCKY RES FOUND.

XX PI Chatterjee M, Foon KA;

XX DR WPI; 1999-347407/29.

XX DR N-PSDB; AAX60630.

XX PT Treatment of psoriasis

XX PS Disclosure; Fig 3; 48pp; English.

XX CC The invention provides a method of treating of psoriasis by administering an antigen which has similar immunogenic properties to an antigen expressed on cells of psoriatic tissue so that an immunological response is elicited in the individual. The antigen stimulates the generation of anti-idiotypic antibodies that neutralize the aberrant immune response causing the psoriasis. The method is used to treat psoriasis, especially chronic plaque, glutamate, pustular, plaque-type psoriasis or psoriatic arthritis. The compositions allow the individual's own immune system to act against psoriatic tissue. The present sequence represents the heavy chain variable region of monoclonal antibody 1A7.

XX Sequence 152 AA;

Query Match 20.3%; Score 31; DB 20; Length 152;
Best Local Similarity 100.0%; Pred. No. 3.9e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 ALDYGQGTSTVTSSAKTTPPPVPLVPGSL 153

|||||

Db 122 ALDYGQGTSTVTSSAKTTPPPVPLVPGSL 152

|||||

RESULT 7

AA21816

ID AAY21816 standard; Protein: 122 AA.
XX AC AAY21816;
XX DT 10-SEP-1999 (first entry)
XX DE Anti-STX1 heavy chain variable region.
XX KW Humanised; monoclonal antibody; MAb; Shiga toxin; Immunoglobulin;
XX KW Ig constant region; enterohemorrhagic Escherichia coli; EHEC; uremia;
XX KW edema; bloody diarrhoea; hemorrhagic colitis; hemolytic uremic syndrome;
XX KW thrombocytopenia; EHEC-mediated disease; anti-STX1.
XX OS Shigella dysenteriae.
XX FH Key Location/Qualifiers
XX FT Misc-difference 23 /note= "encoded by AAG"
XX FT Region 31..35 /note= "complementarity determining region (CDR) 1;
XX FT Region 50..66 /note= "specifically claimed for in claim 10"
XX FT Region 99..111 /note= "complementarity determining region (CDR) 2;
XX FT Region 99..111 /note= "specifically claimed for in claim 10"
XX FT Region 99..111 /note= "complementarity determining region (CDR) 3;
XX FT Region 99..111 /note= "specifically claimed for in claim 10"
XX PN WO932645-A1.
XX PD 01-JUL-1999.
XX PF 22-DEC-1998; 98WO-US27267.
XX PR 18-DEC-1998; 98US-0215163.
XX PR 23-DEC-1997; 97US-0068635.
XX PA (MELT/) MELTON-CELSA A.
XX PA (OBRI/) O'BRIEN A D.
XX PA (SCHM/) SCHMITT C K.
XX PA (STIN/) STINSON J L.
XX PA (WONG/) WONG H.
XX PI Melton-Celsa A, O'Brien AD, Schmitt CK, Stinson JL;
XX PI Wong H;
XX DR WPI: 1999-418935/35.
XX DR N-PSDB; AAX82028.
XX PT Humanized monoclonal antibodies against Shiga toxins, useful for
XX PT protection against enterohemorrhagic Escherichia coli or other Shiga
XX PT toxin producing bacteria
XX PS Claim 5; Fig 3; 75pp; English.
XX CC The invention relates to humanised monoclonal antibodies (MAb) against
XX CC Shiga toxins. The humanised MAb that binds to Shiga toxin comprises a
XX CC constant and a variable region, where: (a) the constant region contains
XX CC at least part of a human immunoglobulin (Ig) constant region; and (b) the
XX CC variable region contains at least part of a non-human Ig variable region.
XX CC Host cells transformed with vectors encoding a humanised MAb against
XX CC Shiga toxin type 2 is useful for treating a patient with an infection
XX CC caused by enterohemorrhagic Escherichia coli (EHEC) or other Shiga toxin
XX CC producing bacteria. The humanised MAb can also be used to reduce illness
XX CC caused by EHEC or other Shiga toxin producing bacteria. EHEC are
XX CC associated with food-borne outbreaks of bloody diarrhoea (hemorrhagic
XX CC colitis) and the hemolytic uremic syndrome. In particular, the humanised
XX CC MAb ameliorate edema, thrombocytopenia and uremia associated with EHEC-
XX CC mediated disease. The present sequence represents an anti-STX1 heavy
XX CC chain variable region.
XX SQ Sequence 122 AA;

Query Match 17.6%; Score 27; DB 20; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 89 LPADTSSSTAYMQISLTSDSAVYFC 115
DB 70 LTADTSSSTAYMQISLTSDSAVYFC 96
|||||
RESULT 8
AAW03200
ID AAW03200 standard; Protein: 152 AA.
XX AC AAW03200;
XX DT 25-MAR-2003 (updated)
XX DT 26-FEB-1997 (first entry)
XX DE Anti-idiotypic monoclonal antibody 1A7 variable heavy chain.
XX KW Murine; mouse; anti-idiotypic; monoclonal antibody; MAB; 1A7;
XX KW variable heavy chain; ganglioside 2; GD2; 14G2a; neuroblastoma;
XX KW glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;
XX KW malignant melanoma; soft tissue sarcoma; small cell carcinoma;
XX KW vaccine; treatment; palliate; detection; diagnosis;
XX KW recombinant production; purification; probe; primer; assay;
XX KW amplification; gene therapy.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT Region 20..49 /label= sig_peptide
XX FT Region 50..54 /note= "framework region 1"
XX FT Region 55..68 /note= "complementarity determining region 1"
XX FT Region 69..84 /note= "framework region 2"
XX FT Region 85..116 /note= "complementarity determining region 2"
XX FT Region 117..125 /note= "framework region 3"
XX FT Region 126..136 /note= "complementarity determining region 3"
XX FT Misc-difference 125 /note= "framework region 4"
XX FT /note= "corresponding codon TAC"
XX PN WO9622373-A2.
XX PD 25-JUL-1996.
XX PF 17-JAN-1996; 96WO-US00882.
XX PF 17-JAN-1996; 95US-0372676.
XX PR 16-JAN-1996; 96US-0591196.
XX PR 17-JAN-1995; 95US-0372676.
XX PR 16-JAN-1996; 96US-0591196.
XX PA (KENT) UNIV KENTUCKY.
XX PI Chatterjee M, Chatterjee SK, Foon KA;
XX WIPI: 1996-354530/35.
XX DR N-PSDB; AAT31333.
XX PT Monoclonal antibody 1A7 and related polynucleotide(s) and
XX PT polypeptide(s) - useful to treat or palliate a GD2-associated
XX PT disease, e.g. melanoma and glioma
XX PS Claim 9; Fig 2; 141pp; English.

XX The present sequence is that of the murine anti-idiotypic monoclonal
 CC antibody (MAB) 1A7 variable heavy chain. MAB 1A7 was raised against
 CC the anti-ganglioside 2 (GD2) MAB 14G2a, which binds an unique
 CC epitope of GD2. As the glycosphingolipid GD2 is expressed at high
 CC density by human neuroectodermal tumours, e.g. malignant melanoma,
 CC neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma
 CC of the lung, MAB 1A7, or its cDNA can be used in a vaccine to treat
 CC or palliate such diseases. They can also be used to reduce the
 CC risk of recurrence of a clinically detectable tumour, and detect an
 CC anti-GD2 Ab bound to a tumour cell.
 CC MAB 1A7 overcomes immune tolerance and induces an immune response
 CC against GD2, which comprises anti-GD2 Ab (humoral response) and
 CC GD2-specific cells (cellular response). It can be used to purify
 CC anti-1A7 (AB3), anti-GD2 (Ab1) or 14G2a (Ab1), detect anti-1A7 or
 CC anti-GD2 in a sample or measure the level of cellular anti-1A7 or
 CC anti-GD2 activity.
 CC The cDNA can be used in expression systems for 1A7 prodn., and in
 CC the prepn. of probes and primers to respectively assay for 1A7
 CC cDNA, and amplify desired polynucleotides for use in gene therapy.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX

SQ Sequence 152 AA;

Query Match 17.68; Score 27; DB 17; Length 152;

Best Local Similarity 100.0%; Pred. No. 1.6e-16; Indels 0; Gaps 0;
 Matches 27; Conservative 0; Mismatches 0;

OY 127 WGQGTSTVSSAKTTPPPVPLVPGSL 153

|||||

Db 126 WGQGTSTVSSAKTTPPPVPLVPGSL 152

RESULT 9

AAG80224

ID AAG80224 standard; protein; 279 AA.

XX AC AAG80224;

XX DT 22-JAN-2002 (first entry)

XX DE Gamma-glutamyl transferase antibody 138H11 antigen binding region.

XX KW Antigen binding region; antibody; 138H11; VH region; VL region;
 KW human; gamma-glutamyl transferase; gamma-glutamyl transpeptidase;
 KW EC 2.3.2.2; kidney cell; carcinoma; renal cell; cytostatic; tumour;
 KW antirheumatic; antiarthritic; liver; stomach; ovary; breast; glioma;
 KW melanoma; autoimmune disease; rheumatoid arthritis; metabolic disorder;
 KW leukotriene biosynthesis; mercaptoacid; glutathione; metastasis;
 KW differentiation; adenocarcinoma.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 1..141

FT /label= VH

FT Domain 142..279

FT /label= VL

XX DE10020034-A1.

XX PD 31-OCT-2001.

XX PF 22-APR-2000; 2000DE-1020034.

XX PR 22-APR-2000; 2000DE-1020034.

XX PA (FISCHER) FISCHER P.

XX PA (DUEBEL) DUEBEL S.

XX PA (SCHE) SCHERBERICH J E.

XX PI Duebel S, Schmiedl A;

XX

DR WPI; 2002-000467/01.

XX Agent for diagnosis and treatment of carcinoma, especially renal cell
 PT carcinoma, comprises binding partner for gamma-glutamyl transferase -

PS Claim 5; Fig 2; 12pp; German.

XX This invention describes a novel agent (A) for diagnosis and treatment of
 CC carcinoma based on substances (I) that are binding partners for
 CC gamma-glutamyltransferase (II), or its isoforms or enzymatically active
 CC variants. The products of the invention have cytostatic, antirheumatic
 CC and antiarthritic activity. (A) are useful for diagnosis and treatment of
 CC tumours that express (II), especially renal cell carcinoma but also
 CC carcinoma of liver, stomach, ovary and breast, glioma and melanoma,
 CC autoimmune diseases, e.g. rheumatoid arthritis, and metabolic disorders,
 CC e.g. disturbances of leukotriene biosynthesis, formation of mercaptoacids
 CC or of glutathione. Diagnostically, (A) are particularly used for
 CC (differential) diagnosis of tumours (especially by immunoscintigraphy,
 CC immunohistochemistry or immunoassays, or for detecting multiple drug
 CC resistance, metastases and relapse, for differentiation of (II)-positive
 CC tumours (kidney tumours, gliomas or adenocarcinoma of unknown origin).
 CC Recombinantly produced (A) reduce the human anti-mouse antibody response,
 CC allowing repeated administration, and can be prepared efficiently as a
 CC fusion protein in microorganisms, transgenic animals or plants. Also,
 CC where used for radio-diagnosis or -therapy, recombinant antibodies are
 CC quickly cleared from the blood and penetrate tumours better. Where (I) is
 CC coupled to an effector, e.g. interleukin-2, a high local concentration is
 CC achieved and systemic toxicity reduced. This sequence represents the
 CC antigen binding region (VH and VL) from antibody 138H11 against
 CC gamma-glutamyl transferase (also called gamma-glutamyl transpeptidase,
 CC EC number 2.3.2.2).

XX SQ Sequence 279 AA;

Query Match 13.7%; Score 21; DB 23; Length 279;

Best Local Similarity 100.0%; Pred. No. 7.1e-11;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 ALDYWGQGTSTVSSAKTTPP 143

|||||

Db 109 ALDYWGQGTSTVSSAKTTPP 129

RESULT 10

AAB30694

ID AAB30694 standard; protein; 412 AA.

XX AC AAB30694;

XX DT 02-APR-2001 (first entry)

XX DE A fusion of anti-CD20 single chain antibody/streptavidin.

XX KW Streptavidin; tumour cell; cancer; adenocarcinoma;

XX KW hematological malignancy; B9E9.

XX OS Synthetic.

XX OS Streptomyces avidinii.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Protein 1..108

FT /note= "VL chain"

FT Peptide 109..126

FT /note= "linker"

FT Protein 127..248

FT /note= "VH chain"

FT Peptide 249..253

FT /note= "linker"

FT Protein 254..412

FT /note= "streptavidin"

XX W0200075333-A1.

PN


```

XX PD 14-DEC-2000.
XX PF
XX PF 05-JUN-2000; 2000WO-US15595.
XX PR 07-JUN-1999; 99US-0137900.
XX PR 03-DEC-1999; 99US-0168976.
XX PA (NEOR-) NEORX CORP.
XX PI Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
XX PD WPI: 2001-091213/10.
XX DR N-PSDB; AAC86563.
XX
XX New vector constructs for expressing genomic streptavidin fusion
XX PT proteins which are useful for targeting tumour cells associated with
XX PT cancer, e.g. adenocarcinomas -
XX PA (NEOR-) NEORX CORP.
XX PS Example 2; Fig 11B; 100pp; English.
XX
XX The present sequence represents a fusion of an anti-CD20 single chain
XX antibody (B9E9) streptavidin. The fusion protein is expressed using
XX vectors of the invention. The specification describes vector constructs
XX for expressing streptavidin fusion proteins. The vector comprises a
XX nucleic acid encoding streptavidin or its functional variant operatively
XX linked to a promoter, and a cloning site for insertion of a second
XX nucleic acid sequence encoding a polypeptide to be fused with
XX streptavidin, interposed between the promoter and the first nucleic
XX acid sequence. Alternatively, the vector construct comprises a nucleic
XX acid, operatively linked to a promoter, encoding a polypeptide to be
XX fused with streptavidin, and a cloning site for insertion of a second
XX nucleic acid encoding at least 129 amino acids of streptavidin or its
XX functional variant. The fusion proteins are useful for targeting tumour
XX cells, particularly tumour cells associated with cancer,
XX e.g. adenocarcinomas or hematological malignancies. The vector construct
XX is useful for expressing of streptavidin fusion proteins. In particular,
XX these are useful as tools for medical diagnostics and therapeutic
XX purposes, e.g. for detecting the presence or absence of, or treating, a
XX target site within a mammalian host.
XX SQ Sequence 412 AA;
XX
XX Query Match 13.1%; Score 20; DB 22; Length 412;
XX Best Local Similarity 100.0%; Pred. No. 7.9e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 49 TSYNHHWVKQTGGGLEWIG 68
XX 157 TSYNHHWVKQTGGGLEWIG 176
XX
XX RESULT 11
XX ID AAB30695
XX XX AAB30695 standard; Protein; 423 AA.
XX AC AAB30695;
XX
XX 02-APR-2001 (first entry)
XX
XX A fusion of anti-CD20 single chain antibody/streptavidin.
XX
XX Streptavidin; tumour cell; cancer; adenocarcinoma;
XX hematological malignancy; B9E9.
XX
XX Synthetic.
XX Streptomyces avidinii.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Protein 1..126
XX FT /note= "VH chain"
XX FT Peptide 127..150

```

```

FT /note= "linker"
FT 151..259
FT /note= "VL chain"
FT Peptide 260..264
FT /note= "linker"
FT Protein 265..423
FT /note= "streptavidin"
XX
XX WO200075333-A1.
XX
XX 14-DEC-2000.
XX
XX 05-JUN-2000; 2000WO-US15595.
XX
XX 07-JUN-1999; 99US-0137900.
XX PR 03-DEC-1999; 99US-0168976.
XX
XX (NEOR-) NEORX CORP.
XX
XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
XX PI WPI: 2001-091213/10.
XX DR N-PSDB; AAC86564.
XX
XX New vector constructs for expressing genomic streptavidin fusion
XX PT proteins which are useful for targeting tumour cells associated with
XX PT cancer, e.g. adenocarcinomas -
XX PA (NEOR-) NEORX CORP.
XX
XX Example 2; Fig 11C; 100pp; English.
XX
XX The present sequence represents a fusion of an anti-CD20 single chain
XX antibody (B9E9) streptavidin. The fusion protein is expressed using
XX vectors of the invention. The specification describes vector constructs
XX for expressing streptavidin fusion proteins. The vector comprises a
XX nucleic acid encoding streptavidin or its functional variant operatively
XX linked to a promoter, and a cloning site for insertion of a second
XX nucleic acid sequence encoding a polypeptide to be fused with
XX streptavidin, interposed between the promoter and the first nucleic
XX acid sequence. Alternatively, the vector construct comprises a nucleic
XX acid, operatively linked to a promoter, encoding a polypeptide to be
XX fused with streptavidin, and a cloning site for insertion of a second
XX nucleic acid encoding at least 129 amino acids of streptavidin or its
XX functional variant. The fusion proteins are useful for targeting tumour
XX cells, particularly tumour cells associated with cancer,
XX e.g. adenocarcinomas or hematological malignancies. The vector construct
XX is useful for expressing of streptavidin fusion proteins. In particular,
XX these are useful as tools for medical diagnostics and therapeutic
XX purposes, e.g. for detecting the presence or absence of, or treating, a
XX target site within a mammalian host.
XX SQ Sequence 423 AA;
XX
XX Query Match 13.1%; Score 20; DB 22; Length 423;
XX Best Local Similarity 100.0%; Pred. No. 8.1e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 49 TSYNHHWVKQTGGGLEWIG 68
XX 32 TSYNHHWVKQTGGGLEWIG 51
XX
XX RESULT 12
XX ID AAY84965
XX XX AAY84965 standard; Protein; 633 AA.
XX AC AAY84965;
XX
XX 21-AUG-2000 (first entry)
XX
XX Amino acid sequence of a CD-20 specific chimeric receptor.
XX
XX CD20-specific receptor; CD-20 specific redirected T cell; leukemia;
XX CD20+ malignancy; non-Hodgkin's lymphoma; myeloablative chemotherapy;

```


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OM protein - protein search, using sw model

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Gapop 60.0 , Gapext 60.0

Searched: 510680 seqs, 136781880 residues

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Post-processing: Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Result No.	Query Match	Length	DB ID	Description
1	153	100.0	153	9 US-09-861-294-4
2	153	100.0	153	12 US-10-367-506-4
3	32	20.9	32	9 US-09-861-294-16
4	32	20.9	32	12 US-10-367-506-16
5	31	20.3	152	10 US-09-990-205-4
6	31	20.3	152	15 US-10-153-401-4
7	30	19.6	30	9 US-09-861-294-12
8	30	19.6	30	12 US-10-367-506-12
9	20	13.1	412	12 US-10-244-821-6
10	20	13.1	412	15 US-10-013-173-6
11	20	13.1	412	15 US-10-150-762-6
12	20	13.1	423	12 US/10/244
13	20	13.1	423	15 US/10/013
14	20	13.1	423	15 US/10/150
15	19	12.4	119	15 US-10-194-975-121

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	153	100.0	153	9 US-09-861-294-4
2	153	100.0	153	12 US-10-367-506-4
3	32	20.9	32	9 US-09-861-294-16
4	32	20.9	32	12 US-10-367-506-16
5	31	20.3	152	10 US-09-990-205-4
6	31	20.3	152	15 US-10-153-401-4
7	30	19.6	30	9 US-09-861-294-12
8	30	19.6	30	12 US-10-367-506-12
9	20	13.1	412	12 US-10-244-821-6
10	20	13.1	412	15 US-10-013-173-6
11	20	13.1	412	15 US-10-150-762-6
12	20	13.1	423	12 US/10/244
13	20	13.1	423	15 US/10/013
14	20	13.1	423	15 US/10/150
15	19	12.4	119	15 US-10-194-975-121

Result No.	Query Match	Length	DB ID	Description
1	153	100.0	153	9 US-09-861-294-4
2	153	100.0	153	12 US-10-367-506-4
3	32	20.9	32	9 US-09-861-294-16
4	32	20.9	32	12 US-10-367-506-16
5	31	20.3	152	10 US-09-990-205-4
6	31	20.3	152	15 US-10-153-401-4
7	30	19.6	30	9 US-09-861-294-12
8	30	19.6	30	12 US-10-367-506-12
9	20	13.1	412	12 US-10-244-821-6
10	20	13.1	412	15 US-10-013-173-6
11	20	13.1	412	15 US-10-150-762-6
12	20	13.1	423	12 US/10/244
13	20	13.1	423	15 US/10/013
14	20	13.1	423	15 US/10/150
15	19	12.4	119	15 US-10-194-975-121

US-09-861-294-4

Sequence 4, Application US/09861294

Patent No. US20020098190A1

GENERAL INFORMATION:

APPLICANT: Malaya CHATTERJEE

APPLICANT: Kenneth A. FOON

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TUMORS BEARING HMFG AND CEA ANTIGENS

FILE REFERENCE: 304142000620

CURRENT APPLICATION NUMBER: US/09/861.294

CURRENT FILING DATE: 2001-05-17

PRIOR APPLICATION NUMBER: 60/049,540

PRIOR FILING DATE: 1997-06-13

PRIOR APPLICATION NUMBER: 09/096,244

PRIOR FILING DATE: 1998-06-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 153

TYPE: PRT

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: SIGNAL

LOCATION: (1)....(19)

US-09-861-294-4

Query Match 100.0%; Score 153; DB 9; Length 153;

Best Local Similarity 100.0%; Pred. No. 5.3e-131;

Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MECSWVFLLSITGTVHQSAYLQOQGAELVRSGASVYKMSCKASGYTLTSTNMHWKTP 60

Db 1 MECSWVFLLSITGTVHQSAYLQOQGAELVRSGASVYKMSCKASGYTLTSTNMHWKTP 60

Qy 61 GQGLEWIGNIPFGNGDYNNKFKGKSLTADTSSSTAYMGISSITSDSAYVFCARGNW 120

Db 61 GQGLEWIGNIPFGNGDYNNKFKGKSLTADTSSSTAYMGISSITSDSAYVFCARGNW 120

Result No.	Query Match	Length	DB ID	Description
1	153	100.0	153	9 US-09-861-294-4
2	153	100.0	153	12 US-10-367-506-4
3	32	20.9	32	9 US-09-861-294-16
4	32	20.9	32	12 US-10-367-506-16
5	31	20.3	152	10 US-09-990-205-4
6	31	20.3	152	15 US-10-153-401-4
7	30	19.6	30	9 US-09-861-294-12
8	30	19.6	30	12 US-10-367-506-12
9	20	13.1	412	12 US-10-244-821-6
10	20	13.1	412	15 US-10-013-173-6
11	20	13.1	412	15 US-10-150-762-6
12	20	13.1	423	12 US/10/244
13	20	13.1	423	15 US/10/013
14	20	13.1	423	15 US/10/150
15	19	12.4	119	15 US-10-194-975-121

```
Oy 121 EGALDYGQGTSTVSSAKTTPPPVPLVPGSL 153
|||||
Db 121 EGALDYGQGTSTVSSAKTTPPPVPLVPGSL 153

RESULT 2
US-10-367-506-4
; Sequence 4, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-367-506-4

Query Match 100.0%; Score 153; DB 12; Length 153;
Best Local Similarity 100.0%; Pred. No. 5.3e-131; Indels 0; Gaps 0;
Matches 153; Conservative 0; Mismatches 0;

Oy 1 MECSWVFLFLSIITGVHSGAYLQSGAELVRSGASVKMSCKASGYTLTTSYNMHWKTP 60
|||||
Db 1 MECSWVFLFLSIITGVHSGAYLQSGAELVRSGASVKMSCKASGYTLTTSYNMHWKTP 60

Oy 61 GQGLEWIGNIPPGNDYYNOKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCARNW 120
|||||
Db 61 GQGLEWIGNIPPGNDYYNOKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCARNW 120

Oy 121 EGALDYGQGTSTVSSAKTTPPPVPLVPGSL 153
|||||
Db 121 EGALDYGQGTSTVSSAKTTPPPVPLVPGSL 153

RESULT 3
US-09-861-294-16
; Sequence 16, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus

Query Match 100.0%; Score 31; DB 10; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.8e-20; Indels 0; Gaps 0;
Matches 31; Conservative 0; Mismatches 0;

Oy 86 KASLTADTSSSTAYMQISLTSEDSAVYFCAR 117
|||||
Db 1 KASLTADTSSSTAYMQISLTSEDSAVYFCAR 32

RESULT 4
US-10-367-506-16
; Sequence 16, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus

US-10-367-506-16

Query Match 100.0%; Score 32; DB 12; Length 32;
Best Local Similarity 100.0%; Pred. No. 6e-22; Indels 0; Gaps 0;
Matches 32; Conservative 0; Mismatches 0;

Oy 86 KASLTADTSSSTAYMQISLTSEDSAVYFCAR 117
|||||
Db 1 KASLTADTSSSTAYMQISLTSEDSAVYFCAR 32

RESULT 5
US-09-990-205-4
; Sequence 4, Application US/09990205
; Patent No. US20020150572A1
; GENERAL INFORMATION:
; APPLICANT: FOON, Kenneth A.
; APPLICANT: CHATTERJEE, Malaya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000501
; CURRENT APPLICATION NUMBER: US/09/990,205
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: U.S. 09/192,838
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/065,774
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus Musculus

US-09-990-205-4

Query Match 100.0%; Score 31; DB 10; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.8e-20; Indels 0; Gaps 0;
Matches 31; Conservative 0; Mismatches 0;
```

QY 123 ALDWGQGTSTVSSAKTTPPPYPLVPGSL 153
|||||
Db 122 ALDWGQGTSTVSSAKTTPPPYPLVPGSL 152

RESULT 6

US-10-153-401-4
; Sequence 4, Application US/10153401
; Publication No. US20030114398A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; Foon, Kenneth A.
; Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,401
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/293,533
; FILING DATE: 1999-04-15
; APPLICATION NUMBER: US 08/372,676
; FILING DATE: 1995-01-17
; APPLICATION NUMBER: US 08/591,196
; FILING DATE: 1996-01-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine M. Polizzi
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 304142000202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-153-401-4

Query Match 20.3%; Score 31; DB 15; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 ALDWGQGTSTVSSAKTTPPPYPLVPGSL 153
|||||
Db 122 ALDWGQGTSTVSSAKTTPPPYPLVPGSL 152

RESULT 7

US-09-861-294-12
; Sequence 12, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-861-294-12

Query Match 19.6%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.7e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 QAYLQSGAELVRSGASVKMSCKASGYTLT 49
|||||
Db 1 QAYLQSGAELVRSGASVKMSCKASGYTLT 30

RESULT 8

US-10-367-506-12
; Sequence 12, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-367-506-12

Query Match 19.6%; Score 30; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.7e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 QAYLQSGAELVRSGASVKMSCKASGYTLT 49
|||||
Db 1 QAYLQSGAELVRSGASVKMSCKASGYTLT 30

RESULT 9

US-10-244-821-6
; Sequence 6, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.

```

; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 s
; OTHER INFORMATION: antibody-genomic streptavidin fusion
US-10-244-821-6

```

Query Match	13.1%	Score 20;	DB 12;	Length 412;
Best Local Similarity	100.0%;	Pred. No. 3.9e-10;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```

RESULT 10
US-10-013-173-6
; Sequence 6, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain
; OTHER INFORMATION: antibody-genomic streptavidin fusion
US-10-013-173-6

```

```

Query Match      13.1%; Score 20; DB 15; Length 412;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      49  TSYNMHWVKOTPGGLEWIG 68
          |||||
Db      157 TSYNMHWVKOTPGGLEWIG 176
          |||||

```

RESULT 11
US-10-150-762-6
; Sequence 6, Application US/10150762
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne B.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; APPLICANT: Dearthstyne, Erica A.

```

; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
;
; TITLE OF INVENTION: METHODS OF USE THEREOF
;
; FILE REFERENCE: 690022.547C2
;
; CURRENT APPLICATION NUMBER: US/10/150,762
;
; CURRENT FILING DATE: 2002-05-17
;
; NUMBER OF SEQ ID NOS: 90
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 6
;
; LENGTH: 412
;
; TYPE: PRT
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 s
;
; OTHER INFORMATION: antibody-genomic streptavidin fusion
;
; US-10-150-762-6

```

Query Match	13.1%	Score 20;	DB 15;	Length 412;
Best Local Similarity	100.0%;	Pred. No. 3.9e-10;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT 12
 US/10/244
 ; Sequence 8, Application US/10244821
 ; Publication No. US20030143233A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goshorn, Stephen Charles
 ; APPLICANT: Graves, Scott Stoll
 ; APPLICANT: Schultz, Joanne Elaine
 ; APPLICANT: Lin, Yukang
 ; APPLICANT: Sanderson, James Allen
 ; APPLICANT: Reno, John M.
 ; APPLICANT: Dearstyn, Erica A.
 ; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 690022.547C3
 ; CURRENT APPLICATION NUMBER: US/10/244, 821
 ; CURRENT FILING DATE: 2002-09-16
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 423
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Predicted amino acid sequence of B9E9 s
 ; US/10/244, 821-8

Query Match	13.1%	Score 20;	DB 12;	Length 423;
Best Local Similarity	100.0%;	Pred. No. 3.9e-10;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	49	TSYNHWVKOTPGGQLEWIG	68	
Db	32	TSYNHWVKOTPGGQLEWIG	51	

RESULT 13
US/10/013
; Sequence 8, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshora, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND

; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain antibody- gend
US/10/013,173-8

Query Match 13.1%; Score 20; DB 15; Length 423;
Best Local Similarity 100.0%; Pred. No. 3.9e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 49 TSYNMHWVKQTGGGLEWIG 68
Db 32 TSYNMHWVKQTGGGLEWIG 51
|||||

RESULT 14
US/10/150
; Sequence 8, Application US/10150762
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150,762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain antibody- gend
US/10/150,762-8

Query Match 13.1%; Score 20; DB 15; Length 423;
Best Local Similarity 100.0%; Pred. No. 3.9e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 49 TSYNMHWVKQTGGGLEWIG 68
Db 32 TSYNMHWVKQTGGGLEWIG 51
|||||

RESULT 15
US-10-194-975-121
; Sequence 121, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 121
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-194-975-121

Query Match 12.4%; Score 19; DB 15; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.1e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY 50 SYNMHWVKQTGGGLEWIG 68
Db 31 SYNMHWVKQTGGGLEWIG 49
|||||

Search completed: August 30, 2003, 22:12:33
Job time : 17.4295 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2003, 22:07:01 ; Search time 10.7819 Seconds
(without alignments)
1364.679 Million cell updates/sec

Title: US-08-836-455-4

Perfect score: 153

Sequence: 1 MDCSWVFLFLSITTCVHSQ.....TVSSAKTTPPVPLVPGSL 153

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96169682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	14.4	119	2	PL0089
2	22	14.4	151	2	PL0011
3	20	13.1	93	2	S42182
4	20	13.1	94	2	S42177
5	20	13.1	95	2	S42178
6	20	13.1	97	2	S42181
7	20	13.1	101	2	S42179
8	20	13.1	101	2	S42184
9	20	13.1	102	2	S42180
10	19	12.4	140	2	S14238
11	19	12.4	149	2	S30752
12	19	12.4	150	2	PN0444
13	19	12.4	152	2	B26471
14	19	12.4	178	2	S29594
15	18	11.8	124	2	S06824
16	17	11.1	112	2	S26473
17	17	11.1	246	2	S38950
18	17	11.1	446	2	S40295
19	16	10.5	109	2	PH1001
20	16	10.5	111	2	PH0998
21	16	10.5	116	2	S09962
22	16	10.5	119	2	PH1512
23	16	10.5	140	2	S09216
24	15	9.8	43	2	S11111
25	15	9.8	67	2	H28833
26	15	9.8	91	2	PL0242
27	15	9.8	94	2	G32513
28	15	9.8	96	2	H28195
29	15	9.8	106	2	PH1002

30 15 9.8 107 2 PL0240 Ig heavy chain V r
31 15 9.8 107 2 PL0241 Ig heavy chain V r
32 15 9.8 108 2 S26316 Ig heavy chain V r
33 15 9.8 109 2 PH0997 Ig heavy chain V r
34 15 9.8 110 2 S26317 Ig heavy chain V r
35 15 9.8 110 2 PH1000 Ig heavy chain V r
36 15 9.8 111 2 S25033 Ig heavy chain V r
37 15 9.8 111 2 S25034 Ig heavy chain V r
38 15 9.8 112 2 S09957 Ig heavy chain V-D
39 15 9.8 113 2 S55335 Ig heavy chain V r
40 15 9.8 115 2 PL0238 Ig heavy chain V r
41 15 9.8 115 2 A54378 Ig heavy chain V r
42 15 9.8 117 2 PL0237 Ig heavy chain V r
43 15 9.8 117 2 PL0235 Ig heavy chain V r
44 15 9.8 117 2 PL0234 Ig heavy chain V r
45 15 9.8 117 2 S19966 Ig heavy chain V r

ALIGNMENTS

RESULT 1

PL0089
Ig heavy chain V region (12s18-1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Mar-2000
C;Accession: PL0089

R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Siaoui, M.; Urbain, J.;
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antidiotypic antibodies; evidence that Ab2s
A;Reference number: PL0080; MUID:89094248; PMID:2492056
A;Accession: PL0089

A;Molecule type: mRNA

A;Residues: 1-119 <MEE>

A;Cross-references: GB:X58580; GB:Y00794; NID:951591; PIDN:CAA1456.1; PID:9930150

A;Note: the sequence shown here is from the VH region of an antidiotypic monoclonal
A;Note: sequences from two other clones (18S28-16 and 12S84-3) were almost identical
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 14.4%; Score 22; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 1.4e-14;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 DTSSSTAYMOISLTSEDSAVY 113

|||||

Db 73 DTSSSTAYMOISLTSEDSAVY 94

RESULT 2

PL0011

Ig heavy chain precursor V region (4C11) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C;Accession: PL0011

R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kiebler-Emmons, T.; Kohler, H.

Mol. Immunol. 25, 33-40, 1988

A;Title: Structural basis of stimulatory anti-idiotypic antibodies.

A;Reference number: PL0011; MUID:88142863; PMID:3125424

A;Accession: PL0011

A;Molecule type: mRNA

A;Residues: 1-151 <CHE>

A;Experimental source: cell line 4C11

C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphoryl

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-136/Product: Ig heavy chain V region 4C11 #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

F;50-54/Region: complementarity-determining 1

F;69-85/Region: complementarity-determining 2

F;118-125/Region: complementarity-determining 3

F:137-151/Domain: C region (fragment) #status predicted <COR>

Query Match 14.4%; Score 22; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.7e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 GADYWGQGRSVTVSSAKTTPP 143
|||||
Db 121 GADYWGQGRSVTVSSAKTTPP 142
|||||

RESULT 3

S42182

Ig gamma chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999

C:Accession: S42182

R:Mo, J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42182

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-93 <MOJ>

A:Cross-references: EMBL:Z25443; NID:g407822; PIDN:CAA80940.1; PID:g407823

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 13.1%; Score 20; DB 2; Length 93;

Best Local Similarity 100.0%; Pred. No. 1.1e-12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 TSYNMHWVKTPGGGLEWIG 68
|||||

Db 23 TSYNMHWVKTPGGGLEWIG 42
|||||

RESULT 4

S42177

Ig gamma chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999

C:Accession: S42177

R:Mo, J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42177

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-94 <MOJ>

A:Cross-references: EMBL:Z25443; NID:g407812; PIDN:CAA80930.1; PID:g407813

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 13.1%; Score 20; DB 2; Length 94;

Best Local Similarity 100.0%; Pred. No. 1.2e-12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 TSYNMHWVKTPGGGLEWIG 68
|||||

Db 23 TSYNMHWVKTPGGGLEWIG 42
|||||

RESULT 5

S42178

Ig gamma chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999

C:Accession: S42178

R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42178

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-95 <MOJ>

A:Cross-references: EMBL:Z25445; NID:g407814; PIDN:CAA80932.1; PID:g407815

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 13.1%; Score 20; DB 2; Length 95;

Best Local Similarity 100.0%; Pred. No. 1.2e-12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 TSYNMHWVKTPGGGLEWIG 68
|||||

Db 23 TSYNMHWVKTPGGGLEWIG 42
|||||

RESULT 6

S42181

Ig gamma chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999

C:Accession: S42181

R:Mo, J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42181

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-97 <MOJ>

A:Cross-references: EMBL:Z25451; NID:g407820; PIDN:CAA80938.1; PID:g407821

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 13.1%; Score 20; DB 2; Length 97;

Best Local Similarity 100.0%; Pred. No. 1.2e-12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 TSYNMHWVKTPGGGLEWIG 68
|||||

Db 23 TSYNMHWVKTPGGGLEWIG 42
|||||

RESULT 7

S42179

Ig gamma chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999

C:Accession: S42179

R:Mo, J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42179

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-101 <MOJ>

A:Cross-references: EMBL:Z25447; NID:g407816; PIDN:CAA80934.1; PID:g407817

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 13.1%; Score 20; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 1.2e-12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A;Accession: S14238
A;Molecule type: mRNA

Q7 123 DWGQGISVIVSSAKITFF 143
 125 DWGQGTSVTVSSAKITPP 143

RESULT 13

Ig heavy chain precursor V region (MAK33) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
 R:Accession: B26471; S70410
 C:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
 Gene 51, 13-19, 1987
 A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine
 A:Reference number: A91572; MUID:87248058; PMID:3110009
 A:Accession: B26471
 A:Molecule type: mRNA
 A:Residues: 1-152 <BUC>
 A:Cross-references: GB:M1613; NID:gl95405; PIDN:AAA38292.1; PID:gl95406
 R:Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 172, 1717-1727, 1990
 A:Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary
 A:Reference number: S70410; MUID:91079775; PMID:2258702
 A:Accession: S70410
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-19 <LEB>
 A:Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476
 C:Genetics:
 A:Introns: 16/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-152/Product: Ig heavy chain V region MAK33 #status predicted <MAT>
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 12.4%; Score 19; DB 2; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.8e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 DYWGQGTSTVTSSAKTTPP 143
 |||||
 DB 130 DYWGQGTSTVTSSAKTTPP 148

RESULT 14

Ig gamma chain (WM65) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S29594
 R:Seymour, R.
 submitted to the EMBL Data Library, February 1991
 A:Reference number: S29593
 A:Accession: S29594
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-178 <SEY>
 A:Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
 C:Keywords: immunoglobulin

Query Match 12.4%; Score 19; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 2.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 DYWGQGTSTVTSSAKTTPP 143
 |||||
 DB 119 DYWGQGTSTVTSSAKTTPP 137

RESULT 15

Ig heavy chain V region (clone 12D4) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1991 #sequence_revision 11-Nov-1994 #text_change 23-Jul-1999
 C:Accession: S06824
 R:Miller III, A.; Glasel, J.A.
 J. Mol. Biol. 209, 763-778, 1989

A:Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-m
 A:Reference number: S06815; MUID:90064531; PMID:2555519
 A:Accession: S06824
 A:Molecule type: mRNA
 A:Residues: 1-124 <MIL>
 A:Cross-references: EMBL:X17166; NID:g51918; PIDN:CAA35044.1; PID:g930156
 A>Note: The authors did not translate the codon TGG for residue 36
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;22-96/Disulfide bonds: #status predicted

Query Match 11.8%; Score 18; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 DYWGQGTSTVTSSAKTTP 142
 |||||
 DB 107 DYWGQGTSTVTSSAKTTP 124

Search completed: August 30, 2003, 22:11:49
 Job time : 10.7819 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2003, 22:04:41 ; Search time 9.24161 Seconds
(without alignments)
778.553 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 153
Sequence: 1 MECSWFLFLSLTTGVHSQ.....TVSSAKTTPPPVPLVPSL 153

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	9.2	117	1	HV12_MOUSE
2	14	9.2	117	1	HV13_MOUSE
3	14	9.2	120	1	HV03_MOUSE
4	14	9.2	140	1	HV02_MOUSE
5	14	9.2	144	1	HV43_MOUSE
6	13	8.5	136	1	HV16_MOUSE
7	12	7.8	117	1	HV42_MOUSE
8	11	7.2	117	1	HV04_MOUSE
9	11	7.2	117	1	HV05_MOUSE
10	11	7.2	117	1	HV06_MOUSE
11	11	7.2	117	1	HV10_MOUSE
12	11	7.2	117	1	HV14_MOUSE
13	11	7.2	117	1	HV49_MOUSE
14	11	7.2	121	1	HV01_MOUSE
15	11	7.2	137	1	HV11_MOUSE
16	11	7.2	139	1	HV07_MOUSE
17	10	6.5	117	1	HV09_MOUSE
18	10	6.5	118	1	HV51_MOUSE
19	9	5.9	114	1	HV00_MOUSE
20	9	5.9	117	1	HV52_MOUSE
21	9	5.9	120	1	HV50_MOUSE
22	9	5.9	130	1	TVB8_MOUSE
23	9	5.9	133	1	TVB2_MOUSE
24	9	5.9	136	1	HV15_MOUSE
25	9	5.9	138	1	HV48_MOUSE
26	8	5.2	117	1	HV03_CARAU
27	8	5.2	117	1	HV1B_HUMAN
28	8	5.2	117	1	HV1G_HUMAN
29	8	5.2	130	1	TVAI_MOUSE
30	8	5.2	131	1	TVAI_HUMAN
31	8	5.2	135	1	TVB1_HUMAN
32	8	5.2	139	1	TVA2_HUMAN
33	8	5.2	147	1	HV1C_HUMAN

34	7	4.6	111	1	HV35_MOUSE	P01804 mus musculus
35	7	4.6	116	1	HV01_HETFR	P03983 heterodontu
36	7	4.6	116	1	HV3T_HUMAN	P01781 homo sapien
37	7	4.6	117	1	HV1A_HUMAN	P01742 homo sapien
38	7	4.6	118	1	HV39_MOUSE	P01809 mus musculus
39	7	4.6	120	1	HV1H_HUMAN	P80421 homo sapien
40	7	4.6	126	1	HV3K_HUMAN	P01772 homo sapien
41	7	4.6	135	1	HV02_XENLA	P20957 xenopus lae
42	7	4.6	137	1	HV46_MOUSE	P01822 mus musculus
43	7	4.6	143	1	Y880_MYCLE	O33060 mycobacteri
44	7	4.6	155	1	Y1E1_ECOLI	P31468 escherichia
45	7	4.6	182	1	YH66_HALN1	Q9HmV9 halobacteri

ALIGNMENTS

RESULT 1

HV12_MOUSE

ID HV12_MOUSE STANDARD; PRT; 117 AA.

AC P01756;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region MOPC 104E.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.

RX MEDLINE=83075344; PubMed=6816276;

RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,

RA Hood L.E.;

RT "Complete amino acid sequence of a mouse mu chain: homology among

RT heavy chain constant region domains.";

RL Biochemistry 21:5415-5424(1982).

CC -|- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA

CC PROTEIN HAS ALSO BEEN DETERMINED.

CC -|- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.

CC PIR: A02039; MHMS4E.

DR HSSP; P01789; IMCP.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG_LIKE; 1.

KW Immunoglobulin V region; Glycoprotein.

FT DOMAIN 1 116

FT DISULFID 22 96

FT CARBOHYD 55 55

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 9.2%; Score 14; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 5e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 34 GASVKMSCKASGYT 47

Db 15 GASVKMSCKASGYT 28

|||||

RESULT 2

HV13_MOUSE

ID HV13_MOUSE STANDARD; PRT; 117 AA.

AC P01757;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region J558.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80078170; PubMed=6765983;
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 rearrangements in heavy chain V-region gene segments."
 RL Nature 283:35-40(1980).
 CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
 WHICH OCCUR IN THE D AND J SEGMENTS.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CR PIR; A26242; MHMSJ5.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 116
 FT DISULFID 22 96
 FT NON_TER 117 117
 FT SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
 Query Match 9.2%; Score 14; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 5e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 34 GASVKMSCKASGYT 47
 DB 15 GASVKMSCKASGYT 28
 RESULT 3
 HV03_MOUSE
 ID HV03_MOUSE STANDARD; PRT; 120 AA.
 AC P01747;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 36-65.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83131846; PubMed=6186498;
 RA Siekevitz M., Geffer M.L., Brodeur P., Riblet R.,
 RA Marshak-Rothstein A.;
 RT "The genetic basis of antibody production: the dominant anti-arsenate
 idiotypic response of the strain A mouse."
 RL Eur. J. Immunol. 12:1023-1032(1982).
 CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
 DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
 CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
 SEGMENT, JH2.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 111
 FT IG-LIKE.

FT NON_TER 120
 SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
 Query Match 9.2%; Score 14; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 104 SLTSEDSAVYFCAR 117
 DB 84 SLTSEDSAVYFCAR 97
 RESULT 4
 HV02_MOUSE
 ID HV02_MOUSE STANDARD; PRT; 140 AA.
 AC P01746;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 93G7 precursor.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-A/J;
 RX MEDLINE=82152818; PubMed=6801765;
 RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
 RA Capra J.D.;
 RT "Somatic mutation in genes for the variable portion of the
 immunoglobulin heavy chain."
 RL Science 216:309-311(1982).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J00493; AAA38128.1;
 CC PIR; A94264; HVMSG7.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region; Hybridoma; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
 FT DOMAIN 20 139 IG-LIKE.
 FT NON_TER 140 140
 SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
 Query Match 9.2%; Score 14; DB 1; Length 140;
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 104 SLTSEDSAVYFCAR 117
 DB 104 SLTSEDSAVYFCAR 117
 RESULT 5
 HV43_MOUSE
 ID HV43_MOUSE STANDARD; PRT; 144 AA.
 AC P01819;
 DT 21-JUL-1986 (Rel. 01, Created)


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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DI Ig heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1990).
CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; V00768; CAA24149.1; -.
CC PIR; A02094; G2MS14.
CC HSP; P01825; 7FAB.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL
CC 1 19
CC CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
CC DOMAIN 20 130 IG-LIKE.
CC NON_TER 144 144
CC SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 9.2%; Score 14; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 LDYWGQGTSTVSS 137
DB 131 LDYWGQGTSTVSS 144
|||||
RESULT 6
HV16_MOUSE STANDARD; PRT; 136 AA.
ID HV16_MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
```

```
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC -----
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CC -----
CC EMBL; J00522; AAD15290.1; -.
CC PIR; E90809; GIMS21.
CC PDB; 1IGC; O3-JUN-95.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal; 3D-structure.
CC NON_TER 1 16
CC SIGNAL
CC <1 16
CC CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
CC DOMAIN 115 119 D SEGMENT.
CC DOMAIN 120 136 JH4 SEGMENT.
CC DISULFID 38 112
CC CONFLICT 75 78
CC CONFLICT 89 90
CC CONFLICT 115 115
CC CONFLICT 120 120
CC NON_TER 136 136
CC SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;

Query Match 8.5%; Score 13; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 DYWGQGTSTVSS 137
DB 124 DYWGQGTSTVSS 136
|||||
RESULT 7
HV42_MOUSE STANDARD; PRT; 117 AA.
ID HV42_MOUSE
AC P01812;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-104.
RX MEDLINE=72105531; PubMed=5062012;
RA Bourgois A., Fougereau M., de Preval C.;
RT "Sequence of amino acids of the NH 2 -terminal region of a
RT mouse-clonal immunoglobulin heavy chain.";
RL Eur. J. Biochem. 24:446-455(1972).
RN [2]
RP SEQUENCE OF 105-117.
RX MEDLINE=76091933; PubMed=812695;
RA Rocca-Serra J., Milili M., Fougereau M.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin. Amino-acid sequence of the H4 cyanogen-bromide
RT fragment.";
RL Eur. J. Biochem. 59:511-523(1975).
RN [3]
```

RP SEQUENCE OF 96-117 FROM N.A.
RX MEDLINE-81223769; PubMed-6787590;
RA Gough N.M., Bernard O.;
RT "Sequences of the joining region genes for immunoglobulin heavy
RT chains and their role in generation of antibody diversity.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:509-513(1981).
RN [4]
RP DISULFIDE BOND.
RA Bourgois A., Fougereau M.;
RT "Partial amino acid sequence of the variable region of a mouse
RT gammac2a immunoglobulin heavy chain. Evidence for the existence of a
RT third sub-group of variability for the heavy chain pool.";
RL FEBS Lett. 8:263-268(1970).
CC -1- MISCELLANEOUS: THIS GAMMA-2A CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A91190; G2MS73.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96
FT CONFLICT 105 105 N -> D (IN REF. 2).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13051 MW; 156DCCC259380F19 CRC64;
Query Match 7.8%; Score 12; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 126 YWGQGSTVTSS 137
DB 106 YWGQGSTVTSS 117
RESULT 8
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE-81234548; PubMed-6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC EMBL; J00536; AAA38605.1;
DR PIR: A02031; HVMS3.
DR HSSP; P01810; 2FBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;
Query Match 7.2%; Score 11; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 60 PGQGLEWIGNI 70
DB 60 PGQGLEWIGNI 70
RESULT 9
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain v region 3 precursor.
DE IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE-81234548; PubMed-6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC EMBL; J00536; AAA38605.1;
DR PIR: A02031; HVMS3.
DR HSSP; P01810; 2FBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

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Query Match          7.2%; Score 11; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 PGQGLEWIGNI 70
DB 60 PGQGLEWIGNI 70
|||||

RESULT 10
HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
DR EMBL: J00533; AAA38602.1;
DR PIR: C90809; HVMS45.
DR HSP; P01810; 2FBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match          7.2%; Score 11; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SSLTSEDSAVY 113
DB 103 SSLTSEDSAVY 113
|||||

RESULT 12
HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain v region 108A precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----

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DR EMBL; J00488; AAA38519.1; -
 DR PIR; A02041; HVMS8A.
 DR HSSP; P01810; 2FBJ.
 DR MGD; MGI:96486; Igh-VJ558.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
 FT DOMAIN 20 >117 IG-LIKE.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 7.2%; Score 11; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.00058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SSLTSEDSAVY 113
 ID HV49_MOUSE STANDARD; PRT; 117 AA.
 DB 103 SSLTSEDSAVY 113

RESULT 13

ID HV49_MOUSE STANDARD; PRT; 117 AA.
 AC P06328;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region VH558 B4 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8509340; PubMed=2578321;
 RA Yancopoulos G.D., Alt F.W.;
 RT "Developmentally controlled and tissue-specific expression of
 RL Cell 40:271-281(1985).
 CC -----

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 CC -----

DR EMBL; M13788; AAA38506.1; -
 DR PIR; A02035; MHMSB4.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Igv; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 7.2%; Score 11; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.00058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SSLTSEDSAVY 113
 ID HV01_MOUSE STANDARD; PRT; 121 AA.
 DB 103 SSLTSEDSAVY 113

RESULT 14

ID HV01_MOUSE STANDARD; PRT; 121 AA.
 AC P01745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MPC 11.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81053741; PubMed=6253904;
 RA Zakut R., Cohen J., Givol D.;
 RT "Cloning and sequence of the cDNA corresponding to the variable
 RL region of immunoglobulin heavy chain MPC11.";
 RN [2]
 RP REVISIONS.
 RA Zakut R., Cohen J., Givol D.;
 RL Nucleic Acids Res. 8:4839-4840(1980).
 CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
 CC FROM A MYELOMA THAT SECRETES IGG2B.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A93708; GVMS11.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Igv; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 112 IG-LIKE.
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 7.2%; Score 11; DB 1; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.0006;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 LTADTSSSTAY 99
 DB 70 LTADTSSSTAY 80

RESULT 15

ID HV11_MOUSE STANDARD; PRT; 137 AA.
 AC P01755;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel..38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00539; AAA38172.1; -.
DR PIR: A02038; G2MS43.
DR HSSP: P01810; 2FBJ
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 137 FRAMEWORK-1.
FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 54 FRAMEWORK-2.
FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 69 85 FRAMEWORK-3.
FT DOMAIN 86 117 D SEGMENT.
FT DOMAIN 118 122 JH2 SEGMENT.
FT DOMAIN 123 137 BY SIMILARITY.
FT DISULFID 41 115
FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 7.2%; Score 11; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SSLTSEDSAVY 113
Db 103 SSLTSEDSAVY 113
|||||

Search completed: August 30, 2003, 22:10:22
Job time : 9.24161 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2003, 22:06:06 ; Search time 23.6174 Seconds
(without alignments)
1671.732 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 153
Sequence: 1 MECSWFLFLSITGVHSQ.....TVSSAKTTPPVYPLVPGSL 153

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- SPTREMBL_23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	10.5	481	11	Q91WT3 mus musculus
2	15	9.8	111	11	Q9DB88 mus musculus
3	15	9.8	426	11	Q9DCD9 mus musculus
4	15	9.8	463	11	Q9DLC4 mus musculus
5	15	9.8	473	11	Q9B8L4 mus musculus
6	14	9.2	109	11	Q9JL75 mus musculus
7	14	9.2	117	11	Q9QXE9 mus musculus
8	14	9.2	117	11	Q9QXF0 mus musculus
9	14	9.2	143	11	Q924Q0 mus musculus
10	14	9.2	147	11	Q923S3 mus musculus
11	14	9.2	474	11	Q8R3H6 mus musculus
12	13	8.5	110	11	Q9JL77 mus musculus
13	13	8.5	121	11	Q99NG4 mus musculus
14	13	8.5	140	11	Q924R2 mus musculus
15	13	8.5	142	11	Q924Q1 mus musculus
16	13	8.5	142	11	Q924Q2 mus musculus

17	13	8.5	143	11	Q924P6 mus musculus
18	13	8.5	143	11	Q924R0 mus musculus
19	13	8.5	145	11	Q924Q6 mus musculus
20	13	8.5	145	11	Q924Q9 mus musculus
21	13	8.5	145	11	Q924P7 mus musculus
22	13	8.5	145	11	Q924R1 mus musculus
23	13	8.5	145	11	Q924R4 mus musculus
24	13	8.5	146	11	Q924Q3 mus musculus
25	13	8.5	481	11	Q91WT1 mus musculus
26	13	8.5	482	11	Q91X92 mus musculus
27	13	8.5	482	11	Q8K172 mus musculus
28	13	8.5	484	11	Q99LA6 mus musculus
29	13	8.5	488	11	Q8K0F2 mus musculus
30	13	8.5	489	11	Q8VCX4 mus musculus
31	11	7.2	137	11	Q924R6 mus musculus
32	11	7.2	139	11	Q924R5 mus musculus
33	11	7.2	140	11	Q924P8 mus musculus
34	11	7.2	141	11	Q924Q4 mus musculus
35	11	7.2	143	11	Q91VA2 mus musculus
36	11	7.2	143	11	Q924Q5 mus musculus
37	11	7.2	143	11	Q91V67 mus musculus
38	11	7.2	143	11	Q924R7 mus musculus
39	11	7.2	143	11	Q924P9 mus musculus
40	11	7.2	144	11	Q924P5 mus musculus
41	11	7.2	145	11	Q924R3 mus musculus
42	11	7.2	145	11	Q924Q7 mus musculus
43	11	7.2	146	11	Q924R8 mus musculus
44	11	7.2	146	11	Q924Q8 mus musculus
45	11	7.2	168	11	Q8VDC9 mus musculus

ALIGNMENTS

RESULT 1

Q91WT3 Q91WT3 PRELIMINARY; PRT; 481 AA.
AC Q91WT3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical 52.0 kDa protein.
GN IGH-VJ558 OR AI893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013488; AAH13488.1; -
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Igh-Like.
DR InterPro; IPR003006; Igh_MHC.
DR InterPro; IPR003596; Igh_V.
DR Pfam; PF00047; Igh; 4.
DR SMART; SM00406; Igh; 1.
DR PROSITE; PS00835; IGH_LIKE; 4.
DR PROSITE; PS00290; IGH_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52022 MW; 4EBB5C253038B718 CRC64;

Query Match 10.5%; Score 16; DB 11; Length 481;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SSLTSEDSAVYFCARG 118

DB 102 SSLTSEDSAVYFCARG 117

```
RESULT 2
Q9D9B8      PRELIMINARY;      PRT;      111 AA.
AC Q9D9B8;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Adult male testis cDNA, RIKEN full-length enriched library,
DE clone:1700110L1, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUP=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli J., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007163; BAB24877.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-CL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 2.
SQ SEQUENCE 436 AA; 45819 MW; 56E1275BA48F6FB1 CRC64;

Query Match      9.8%; Score 15; DB 11; Length 426;
Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SSLTSEDSAVYFCAR 117
Db 46 SSLTSEDSAVYFCAR 60

RESULT 4
Q99LC4      PRELIMINARY;      PRT;      463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEF-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match      9.8%; Score 15; DB 11; Length 463;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SSLTSEDSAVYFCAR 117
Db 46 SSLTSEDSAVYFCAR 60

RESULT 3
Q9DCD9      PRELIMINARY;      PRT;      426 AA.
AC Q9DCD9;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Adult male kidney cDNA, RIKEN full-length enriched library,
DE clone:0610041A01, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUP=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli J., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007163; BAB24877.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;

Query Match      9.8%; Score 15; DB 11; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SSLTSEDSAVYFCAR 117
Db 90 SSLTSEDSAVYFCAR 104

RESULT 3
Q9DCD9      PRELIMINARY;      PRT;      426 AA.
AC Q9DCD9;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Adult male kidney cDNA, RIKEN full-length enriched library,
DE clone:0610041A01, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUP=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
```


OY 103 SSLTSEDSAVYFCAR 117
 Db 103 SSLTSEDSAVYFCAR 117

RESULT 5

Q9D8L4 PRELIMINARY; PRT; 473 AA.
 AC Q9D8L4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE 181006009Rik protein.
 GN IGH-1 OR 181006009R1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK007918; BAB25349.1; -
 DR HSP; P01842; 7FAB.
 DR MGD; MGI:96443; Igh-1.
 DR InterPro; IPR007110; Igh-like.
 DR InterPro; IPR003006; IGH_MHC.
 DR Pfam; PF00047; Igh; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 9.8%; Score 15; DB 11; Length 473;
 Best Local Similarity 100.0%; Pred. No. 7.6e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 SSLTSEDSAVYFCAR 117
 Db 103 SSLTSEDSAVYFCAR 117

RESULT 6

Q9JL75 PRELIMINARY; PRT; 109 AA.
 AC Q9JL75;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Anti-myosin immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=20448942; PubMed=10992488;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of
 streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 with cardiac myosin.";
 RL Infect. Immun. 68:5803-5808(2000).
 DR EMBL; AF206031; AAF69329.1; -
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; IGH_MHC.
 DR InterPro; IPR003596; Igh_v.
 DR Pfam; PF00047; Igh; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00406; IGH_MHC; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match 9.2%; Score 14; DB 11; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 GASVKMSCKASGYT 47
 Db 6 GASVKMSCKASGYT 19
 I|||||I|||||I

RESULT 7

Q9QXE9 PRELIMINARY; PRT; 117 AA.
 AC Q9QXE9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Immunoglobulin heavy chain V-D-J region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ225174; CAB65237.1; -
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; IGH_MHC.
 DR InterPro; IPR003596; Igh_v.
 DR Pfam; PF00047; Igh; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 9.2%; Score 14; DB 11; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 GASVKMSCKASGYT 47
 Db 15 GASVKMSCKASGYT 28
 I|||||I|||||I

RESULT 8

Q9QXF0 PRELIMINARY; PRT; 117 AA.
 ID Q9QXF0

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AC Q90XF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1; -
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match          9.2%; Score 14; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GASVKMSCKASGYT 47
DB 15 GASVKMSCKASGYT 28

RESULT 9
Q924Q0
ID Q924Q0 PRELIMINARY; PRT; 143 AA.
AC Q924Q0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE V165-D-J-C mu protein (Fragment).
GN V165-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kozono Y., Kozono H., Azuma T.;
RL "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069915; BAB63931.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;

Query Match          9.2%; Score 14; DB 11; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GASVKMSCKASGYT 47
DB 15 GASVKMSCKASGYT 28

AC Q925S3 PRELIMINARY; PRT; 147 AA.
AC Q925S3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MRP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RX PubMed-11819679;
RC STRAIN-BALB/c;
EX PubMed-11819679;
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240166; AAK43731.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match          9.2%; Score 14; DB 11; Length 147;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 LTSSEDSAVYFCARG 118
DB 88 LTSSEDSAVYFCARG 101

RESULT 11
Q8R3H6
ID Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 51.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; -
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
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DR PROSITE; PS50835; IG_LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;  
  
Query Match 9.2%; Score 14; DB 11; Length 474;  
Best Local Similarity 100.0%; Pred. No. 8.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 104 SLTSEDSAVYFCAR 117  
Db 104 SLTSEDSAVYFCAR 117  
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RESULT 12  
Q9JL77 PRELIMINARY; PRT; 110 AA.  
AC Q9JL77;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Anti-myosin immunoglobulin heavy chain variable region  
DE (Fragment).  
DE Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DBA/2;  
RX MEDLINE=20448942; PubMed=10992488;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "T-Cell-dependent antibody response to the dominant epitope of  
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
with cardiac myosin".  
RL Infect. Immun. 68:5803-5808(2000).  
DR EMBL; AF206029; AAF69327.1; -;  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG_LIKE; 1.  
FT NON_TER 1 110  
FT NON_TER 110 110  
SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;  
  
Query Match 8.5%; Score 13; DB 11; Length 110;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 125 DYWGQGTSTVTSS 137  
Db 98 DYWGQGTSTVTSS 110  
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RESULT 13  
Q99NG4 PRELIMINARY; PRT; 121 AA.  
AC Q99NG4;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Single chain Fv (Fragment).  
DE Mus musculus (Mouse).  
OS Plasmid pHEN1.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
  
QY 125 DYWGQGTSTVTSS 137  
Db 103 DYWGQGTSTVTSS 115  
|||||  
  
RESULT 15  
Q924Q1 PRELIMINARY; PRT; 142 AA.  
AC Q924Q1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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RX MEDLINE=98169018; PubMed=9510199;  
RA Hawlisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,  
RA Bautsch W., Kola A., Klos A., Koehl J.;  
RT "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";  
J Immunol. 160:2947-2958(1998).  
RL EMBL; AJ222590; CAA10890.1; -;  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG_LIKE; 1.  
KW Plasmid.  
FT NON_TER 1 121  
FT NON_TER 121 121  
SQ SEQUENCE 121 AA; 13255 MW; D293E4EBC8C59D5B CRC64;  
  
Query Match 8.5%; Score 13; DB 11; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 125 DYWGQGTSTVTSS 137  
Db 108 DYWGQGTSTVTSS 120  
|||||  
  
RESULT 14  
Q924R2 PRELIMINARY; PRT; 140 AA.  
AC Q924R2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE VH186.2-D-J-C mu protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
Hydroxy-3-Nitrophenyl)Acetyl (NP)."  
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB067788; BAB63273.1; -;  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG_LIKE; 1.  
FT NON_TER 1 140  
FT NON_TER 140 140  
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;  
  
Query Match 8.5%; Score 13; DB 11; Length 140;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 125 DYWGQGTSTVTSS 137  
Db 103 DYWGQGTSTVTSS 115  
|||||  
  
RESULT 15  
Q924Q1 PRELIMINARY; PRT; 142 AA.  
AC Q924Q1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
```

```

DT 01-MAR-2003 (trEMBLrel. 23, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN V23-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB069913; BAB63929.1;
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 142
FT NON_TER 142
SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Query Match 8.5%; Score 13; DB 11; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 DWYQGQGTSTVSS 137
Db 105 DWYQGQGTSTVSS 117

```

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 30, 2003, 22:10:26 ; Search time 3130.85 Seconds
(without alignments)
1999.191 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 816
Sequence: 1 MECSWVFLLSITGVHSQ.....TVSSAKTTPPPVPLPGSL 153

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_plus.p2n.model -DEV=xlh
-Q/cgn2_1/USPTO.spool/US08836455/runat_29082003_132901_22281/app_query.fasta_1.654
-DB=GenEmbl -QFWT-fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdl -LIST=45
-DOALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08836455_@CGN_1_1_3608_@runat_29082003_132901_22281 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -FGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl :
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*

29: em.vi.*
30: em.htg_hum.*
31: em.htg_inv.*
32: em.htg_other.*
33: em.htg_mus.*
34: em.htg_pin.*
35: em.htg_rod.*
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37: em.htg_vrt.*
38: em.sy.*
39: em.htgo_hum.*
40: em.htgo_mus.*
41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	816	100.0	461	6	AR164506 Sequence
2	816	100.0	461	6	BD085738 Methods o
3	725	88.8	411	10	AF124720 Mus muscu
4	630	77.2	471	10	AB050080 Mus muscu
5	621	76.1	1553	6	E08434 cDNA encodi
6	609	74.6	483	10	U39899 Mus musculu
7	603	73.9	1542	10	BC002121 Mus muscu
8	602	73.8	525	10	M28834 Mus musculu
9	602	73.8	540	6	A13735 variable re
10	601.5	73.7	1526	10	MMU555622 Mus muscu
11	599.5	73.5	1544	10	MUSIGBIH1
12	597.5	73.2	457	10	AY178830 Mus muscu
13	595	72.9	489	10	MU039900
14	590	72.3	489	10	AB050070 Mus muscu
15	581	71.2	1557	10	BC003435 Mus muscu
16	580	71.1	473	10	AB050071 Mus muscu
17	575	70.5	1573	10	BC018280 Mus muscu
18	574.5	70.4	1568	6	E33134 Humanized a
19	574.5	70.4	1570	6	A22261 M.musculus
20	574.5	70.4	1570	6	A77138 Sequence 6
21	569	69.7	1620	10	BC003888 Mus muscu
22	568.5	69.7	453	6	AR109947 Sequence
23	568.5	69.7	509	10	M19903 Mouse Ig re
24	568	69.6	1579	10	X13188 Mouse mRNA
25	568	69.6	1683	6	E35543 Transgenic
26	567.5	69.5	416	10	AF045892 Mus muscu
27	567.5	69.5	902	12	U49832 Synthetic s
28	566.5	69.4	450	10	AY178829 Mus muscu
29	565.5	69.3	1570	6	AR029102 Sequence
30	565	69.2	458	6	I05921 Sequence 37
31	565	69.2	458	6	I08811 Sequence 12
32	565	69.2	458	6	I09199 Sequence 38
33	565	69.2	458	10	M17953 Mouse Ig re
34	563	69.0	1500	10	MMAMST2
35	563	69.0	1581	6	A78881 Sequence 1
36	563	69.0	1581	10	MMIGHC2AA
37	563	69.0	1629	10	BC033451 Mus muscu
38	562.5	68.9	460	10	AB050073 Mus muscu
39	562	68.9	405	10	AB069863 Mus muscu
40	561.5	68.8	1083	6	AX556950 Sequence
41	561.5	68.8	1083	6	AX709549 Sequence
42	561.5	68.8	1413	6	AX556949 Sequence
43	561.5	68.8	1413	6	AX709548 Sequence
44	561.5	68.8	1558	10	AF466769 Mus muscu
45	561.5	68.8	9209	6	AR000007 Sequence

ALIGNMENTS

RESULT 1

REFERENCE AUTHORS TITLE	JOURNAL	COMMENT
<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 100-101.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 100-101.</p>		

FEATURES	SOURCE	BASE COUNT
1. <u>Age</u>	1990 Census	100,000
2. <u>Gender</u>	1990 Census	100,000
3. <u>Ethnicity</u>	1990 Census	100,000
4. <u>Marital Status</u>	1990 Census	100,000
5. <u>Occupation</u>	1990 Census	100,000
6. <u>Income</u>	1990 Census	100,000
7. <u>Home Ownership</u>	1990 Census	100,000
8. <u>Neighborhood</u>	1990 Census	100,000
9. <u>Crime Rate</u>	1990 Census	100,000
10. <u>Population Density</u>	1990 Census	100,000
11. <u>Unemployment Rate</u>	1990 Census	100,000
12. <u>Healthcare Access</u>	1990 Census	100,000
13. <u>Education Level</u>	1990 Census	100,000
14. <u>Transportation</u>	1990 Census	100,000
15. <u>Environmental Quality</u>	1990 Census	100,000
16. <u>Public Services</u>	1990 Census	100,000
17. <u>Community Engagement</u>	1990 Census	100,000
18. <u>Local Economy</u>	1990 Census	100,000
19. <u>Infrastructure</u>	1990 Census	100,000
20. <u>Quality of Life</u>	1990 Census	100,000

ORIGIN

Alignment
Pred. No.
Score:
Percent S
Best Loca
Query Matc
DB:

US-08-836

QY

Db

QY

Db QY Db QY

QY Db QY Db

Q \bar{Y} D \bar{b} Q \bar{Y} D \bar{b}

QY
Db
RESULT 3
AF124720

LOCUS AF124720 411 bp mRNA linear ROD 22-MAY-2001
DEFINITION Mus musculus immunoglobulin heavy chain mRNA, partial cds.
ACCESSION AF124720
VERSION AF124720.1 GI:14164544
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 411)
Tripathi, P.K., Qin, H., Bhattacharya-Chatterjee, M., Ceriani, R.L., Foon, K.A. and Chatterjee, S.K.
TITLE Construction and characterization of a chimeric fusion protein consisting of an anti-idiotypic antibody mimicking a breast cancer-associated antigen and the cytokine GM-CSF
JOURNAL Hybridoma 18 (2), 193-202 (1999)
MEDLINE 99306687
PUBMED 10380019
REFERENCE 2 (bases 1 to 411)
Chatterjee, S.K. and Tripathi, P.K.
AUTHORS Direct Submission
TITLE Submitted (29-JAN-1999) Internal Medicine, University of Kentucky,
JOURNAL 800 Rose Street, Lexington, KY 40536, USA
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1..411
/organism="Mus musculus"
/mol_type="mRNA"
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GTYLTSNMHWKQTPGGQLEWIGYIFLNAGTNYNOKFKGKATLTADTSSSTAYMQI
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BASE COUNT 102 a 101 c 107 g 101 t
ORIGIN
Alignment Scores:
Pred. No.: 1.12e-65 Length: 411
Score: 725.00 Matches: 136
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.27% Mismatches: 0
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DB: 10 Gaps: 0
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QY 1 MetGluCysSerTrpValPheLeuSerIleThrGlyValHisSerGln 20
Db 1 ATGAATGACGTGGGTCTTCCTCCCTGCTCAATACTACAGGTGCCACTCCGAC 60
QY 21 AlaTyrLeuGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
Db 61 GCTTATCTACAGCAGCTGGGGCTGAGCTGGTGGCTGGGCGCTCAGTGAAGATGTC 120
QY 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethIstTrpValLysGlnThrPro 60
Db 121 TGAAGGCTTCTGGCTACACATTGACAGTACATATGACATGCTGGGTAAGACAGACCT 180
QY 61 GlyGlnGlyLeuGlnTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrAsn 80
Db 181 GGACAGGGCTGGAATGGATGGAAATATTTTCCTGGAAATGCTGATCTACTACAAT 240
QY 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet 100
Db 241 CAGAAGTTTAAAGCGAGGCTCATTTGACTGCAGACACATCTCCACAGCAGCTCAATG 300
QY 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120

Db 301 CAGATCAGCAGCCTGACATCTGAAGACTCTCGGCTCTATTCTCTGCAAGAGGAACTGG 360
QY 121 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 137
Db 361 GAGGGTCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
RESULT 4
LOCUS AB050080 471 bp mRNA linear ROD 02-APR-2002
DEFINITION Mus musculus VH9H8 mRNA for anti-A/U antibody, partial cds.
ACCESSION AB050080
VERSION AB050080.1 GI:19909935
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Kitagawa, Y. and Okuhara, E.
TITLE The separation of three antibody populations from anti-poly(A).poly(U) antibodies elicited in mice or rabbits and antigenic features of poly(A).poly(U)
JOURNAL Mol. Immunol. 19 (2), 257-266 (1982)
MEDLINE 82245325
PUBMED 6178956
REFERENCE 2
AUTHORS Kitagawa, Y.
TITLE anti-dsRNA (A/U) Ab VH region VH9H8
JOURNAL Published Only in Database (2002)
REFERENCE 3 (bases 1 to 471)
AUTHORS Kitagawa, Y.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural University, Biotechnology Institute; Minami 2-2, Ogata, Akita 010-0444, Japan (E-mail: kitagawa@agri.akita-pu.ac.jp, URL: www.akita-pu.ac.jp, Tel: 81-185-45-2026 (ex.400), Fax: 81-185-45-2678)
FEATURES
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BASE COUNT 114 a 126 c 121 g 110 t
ORIGIN
Alignment Scores:
Pred. No.: 7.75e-56 Length: 471
Score: 630.00 Matches: 128
Percent Similarity: 85.26% Conservative: 5
Best Local Similarity: 82.05% Mismatches: 19
Query Match: 77.21% Indels: 4
DB: 10 Gaps: 3
US-08-836-455-4 (1-153) x AB050080 (1-471)
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Db 5 GTCGACATGGGATGGACCGGGGTCTTCCTCATCTCCATCAATAACTACAGGTGTCAC 64

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Qy 19 SerGlnAlaTyrIleuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLys 38
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Qy 39 MetSerCysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGln 58
Db 125 ATGTCCTGCAAGGCTTCTGGCTACACATTACCAATGATACATATGCAATGCTGGTAAACAG 184

Qy 59 ThrProGlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyr 78
Db 185 ACACCTGGACAGGCGCTGGATGGATGATATATTTCTCG---AATGCTGGTACTAAC 241

Qy 79 TyrAsnGlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAla 98
Db 242 TACAATCAGAAGTTCAAGGCGCAAGCCACATTCAGCCGACACACATCTCCAGCACAGCC 301

Qy 99 TyrMetGlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGly 118
Db 302 TACATGCAGATCAGCAGCCCTGACATCTGAAGACTCTCGGTCTATTCTGTGCAAGAGGG 361

Qy 119 AsnTrpGluGlyAla---LeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 137
Db 362 GAGTATGGTAAACCCCTGGTTGGTTACTGGGGCCAGGGACTCTGGTCACTGTCTCTGCA 421

Qy 138 AlaLysThrThrProProValTyrProLeuValProGlySerLeu 153
Db 422 GCCAAACACAGCCCAACCGTTTATCCCTTGGCCCTGGCCCTGGAAGCTTG 469

RESULT 5
E08434
LOCUS E08434 1553 bp DNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding H-chain of anti-TMV-antibody.
ACCESSION E08434
VERSION E08434.1 GI:2176551
KEYWORDS JP 1994319396-A/7.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1553)
AUTHORS Saito,Y., Kogiku,T., Kamishiro,T., Murafuji,H., Takami,M. and Fumino,M.
TITLE PLANT FOR PRODUCTION ANTIVIRAL ANTIBODY AND METHOD FOR CREATING THE SAME PLANT
JOURNAL Patent: JP 1994319396-A 7 22-NOV-1994; JAPAN TOBACCO INC, KURARAY CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1994319396-A/7
PD 22-NOV-1994
PF 07-MAY-1993 JP 1993131208
PI SAITO YASUO, KOGIKU TOSHIHIKO, KAMISHIRO TAKASHI, PI MURAFUJI HITOAKI, TAKAMI MASAOKI, FUMINO MASAYASU
PC A01H5/00,C12N15/13,C12P21/08;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT source 1..1553
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FT anti-TMV-antibody'
FT 5'UTR 1..55
FT CDS 56..1453
FT /product='H-chain of anti-TMV-antibody' FT
3'UTR 1454..1553.
Location/Qualifiers
source 1..1553
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Query Match: 76.10% Indels: 4
DB: 6 Gaps: 2

US-08-836-455-4 (1-153) x E08434 (1-1553)
Qy 1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln 20
Db 56 ATGAATGTAACCTGGATACCTCTTTTATCTGCTCACTAACTTCAGGTGCTACTCAG 115
Qy 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
Db 116 GTTCAGCTCCAGCAGTCTGGGGCTGAGCTGCAAGACCTGGGCTTCAGTCAAGTTGCT 175
Qy 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro 60
Db 176 TGAAGGCTTCTGGCTACACCTTTTACTAGCTACGATGAGTGGTGGTAAACACAGAGCC 235
Qy 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
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Qy 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet 100
Db 296 CAGAAATTCAAGGGCAAGGCCACATTGACTGCAATAAATCCTCCACAGCAGCCTACATG 355
Qy 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGly----- 118
Db 356 CAACTCAGCGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGAGGGGGT 415
Qy 119 ---AsnTrp---GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSer 136
Db 416 TACTCTGGTCCGACTATGCTATGAGTACTGGGTCAAGGAACCTCAGTCACGCTCTCC 475
Qy 137 SerAlaLysThrThrProProValTyrProLeuValProGlySer 152
Db 476 TCAGCCAAACAGCACACCCCATCTGTCTATCCACTGGCCCTGGATCT 523

RESULT 6
MMU39899 483 bp DNA linear ROD 21-NOV-1996
LOCUS MMU39899
DEFINITION Mus musculus anti-glycoprotein-B of human Cytomegalovirus immunoglobulin Vh chain gene, partial cds.
ACCESSION U39899
VERSION U39899.1 GI:1680666
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 483)
AUTHORS Schoppel,K., Hassfurth,E., Britt,W., Ohlin,M., Borrebaeck,C.A. and Mach,M.
TITLE Antibodies specific for the antigenic domain 1 of glycoprotein B (gpUL55) of human cytomegalovirus bind to different substructures
JOURNAL Virology 216 (1), 133-145 (1996)
MEDLINE 96187797
REFERENCE 8614980
AUTHORS 2 (bases 1 to 483)
Schoppel,K.
Direct Submission
Submitted (02-NOV-1995) Michael Mach, Institute of Virology, University Erlangen-Nuernberg, Schlossgarten 4., 91054 Erlangen, Germany
FEATURES Location/Qualifiers

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BASE COUNT 117 a 118 c 130 g 118 t
ORIGIN

Alignment Scores:
Pred. No.: 1.15e-53 Length: 483
Score: 609.00 Matches: 117
Percent Similarity: 85.06% Conservative: 14
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Query Match: 74.63% Indels: 4
DB: 10 Gaps: 1

US-08-836-455-4 (1-153) x MMU39899 (1-483)
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QY 21 AlaTyrLeuGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
DB 61 GTTCAGCTCCAGCAGCTCTGGGCTGAGCTGGTGAGCCCTGGTCCCTCAGTGAAGATTCC 120
QY 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro 60
DB 121 TGCAGAGCTCTGGCTATGCATTCAGTCTGCTACTGCTAACTGGTGAAGCAGAGGCCT 180
QY 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
DB 181 GGACAGGGTCTTGAGTGGATGGACAGATTTATCTCGAGATGGTGATATGACTACAAAT 240
QY 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet 100
DB 241 GGAAATTCAGGGTAAAGCCACACTGACTGACGACAAATCTCCAGCAGCAGCTACATG 300
QY 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGly----- 118
DB 301 CAGCTCAGCAGCCTAACATCTGAGGACTCTGGGCTCTATTCTGTGCAAGAGGTTACGAC 360
QY 119 -----AsnTrpGluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSer 136
DB 361 GAAGTGGATATTACTTTCTTGGACTACTGGGGTCAAGGAACCTCAGTCCACCGTCTCC 420
QY 137 SerAlaLysThrThrProProValTyrProLeuValPro 150
DB 421 TCAGGCAAAACACACACCCCATCAGTCTATCCACTGGCTCCT 462

RESULT 7
BC002121 1542 bp mRNA linear ROD 16-APR-2003
LOCUS Mus musculus immunoglobulin heavy chain 4 (serum IgG1), mRNA (cDNA
DEFINITION clone MGC:6628 IMAGE:3491766), complete cds.
ACCESSION BC002121
VERSION BC002121.1 GI:12805308
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

REFERENCE
AUTHORS

1 (bases 1 to 1542)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Hellon,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>
Contact: (Dickson, Mark) mcdpaxil@stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 8 Row: a Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, similarity but not identity to protein.

FEATURES

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CDS

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VVDISKDDPEVQESWFDVVEHTAQPKPREQFNSTFRSVELPIMHQDLNGLNGKEFK
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Query Match: 73.90% Indels: 0
Gaps: 10
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QY 1 MetGluCysSerTrpValPheLeuLeuSerIleThrThrGlyValHisSerGln 20
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QY 21 AlaTyrLeuGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
Db 93 GTTCAGCTGCAGCAGCTCGAGCTGAGCTGGCAGGCGCTGGGCTTCAGTGAAGATGCC 152
QY 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethHisTrpValLysGlnThrPro 60
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QY 61 GlyGlnGlyLeuGluTyrPileGlyAsnIlePheProGlyAsnGlyAspThrTyrAsn 80
Db 213 AGCAGGGCTTGGATGGATGGAGATTATCTCTGGAAGTGTAACACTTACTACAAT 272
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Db 273 GAAAGTTCAGGCGCAAGCCACACTGACTGCAGACAAATCTCCACAGCAGCTACATG 332
QY 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
Db 333 CAGCTCAGCAGCTGACATCTGAGGACTGCGAGCTCTATTCTCTGCAAGATGGGGGAG 392
QY 121 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr 140
Db 393 CCTGGCAGCTGGACTACTGGGCGCAAGCCACCATCATCATCAGTCTCTCTCAGCCAAA 452
QY 141 ThrProProValTyrProLeuValProGlySer 152
Db 453 ACACCCCATCTGTCTATCCACTGGCCCTGGATCT 488
RESULT 8
MUSIGHALPA
LOCUS
DEFINITION
Mus musculus IgG2a chain (anti-pseudomonas aeruginosa lipoprotein I
antibody) mRNA, 5' end.
ACCESSION
M28834.1 GI:576597
KEYWORDS
V-segment; anti-lipoprotein antibody; immunoglobulin G2a gamma
chain; immunoglobulin heavy chain.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
Marget,M., Eckhardt,A., Ehret,W., von Specht,B.U., Duchene,M. and
Domdey,H.
Cloning and characterization of cDNAs coding for the heavy and
light chains of a monoclonal antibody specific for Pseudomonas
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aeruginosa outer membrane protein I
Gene 74 (2), 335-345 (1988)
MEDLINE
89232725
PUBMED
3149944
COMMENT
On Nov 28, 1994 this sequence version replaced gi:342018.
Original source text: Mus musculus (strain BALB/c, sub_species
domesticus) hybridoma cDNA to mRNA.
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Location/Qualifiers
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Best Local Similarity: 76.32% Mismatches: 25
Query Match: 73.77% Indels: 2
Gaps: 1
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QY 1 MetGluCysSerTrpValPheLeuLeuSerIleThrThrGlyValHisSerGln 20
Db 49 ATGGAAGGCACTGGATCTTCTCTCTCTTTCAGTTACTGCAGGTGCCACTCCAG 108
QY 21 AlaTyrLeuGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
Db 109 GTCCAGCTTCAGCAGCTCGGGCTGAACTGGCAAAACCTGGGCGCTCAGTGAAGATGCC 168
QY 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethHisTrpValLysGlnThrPro 60
Db 169 TGAAGGCTTCTGGCTACACCTTACTTGGATGGTGGTGGTGGTGGTGGTGGTGGTGG 228
QY 61 GlyGlnGlyLeuGluTyrPileGlyAsnIlePheProGlyAsnGlyAspThrTyrAsn 80
Db 229 GGACAGGGCTGGAAAGGATGGATACATTAATCTTAACTGATGTTATCTGATACAA 288
QY 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet 100
Db 289 CAGAAGCTTCAAGGACCAAGCCACATTGACTGCAGACAAATCTCCACAGCAGCTACATG 348
QY 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGly----- 118
Db 349 CAATGAGCAGCTGACATCTGAGGACTCTGAGGACTCTGAGTCTATTATTGTCACAGAA 408
QY 119 AsnTrpGluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAla 138
Db 409 AACTAGAGGGGCTATGGACTACTGGGTCAGGAACCTCAGTCAACCGTCTCTCTCAGCC 468
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[illegible]

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polyA_site 1510
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BASE COUNT 396 a 436 c 360 g 334 t
ORIGIN
Alignment Scores:
Pred. No.: 2.5e-52 Length: 1526
Score: 601.50 Matches: 115
Percent Similarity: 82.58% Conservative: 13
Best Local Similarity: 74.19% Mismatches: 24
Query Match: 73.71% Indels: 3
DB: 10 Gaps: 1

US-08-836-455-4 (1-153) x MMU555622 (1-1526)

Qy 1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln 20
Db 13 ATGGAATGGAGTTGGATATTCTCTTCTCTCTGTCAGGAACCTGCAGGTGCCACTCTGAG 72

Qy 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
Db 73 GTCCAGCTGCAGCAGCTCTGGACCTGAGCTGATAGGCTGGGGCTTCAGTGAAGATGTC 132

Qy 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro 60
Db 133 TGCAAGGCTCTGGATACACATTCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 192

Qy 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
Db 193 GGGCAGGCGCTTGATGGATGATATTAATCTTACATGATGCTGCTGCTGCTGCTGCTGCT 252

Qy 81 GlnLysPheLysGlyLysAlaSerLeuThraAlaSerThrSerSerThrAlaTyrMet 100
Db 253 GAGAAGTTCAAGCAGGCGACCTGACTTACAGCAAACTCTCCAGCAGCCTACATG 312

Qy 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
Db 313 GAGCTCAGCAGCCTGACTCTGAGGAGCTCTGCGGTCTATTACTGTGCAAGAGGACTTAT 372

Qy 121 -----GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 137
Db 373 TACTACGGTAGTAGGATTGACTGCTGGGGCGAAGCAGCAGCAGCAGCAGCAGCAGCAGC 432

Qy 138 AlaLysThrThrProProValTyrProLeuValProGlySer 152
Db 433 GCCAAAGCAGACCCCATCTGCTATCCACTGGCCCTGGATCT 477

RESULT 11
MUSIGBIH1
LOCUS Mus musculus mRNA for immunoglobulin gamma-3 heavy chain precursor,
DEFINITION complete cds.
ACCESSION D14625
VERSION D14625.1 GI:286089
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 1544)
Takahashi,S., Itoh,J., Nose,M., Ono,M., Yamamoto,T. and Kyogoku,M.
Cloning and cDNA sequence analysis of nephritogenic monoclonal
antibodies derived from an MRL/lpr lupus mouse
Mol. Immunol. 30 (2), 177-182 (1993)
93156722
8429833
REFERENCE
2
Ono,M., Yamamoto,T., Kyogoku,M. and Nose,M.
Sequence analysis of the germ-line VH gene corresponding to a
nephritogenic antibody in MRL/lpr lupus mice
Clin. Exp. Immunol. 100 (2), 284-290 (1995)
JOURNAL
MEDLINE
AUTHORS
TITLE
JOURNAL

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95262286
PUBMED 7743668
REFERENCE 3 (bases 1 to 1544)
AUTHORS Nose,M.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1993) Masato Nose, Tohoku University School of
Medicine, Dept. of Pathology; 2-1 Seiry-cho Aoba-ku, Sendai,
Miyagi 980, Japan (E-mail:d22181@cctu.cc.tohoku.ac.jp,
Tel:81-22-273-9042, Fax:81-22-234-1986)
FEATURES
Location/Qualifiers
Source 1..1544
/organism="Mus musculus"
/mol_type="mRNA"
/strain="MRL/MpJ-lpr/lpr"
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/chromosome="14"
/clone="pB1H1"
/clone_lib="pbluescript KS(+)"
/dev_stage="adult"
1..32
33..1445
/feature="precursor of C and V-D-J regions from 7B6.8"
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/protein_id="BAA03476.1"
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SSVTGLGVKGYFPEPVTVKWNYSALSGVTVSSVLSGLYSSLSLTVPSSTWPSQ
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DMRKEFKCKVKNNKALPAPIERTISKPKRAQTPQVTTIPPPREQMSKKRSLTCLV
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33..89
sig_peptide
mat_peptide
90..1442
V_region
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90..452
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453..1442
C_region
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1446..1544
3'UTR
polyA_signal 1514..1519
BASE COUNT 402 a 448 c 368 g 326 t
ORIGIN
Alignment Scores:
Pred. No.: 4.08e-52 Length: 1544
Score: 599.50 Matches: 116
Percent Similarity: 84.42% Conservative: 14
Best Local Similarity: 75.32% Mismatches: 21
Query Match: 73.47% Indels: 3
DB: 10 Gaps: 1

US-08-836-455-4 (1-153) x MUSIGBIH1 (1-1544)

Qy 1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln 20
Db 33 ATGGAATGGAGCGGGGCTCTTCTCTCTCTGTCAGTAACCTGCAGGTGCCACTGCCAG 92

Qy 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
Db 93 GTCCAACTGCAGCAGCTCTGAGCTGAGCTGGTAAAGCCCTGGGACTTCAGTGAAGATGCC 152

Qy 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro 60
Db 153 TGCAGGCTCTGGATACACCTTCTACTACTGATAGGTGGGTAAAGCAGAGGCT 212

Qy 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
Db 213 GGACATGGCCCTTGAGTGGAGTATTTACCCCTGGAGGTGGTTTACTACTAACAATACAT 272

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Db	68	GTGCAACTGCAGCAGCTGGGGCTGACCTGGTGAAGCCTGGGGCTCAGTGAAGATGCC	127	
Qy	41	CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethHisTrpValLysGlnThrPro	60	
Db	128	TGCAAGGCTTCTGGCTACACATTTACCAGTTTACAAATATGCAC TGGGTAAAGCAGACACCT	187	
Qy	61	GlyClnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn	80	
Db	188	GGACAGGGCTGGGAATGCGATGGAGTTATTATTCAGGNAATGGTGATACTTCTCAGCT	247	
Qy	81	GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet	100	
Db	248	CAGAAAGTTCAAGCAGGCCACCATGCTGCAGACAAATCTCCACACAGCCTACATG	307	
Qy	101	GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp	120	
Db	308	CAGCTCAGCAGCCTGCATCATCTGAGGACTCTGCGGTCTATTACTGTTCAAGAGGGGGA	364	
Qy	121	GluCysAlaLeuAspTyrTrpGlyClnGlyThrSerValThrValSerSerAlaLysThr	140	
Db	365	CGCGGTATATAATGGCTACTTGGGGTCAAGGAACCTCAGTCACCGCTCTCTCAGCCAAAACG	424	
Qy	141	ThrProProValTyrProLeu	148	
Db	425	ACACCCCACTGTCTATCCACTG	448	
RESULT 13	MMU39900	489 bp	DNA linear	ROD 22-NOV-1996
LOCUS	Mus musculus anti-glycoprotein-B of human Cytomegalovirus			
DEFINITION	immunoglobulin Vh chain gene, partial cds.			
ACCESSION	U39900			
VERSION	U39900.1	GI:1680668		
KEYWORDS				
SOURCE	Mus musculus (house mouse)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 489)			
AUTHORS	Schoppel,K., Hassfurth,E., Britt,W., Ohlin,M., Borrebaeck,C.A. and Mach,M.			
TITLE	Antibodies specific for the antigenic domain 1 of glycoprotein B (gpUL55) of human cytomegalovirus bind to different substructures			
JOURNAL	Virology 216 (1), 133-145 (1996)			
MEDLINE	86187797			
PUBMED	8614980			
REFERENCE	2 (bases 1 to 489)			
AUTHORS	Schoppel,K.			
TITLE	Direct Submission			
JOURNAL	Submitted (02-NOV-1995) Michael Mach, Institute of Virology, University Erlangen-Nuernberg, Schlossgarten 4., 91054 Erlangen, Germany			
FEATURES	Location/Qualifiers			
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	KLK"			
BASE COUNT	112 a 122 c 130 g 125 t			
ORIGIN				
Alignment Scores:				

Pred. No.: 3,22e-52 Length: 489
 Score: 595.00 Matches: 117
 Percent Similarity: 81.65% Conservative: 12
 Best Local Similarity: 74.05% Mismatches: 19
 Query Match: 72.92% Indels: 10
 DB: 10 Gaps: 2

US-08-836-455-4 (1-153) x MMU39900 (1-489)

QY 1 MetGluCysSerTrpValPheLeuLeuSerIleThrGlyValHisSerGln 20
 DB 1 ATGAATGACGCTGGGTCTTCTCTCCCTCAATAACTCAGGTGCCATTGCCAG 60
 QY 21 AlaTyrLeuGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
 DB 61 GTCCAGCTGCAGCAGCTGGACCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATTCC 120
 QY 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethIstTrpValLysGlnThrPro 60
 DB 121 TGCACAGCTTCTGGCTACACATTTCAGTGGCTCTTGGATGAACCTGGGTGAAGCAGAGCCCT 180
 QY 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrAsn 80
 DB 181 GGACAGGCTTTCAGTGGATGGACGGATTATCTCTGGAGATGAGATTAATACTACAGT 240
 QY 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet 100
 DB 241 GGAATAATTCAGGCAAGGCACACTGACTGCAGACAAATCCCTCCAGCAGACGCTACTTG 300
 QY 101 GlnIleSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
 DB 301 CAATCAGCAGCTGACCTCTGTGGACTTGCCTGCTATTTCTGTGCAAGAGAT----- 354
 QY 121 GluGly-----AlaLeuAspTyrTrpGlyGlnGlyThrSer 132
 DB 355 GATGGTACTACCTGCTTTGATTACTATGCTATGACTATTGGGTCAAGGAACCTCA 414
 QY 133 ValThrValSerSerAlaLysThrThrProProValTyrProLeuValPro 150
 DB 415 GTCACCGTCTCTCAGCAAAACAACACCCCATCATCAGTCTATCCCTGCTGCTCT 468

RESULT 14
 AB050070 469 bp mRNA linear ROD 02-APR-2002
 LOCUS
 DEFINITION Mus musculus VH6G9 mRNA for anti-dsRNA (RDV-RNA) antibody, partial cds.

AB050070.1 GI:19909916

AB050070 Mus musculus (house mouse)

AB050070 Mus musculus

AB050070 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AB050070 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AB050070 Kitagawa, Y., Matsumoto, T., Okuhara, E. and Shikata, E.

AB050070 Immunogenicity of rice dwarf virus-ribonucleic acid

AB050070 Tohoku J. Exp. Med. 122 (4), 337-343 (1977)

AB050070 78034786

AB050070 918970

AB050070 Kitagawa, Y.

AB050070 anti-dsRNA (RDV-RNA) Ab VH region-VH6G9

AB050070 Published Only in Database (2002)

AB050070 3 (bases 1 to 469)

AB050070 Direct Submission

AB050070 Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural

AB050070 University, Biotechnology Institute; minami 2-2, Ogata, Akita

AB050070 010-0444, Japan (E-mail: kitagawa@agri.akita-pu.ac.jp,

AB050070 URL: www.akita-pu.ac.jp/, Tel: 81-185-45-2026 (ex.400),

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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALE/c"
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 /cell_type="B cell"
 1. .469
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 9. .>467
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 /db_xref="GI:19909917"
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 GTFSSHWTHGKORPGQGLWGIYPGDSDRYNKKFKGKSLTKADKSSSTAYIQLS
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BASE COUNT 111 a 115 c 123 g 120 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1e-51 Length: 469
 Score: 590.00 Matches: 113
 Percent Similarity: 83.33% Conservative: 17
 Best Local Similarity: 72.44% Mismatches: 20
 Query Match: 72.30% Indels: 6
 DB: 10 Gaps: 3

US-08-836-455-4 (1-153) x AB050070 (1-469)

QY 1 MetGluCysSerTrpValPheLeuLeuSerIleThrGlyValHisSerGln 20
 DB 9 ATGAATGACGCTGGGTCTTCTCTCCCTCAATAACTCAGGTGCCATTGCCAG 68
 QY 21 AlaTyrLeuGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
 DB 69 GTTCAGCTCCAGCAGCTGGGGCTGAAGTGGCAAGACCTGGGCTTCAGTGAAGTTGCTC 128
 QY 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethIstTrpVal-----LysGln 58
 DB 129 TGAAGGCTTCTGGCTACACCTTTAGTAGT-----CACTGGATACATGTTAAACAG 179
 QY 59 ThrProGlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyr 78
 DB 180 AGCCCTGGACAGGGCTCGAGTGGATGGGCCATTATCTCTGGAGATGGTCTTAGG 239
 QY 79 TyrAsnGlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAla 98
 DB 240 TACAATAAGAAGTTCAAGGGCAAGGCTCATTTGACTGCAGATAAATCTCCAGCAGACC 299
 QY 99 TyrMetGlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArg--- 117
 DB 300 TACATACAACTCAGCAGCTGGGATCGAGGACTCTCGGTCTATTACTGTGCANGAAT 359
 QY 118 GlyAsnTrpGluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 137
 DB 360 GGTAACTTCGACCCCTCTTTGATTATTGGGCAAGGAGACTCTGGTCACTGTCTCTGCA 419
 QY 138 AlaLysThrThrProProValTyrProLeuValProGlySerLeu 153
 DB 420 GCCAAAACAGCAGACCCCGCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 467

RESULT 15

BC003435

LOCUS

DEFINITION

BC003435 Mus musculus immunoglobulin heavy chain 4 (serum IgG1), mRNA (cdna

BC003435 clone MGC:6486 IMAGE:2646928), complete cds.

ACCESSION

BC003435.1

VERSION

BC003435.1

KEYWORDS

GI:13097380

SOURCE

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

LOCUS

BC003435

DEFINITION

BC003435 Mus musculus immunoglobulin heavy chain 4 (serum IgG1), mRNA (cdna

BC003435 clone MGC:6486 IMAGE:2646928), complete cds.

ACCESSION

BC003435.1

VERSION

BC003435.1

KEYWORDS

GI:13097380

SOURCE

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 30, 2003, 22:10:01 ; Search time 230.013 Seconds
(without alignments)
1795.608 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 816
Sequence: 1 MEC5WFLFLSITGVSQ.....TVSSAKTTPPVYPLVPGSL 153

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	816	100.0	461	18	AAT85150 Murine monoclonal
2	816	100.0	461	20	AAV83773 Antibody 11D10 hea
3	816	100.0	461	25	AAV51274 Mouse 11D10 antibo
4	621	76.1	1553	16	AAQ79930 Anti-tobacco mosai
5	602	73.8	540	10	AAQ91645 Heavy chain of mon
6	599	73.4	736	25	ABX16571 Mouse DNA encoding
7	574.5	70.4	1570	12	AAQ12637 Monoclonal antibod
8	570	69.9	725	21	AAA43821 Mouse secreted exp
9	568	69.6	1683	20	AAV61084 Mouse immunoglobul
10	565	69.2	458	10	AAV81146 2H7 Vh sequence.
11	565	69.2	459	20	AAV82337 Mouse antibody 2H7
12	565	69.2	459	22	AAH22070 2H7 heavy chain va
13	565	69.2	491	18	AAV70868 Mouse 2H7 antibody
14	565	69.2	491	19	AAV18557 Mouse 2H7 antibody
15	565	69.2	491	19	AAV03926 Mouse 2H7 antibody
16	565	69.2	491	19	AAV18593 Mouse 2H7 antibody
17	565	69.2	518	18	AAT36316 2H7 antibody heavy
18	565	69.2	520	18	AAT51042 Coding sequence fo
19	563	69.0	1392	18	AAV62936 3F4 (Chimeric) hum
20	563	69.0	1395	18	AAV62935 Murine anti-porcine
21	563	69.0	1581	14	AAQ48037 Monoclonal antibod
22	563	69.0	3400	18	AAT62937 3F4 human C2/G4 ch
23	563	69.0	5300	18	AAT62938 3F4 human IgG4 exp
24	561.5	68.8	1083	24	ABD45753 Human CH2 domain d
25	561.5	68.8	1083	25	ABD24017 Antibody C2B8 CH2
26	561.5	68.8	1413	21	AAAG3531 DNA encoding a dim
27	561.5	68.8	1413	24	AAAG4752 Human C2B8 antibod
28	561.5	68.8	1413	25	ABD24016 Antibody C2B8 heav
29	561.5	68.8	9208	15	ABX65629 TCAE8 expression v
30	561.5	68.8	9209	25	ABX94203 Vector contg. TCAE
31	561.5	68.8	19001	19	AAV61793 Traget plasmid Mol
32	560.5	68.7	1392	19	AAV70129 Anti-Fas MAB HFE7A
33	560.5	68.7	1392	21	AAA72108 cDNA encoding mous
34	560.5	68.7	1392	21	AAAL1546 Murine anti-Fas an
35	560.5	68.7	1392	24	ABL45925 Mouse humanised an
36	560.5	68.7	1392	24	ABL48668 Humanised anti-Fas
37	555	68.0	420	22	AAF81910 Anti-CA125 bifunct
38	554.5	68.0	1314	24	ABD29310 Human penton base
39	554.5	68.0	1314	25	ABX12746 DNA encoding porti
40	554.5	68.0	1516	24	ABD29308 Human penton base
41	554.5	68.0	1516	25	ABX12744 DNA encoding mouse
42	554.5	68.0	1582	16	AAQ94037 MAB 55.1 heavy cha
43	552.5	67.7	409	21	AAZ87715 Anti-human VEGF re
44	552.5	67.7	409	22	AAV70192 Anti-human Flt-1 m
45	552	67.6	468	19	AAV05544 Nucleotide sequenc

ALIGNMENTS

RESULT 1
AAT85150
ID AAT85150 standard; cDNA; 461 BP.
XX AAT85150;
AC AAT85150;
XX
DT 25-MAR-2003 (updated)
DT 04-JAN-1998 (first entry)
XX
DE Murine monoclonal anti-idiotypic antibody 11D10 VH cDNA.
XX
KW Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
KW human milk fat globule; HMF; tumour; breast cancer; vaccine; ss.
XX
XX Mus musculus.
OS
XX Key Location/Qualifiers
FH

Pred. No.: 1.53e-70 Length: 461
 Score: 816.00 Matches: 153
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-08-836-455-4 (1-153) x AAV83773 (1-461)

QY 1 MetGluCysSerTrpValPheLeuSerIleThrThrGlyValHisSerGln 20
 DB 1 ATGGAATGACGTGGGTCTTCTCTCTCTCAATACTACAGGTGTCCACTCCAG 60
 QY 21 AlaTyrLeuGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
 DB 61 GCTTATCTACAGCAGCTGGGGCTGAGTGTGAGGTCTGGGGCTCAGTGAAGATGCC 120
 QY 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethIstTrpValLysGlnThrPro 60
 DB 121 TGCAGAGCTTCTGGCTACACATTGACCAATGACATGCGTGGTAAAGCAGACACCT 180
 QY 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrAsn 80
 DB 181 GGACAGGCTTGAATGGATGGAAATATTTTCTGGAATGGTATCTTACTACAA 240
 QY 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet 100
 DB 241 CAGAAGTTTAAGGCAAGGCTCATTTGACTGCAGACACATCTCCAGCAGCCTACATG 300
 QY 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
 DB 301 CAGATCAGCAGCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGAACTGG 360
 QY 121 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr 140
 DB 361 GAGGTGCTCTGACTACTGGGTCAAGGAACCTCAGTCACTCCCTCCTCAGCCAAACG 420

QY 141 ThrProProValTyrProLeuValProGlySerLeu 153
 DB 421 ACACCCGCCCTCTATCCACTGGTCCCTGGAAGCTTG 459

RESULT 3

ID AAL51274 standard; cDNA; 461 BP.

XX AC AAL51274;

XX 20-MAR-2003 (first entry)

XX Mouse 11D10 antibody heavy chain variable region coding sequence.

XX Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; HMFG;
 KW carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour;
 KW CEA-associated tumour; anti-idiotype antibody.

XX Mus musculus.

XX Key Location/Qualifiers

XX CDS 1..459

XX /tag= a

XX /partial

XX /product= "Mouse 11D10 anti-idiotype antibody heavy chain

XX variable region"

XX /note= "No stop codon is given"

XX sig_peptide 1..57

XX /tag= b

XX mat_peptide 58..459

XX /tag= c

XX WO20020292012-A2.

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

PF 17-MAY-2002; 2002WO-US15840.
 XX
 PR 17-MAY-2001; 2001US-0861294.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 PI Chatterjee M, Foon KA;
 XX
 XX WPI; 2003-129216/12.
 DR P-PSDB; AAO16293.
 XX
 XX Use of anti-idiotypic antibodies for human milk fat globules (HMFG)- or
 PT carcinoembryonic antigen (CEA)-associated tumor for delaying the
 PT development of, or treating a HMFG- or CEA-associated tumor (e.g.
 PT breast tumor) in humans
 XX
 XX Disclosure; Fig 2; 98pp; English.
 XX
 CC The invention comprises a method for delaying the development of, or
 CC treating a tumor that is associated with human milk fat globules (HMFG)
 CC or carcinoembryonic antigen (CEA). The method of the invention involves
 CC administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an
 CC anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for
 CC delaying the development, of or treating HMFG/CEA-associated tumours. The
 CC present DNA sequence encodes the heavy chain variable region of the mouse
 CC 11D10 anti-idiotype antibody.
 XX
 SQ Sequence 461 BP; 112 A; 121 C; 119 G; 109 T; 0 other;

Alignment Scores:

Pred. No.: 1.53e-70 Length: 461
 Score: 816.00 Matches: 153
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0

US-08-836-455-4 (1-153) x AAL51274 (1-461)

QY 1 MetGluCysSerTrpValPheLeuSerIleThrThrGlyValHisSerGln 20
 DB 1 ATGGAATGACGTGGGTCTTCTCTCTCTCAATACTACAGGTGTCCACTCCAG 60
 QY 21 AlaTyrLeuGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
 DB 61 GCTTATCTACAGCAGCTGGGGCTGAGTGTGAGGTCTGGGGCTCAGTGAAGATGCC 120
 QY 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethIstTrpValLysGlnThrPro 60
 DB 121 TGCAGAGCTTCTGGCTACACATTGACCAATGACATGCGTGGTAAAGCAGACACCT 180
 QY 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
 DB 181 GGACAGGCTTGAATGGATGGAAATATTTTCTGGAATGGTATCTTACTACAA 240
 QY 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet 100
 DB 241 CAGAAGTTTAAGGCAAGGCTCATTTGACTGCAGACACATCTCCAGCAGCCTACATG 300
 QY 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
 DB 301 CAGATCAGCAGCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGAACTGG 360
 QY 121 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr 140
 DB 361 GAGGTGCTCTGACTACTGGGTCAAGGAACCTCAGTCACTCCCTCCTCAGCCAAACG 420
 QY 141 ThrProProValTyrProLeuValProGlySerLeu 153
 DB 421 ACACCCGCCCTCTATCCACTGGTCCCTGGAAGCTTG 459

RESULT 4

AAQ79930

ID AAQ79930 standard; cDNA to mRNA; 1553 BP.
 XX AC
 XX XX
 XX AAQ79930;
 DT
 XX 01-SEP-1995 (first entry)
 DE
 XX Anti-tobacco mosaic virus monoclonal Ab heavy chain cDNA.
 KW Tobacco mosaic virus; TMV; monoclonal antibody;
 KW heavy chain; virus-resistant plants; biofarming; ss.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 XX CDS 56..1453
 FT /*tag= a
 FT sig_peptide 56..112
 FT /*tag= b
 FT mat_peptide 113..1450
 FT /*tag= c
 XX
 XX JP06319396-A.
 XX
 XX 22-NOV-1994.
 XX
 XX 07-MAY-1993; 93JP-0131208.
 XX
 XX 07-MAY-1993; 93JP-0131208.
 XX
 XX (NLSB) JAPAN TOBACCO INC.
 XX (KURS) KURARAY CO LTD.
 XX
 XX WPI; 1995-040220/06.
 XX P-PSDB; AAR66758.
 XX
 XX Transformed plant producing animal-derived anti-virus antibody -
 PT esp. tobacco plants producing anti-tobacco mosaic virus
 PT monoclonal antibody
 XX
 XX Example 2; Pages 14-15; 26pp; Japanese.
 XX
 CC AAQ79929 and AAQ79930 encode AAR66757 and AAR66758, the light and heavy
 CC chains of an animal derived anti-tobacco mosaic virus (TMV)
 CC monoclonal antibody. The cDNAs were incorporated into a T1
 CC plasmid vector, which was incorporated into A. tumefaciens.
 CC The resultant plant expression vector was used to transform
 CC tobacco plants, making them TMV resistant, the plants could
 CC also be biofarmed for the prodn. of anti-virus antibodies.
 XX
 XX Sequence 1553 BP; 386 A; 450 C; 372 G; 345 T; 0 other;
 SQ

Alignment Scores:
 Pred. No.: 5,92e-51 Length: 1553
 Score: 621.00 Matches: 118
 Percent Similarity: 85.26% Conservative: 15
 Best local Similarity: 75.64% Mismatches: 19
 Query Match: 76.10% Indels: 4
 DB: 16 Gaps: 2

US-08-836-455-4 (1-153) x AAQ79930 (1-1553)

Qy 1 MetGluCysSerTrpValPheLeuPheLeuSerIleThrThrGlyValHisSerGln 20
 Db 56 ATGGAATGTAACGTGATACCTCCCTTTATCTGTGTCAGTAACCTCAGGTGCTACTACAG 115
 Qy 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
 Db 116 GTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTGTCC 175
 Qy 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethIstirpValLysGlnThrPro 60
 Db 176 TGAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGTCAGTGGGTAAACAGAGGCGCT 235

Qy 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
 Db 236 GGACAGGGTCTGGAATGGATTGGGGCTATTATCTCTGGAATGGTATAGTACACT 295
 Qy 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet 100
 Db 296 CAGAAGTTCAGGGCAAGGCCACATGCTGACATGAGATAAATCTCCACAGCAGCTACATG 355
 Qy 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGly----- 118
 Db 356 CAACTCAGCGCTTGGCATCTGAGGACTCTGGGTCTATTACTGTGCAAGAGGGGGGT 415
 Qy 119 ---AsnTrp---GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSer 136
 Db 416 TACTCTGGTCCGACTATGCTATGGACTACTGGGTCAAGGAACTCAGTCACCGTCTCC 475
 Qy 137 SerAlaLysThrThrProProValTyrProLeuValProGlySer 152
 Db 476 TCAGCCAAAACAGACACCCCATCTGTCTATCCACTGGCCCTGGATCT 523

RESULT 5
 AAN91645
 ID AAN91645 standard; DNA; 540 BP.
 XX
 AC AAN91645;
 XX
 XX 25-MAR-2003 (updated)
 DT 31-OCT-2002 (updated)
 DT 15-MAR-1990 (first entry)
 XX
 DE Heavy chain of monoclonal antibody 6A4.
 XX
 KW Monoclonal antibody 6A4; heavy chain; Pseudomonas aeruginosa; OMP-1.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 XX CDS 64..540
 FT /*tag= a
 XX
 XX EP338395-A.
 XX
 XX 25-OCT-1989.
 XX
 XX 12-APR-1989; 89EP-0106463.
 XX
 XX 19-APR-1988; 88DE-3813023.
 XX
 XX (BEHW) BEHRINGWERKE AG.
 XX
 XX Domdey H, Marget M, Vonspecht B;
 XX
 XX WPI; 1989-310861/43.
 XX P-PSDB; AAP93079.
 XX
 XX Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
 XX variable antibody regions.
 XX
 XX Claim 1; page 6; 7pp; german.
 XX
 CC The sequence has a variable and constant region. Monoclonal antibody 6A4
 CC reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa.
 CC It is used for therapy and diagnosis of infection, and as a carrier for
 CC drugs. The antibody is IgG2a subclass.
 CC (Updated on 31-OCT-2002 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 540 BP; 145 A; 144 C; 130 G; 121 T; 0 other;
 SQ

Alignment Scores:
 Pred. No.: 1.17e-49 Length: 540
 Score: 602.00 Matches: 116


```

RESULT 7
AAQ12637
ID AAQ12637 standard; DNA; 1570 BP.
AC
AC
XX
XX
DT 25-MAR-2003. (updated)
DT 03-OCT-1991 (first entry)
XX
XX Monoclonal antibody OK3T heavy chain coding sequence.
XX
XX OK3T; heavy chain; humanised antibodies; CDR-grafting; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX sig_peptide 41..97
XX mat_peptide /*tag= a
XX /*tag= b
XX /product= OK3T heavy chain
XX
XX W09109967-A.
XX W09109968-A.
XX
XX 11-JUL-1991.
XX
XX 21-DEC-1990; 90WO-GB02017.
XX
XX 21-DEC-1990; 90WO-GB02017.
XX 21-DEC-1989; 89GB-0028874.
XX
XX (CULT ) CELLTech LTD.
XX
XX Adair JR, Athwal DS, Emtage JS;
XX
XX WPI; 1991-222915/30.
XX P-PSDB; AARI3061.
XX
XX New humanised antibodies comprising CDR grafted antibody - with
XX heavy and light chains, for use in in vivo therapy and diagnosis
XX
XX Disclosure; Fig 2a; 91pp; English.
XX
XX The OK3T heavy chain sequence was isolated from a cDNA library
XX prepared from OK3T producing cells. The library was screened with a
XX probe complementary to a sequence in the mouse IgG2a constant CH1
XX domain region. The OK3T sequence was used in CDR-grafting experiments
XX to prepare humanised antibodies.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX SQ Sequence 1570 BP; 447 A; 443 C; 356 G; 324 T; 0 other;

Alignment Scores:
Pred. No.: 1.99e-46 Length: 1570
Score: 574.50 Matches: 113
Percent Similarity: 80.13% Conservative: 8
Best Local Similarity: 74.83% Mismatches: 29
Query Match: 70.40% Indels: 1
DB: 12 Gaps: 1

US-08-836-455-4 (1-153) x AAQ12637 (1-1570)
Qy 1 MetGluCysSerTrpValPheLeuPheLeuSerIleThrThrGlyValHisSerGln 20
Db 41 ATGGAAGGCACTGGATCTTCTACTCTGTGTGTCAGTAAGTGCAGGTGCCACTCCAG 100
Qy 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
Db 101 GTCCAGCTGCAGCAGTCTGGGGCTGAACTGGCAAGACCTGGGGCTCAGTGAAGATGCC 160
Qy 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethIstTrpValLysGlnThrPro 60

```

```

Db 161 TGCAAGGCTTCTGGCTACACCTTTTACTAGGTACACGATGCACCTGGGTAAACAGAGCCT 220
Qy 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
Db 221 GGACAGGCTCTGGATGATGGATACATTAATCTAGCCGTGTTATATACTAATACAAT 280
Qy 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet 100
Db 281 CAGAAGTTCAAGGACAAGGCCACATTCGACTACAGACAAATCCTCCAGCAGCCTACATG 340
Qy 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArg--GlyAsn 119
Db 341 CAACTGAGCAGCCTGCATCTGAGGACTCTGCAGCTCTATTACTGTGCAAGATATATGAT 400
Qy 120 TrpGluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLys 139
Db 401 GATCATTTACTGCCTTGACTACTGGGGCCAGGACCACTCTCAGTCTCTCTCAGCCAAA 460
Qy 140 ThrThrProProValTyrProLeuValPro 150
Db 461 ACAACAGCCCATCGGTCTATCCACTGGCCCT 493

RESULT 8
AAA43821
ID AAA43821 standard; cDNA; 725 BP.
XX
XX AAA43821;
XX
XX 21-AUG-2000 (first entry)
XX
XX Mouse secreted expressed sequence tag SEQ ID NO:396.
XX
XX Human; mouse; chicken; rat; secreted expressed sequence tag; sEST;
XX expressed sequence tag; EST; probe; chemotactic; proliferative;
XX immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
XX thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
XX antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;
XX antitumor; osteopathic; neuroprotective; nootropic; antipsoriatic;
XX cerebroprotective; anticonvulsant; antidepressant; gene therapy;
XX vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
XX insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
XX lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
XX central nervous system disorder; Alzheimer's disease; stroke;
XX Parkinson's disease; Huntington's disease; coagulation disorder;
XX haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
XX tumour; infection; depression; psoriasis; ss.
XX
XX Mus musculus.
XX
XX WO200021991-A1.
XX
XX 20-APR-2000.
XX
XX 15-OCT-1999; 99WO-US24206.
XX
XX 15-OCT-1998; 98US-0104436.
XX
XX (GEMY ) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
XX Merberg D, Treacy M, Bowman MR;
XX
XX WPI; 2000-317938/27.
XX
XX Isolated polynucleotides, and encoded proteins, comprising secreted
XX expressed sequence tags (sESTs), useful for treating various disorders
XX such as autoimmune, infectious, and central nervous system disorders -
XX
XX Claim 1; Page 306; 803pp; English.
XX
XX AAA43426 to AAA45925 represent specifically claimed secreted expressed
XX sequence tags (sESTs), isolated from human, mouse, chicken and rat
XX
XX

```


Db	181	GGCAGGCGCTGGAAATGGATTGGATATATTATATTGGATATGGTTATATTAGTATAAT	240
Qy	81	GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaItyrMet	100
Db	241	GAGAAGTTCAAGGCGAAGCCACACTGACTCAGACACATCCTCCAGGACAGCCTACATG	300
Qy	101	GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaAargGlyAsnTrp	120
Db	301	CAACTCAGCAGCGCTGACATCTGAGGACTCTGCAATCTATTCTGTGCAAGATGGGCTTA	360
Qy	121	GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr	140
Db	361	ATCTTTGTATGGACTACTGGGGTCAGGAACCTCAGTCACCTGCTCCTCAGCCTCATC	420
Qy	141	ThrProProValTyrProLeuValPro	150
Db	421	AGGAACCTCAGCTACCCCTTAAAGCC	450
RESULT 10			
ID	AA911146	standard; DNA; 458 BP.	
XX	AA911146;		
DT	25-MAR-2003	(updated)	
DT	06-JUL-1990	(first entry)	
XX	2H7	Vh sequence.	
XX			
KW		Antibodies; passive immunisation; pH3-6a; ss.	
XX			
OS		Synthetic.	
Key		Location/Qualifiers	
FF	CDS	39..458	
FT		/*tag= a	
FT	misc_feature	398..408	
FT		/*tag= b	
FT		/note=Sequence homologous to DSP.2"	
FT	misc_feature	360..406	
FT		/*tag= c	
FT		/note=*JH1 region"	
XX	W08900999-A.		
XX			
XX	09-FEB-1989.		
XX			
XX	25-JUL-1988;	88WO-US02514.	
XX			
XX	24-JUL-1987;	87US-0077528.	
XX			
XX	(ITGB-) INT GENETIC ENG INC.		
PA	(INGE-) INGENE INT GENETIC ENG INC.		
XX			
PI	Robinson RR, Liu AV, Horwitz AH, Wall R, Better M;		
XX			
DR	WPI; 1989-061144/08.		
XX	P-PSDB; AAP94780.		
XX			
PT	Poly nucleotide(s) encoding Immunoglobulin molecules -		
PT	used for efficient prodn. of chimeric human or non-human or		
PT	class switched antibodies.		
XX			
PS	Disclosure; Page ?; 7pp; English.		
XX			
CC	Sequence carries 2H7 VH region of the chimeric immunoglobulin sequence.		
CC	The antibodies are useful in passive immunisation avoiding negative		
CC	immune reactions. They are also useful in assaying and in vitro imaging.		
CC	(Updated on 25-MAR-2003 to correct PA field.)		
XX			
SQ	Sequence 458 BP; 113 A; 120 C; 112 G; 113 T; 0 other;		

(XOMA) XOMA CORP.

Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
Wall R, Wilcox GL;
WPI: 1997-225473/20.
P-PSDB; AAW16343.

Secretate immunoglobulin heavy and light chain fragments - capable
of assembling into chimeric antibodies, useful for e.g. passive
immunisation, diagnosis, etc

Example 4; Fig 21; 96pp; English.

A cDNA clone (AAV70868) codes for the heavy chain variable region
(AAW16343) of the 2H7 mouse monoclonal antibody, which recognises
human B-cell surface antigen Bp35. The sequence was isolated from
a 2H7 cell line cDNA library by PCR amplification. The 2H7 light
chain variable sequence (AAT60869) has also been isolated. The
sequences have been used to construct a human-mouse chimeraic
antibody with specificity for the human B-cell antigen.
(updated on 25-MAR-2003 to correct Pf field.)

XX Sequence 491 BP; 113 A; 153 C; 112 G; 113 T; 0 other;

Alignment Scores:

Pred. No.:	4,13e-46	Length:	491
Score:	565.00	Matches:	112
Percent Similarity:	84.29%	Conservative:	6
Best Local Similarity:	80.00%	Mismatches:	18
Query Match:	69.24%	Indels:	4
DB:	18	Gaps:	1

US-08-836-455-4 (1-153) x AAV70868 (1-491)

QY 1 MetGluCysSerTrpValPheLeuPheLeuSerIleThrThrGlyValHisSerGln 20
Db 72 ATGGGATTTCAGCAGGATCTTTCTCTTCTCTCTCTGTCTGACGTAAGTGTCCACTCCCAG 131

QY 21 AlaTyrlEuGlnSerGlyAlaGlueValArgSerGlyAlaSerVallysMetSer 40
Db 132 GCTTATATCATCACGAGCTCTGGGGCGCTGGAGCTGGTGAGGCCTGGGCCCTCAGTGAAGATGTCC 191

QY 41 CysLysAlaSerGlyTyrrThrLeuthrSerrTyrrAsnMethistrpVallysGlnthrPro 60
Db 192 TGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGACCTGGGTAAAGCAGACACCT 251

QY 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyaspThrrTyrrAsn 80
Db 252 AGACAGGGCCCTGGAATGGATGGTAGCTATTATTCAGGAAATGGTGATCTCTCTTACAAAT 311

QY 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspthrSerrSerThrAlaTyrrMet 100
Db 312 CAGAAGTTCAAGGCAAGGCCACACTGACTGTAGACAAATCTCTCAGCAGACGCCTACATG 371

QY 101 GlnIleSerSerLeuthrSerGluAspSerAlaValtyrPheCysAlaarg----- 117
Db 372 CAGCTCAGCAGCCTGACATCTGAAGACTCTCGCGTCTATTCTCTGTGCAAGAGTGGTGATC 431

QY 118 ---GlyAsnTrpGluGlyAlaLeuAspTyrrTrpGlyClnclyThrSerValthrValser 136
Db 432 TATAGTACTCTTACTGGTACTTCGATGTCTGGGGCACAGGGACCACGGTCTACCGTCTCG 491

RESULT 14
ID AAV18557
ID AAV18557 standard; CDNA; 491 BP.
AC AAV18557;
XX
DT 05-JUN-1998 (first entry)
DE Mouse 2H7 antibody heavy chain variable region cdna.
XX

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 30, 2003, 22:11:56 ; Search time 202.802 seconds
(without alignments)
1730.853 Million cell updates/sec

Title: US-08-836-455-4

Perfect score: 816

Sequence: 1 MEC5WFLFLSITGVSQ.....TVSSAKTTPPVYPLVPGSL 153

Scoring table:

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1533700 seqs, 1147125425 residues

Total number of hits satisfying chosen parameters: 3067400

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPTO.spool/US08836455/runat_29082003_132902/app_query.fasta.1.654
-DB=publishedApplications_NA -QFMT=fastcap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US08836455 -CGN_1_1_271 -runat_29082003_132902_22302
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	816	100.0	461	9	US-09-861-294-3
					Sequence 3, Appli

2	816	100.0	461	12	US-10-367-506-3	Sequence 3, Appli
3	599	73.4	736	13	US-10-006-773-12	Sequence 12, Appl
4	565.5	69.3	1570	11	US-09-795-515-6	Sequence 6, Appli
5	561.5	68.8	9199	11	US-09-911-692-3	Sequence 3, Appli
6	561.5	68.8	9209	10	US-09-911-703-3	Sequence 2, Appli
7	561.5	68.8	9209	11	US-09-905-928-2	Sequence 2, Appli
8	561.5	68.8	9209	12	US-10-238-681-3	Sequence 2, Appli
9	561.5	68.8	9209	14	US-10-096-964-2	Sequence 2, Appli
10	561.5	68.8	18986	13	US-10-109-853-2	Sequence 2, Appli
11	560.5	68.7	1392	14	US-10-216-484-8	Sequence 8, Appli
12	554.5	68.0	1314	10	US-09-903-327A-5	Sequence 5, Appli
13	554.5	68.0	1516	10	US-09-903-327A-1	Sequence 1, Appli
14	552.5	67.7	409	14	US-10-160-232-7	Sequence 7, Appli
15	540	66.2	406	12	US-10-244-821-85	Sequence 85, Appl
16	540	66.2	406	14	US-10-150-762-85	Sequence 85, Appl
17	540	66.2	406	14	US-10-150-762-87	Sequence 87, Appl
18	539.5	66.1	540	9	US-09-748-960-5	Sequence 5, Appli
19	532.5	65.3	5691	10	US-09-897-006-11	Sequence 11, Appl
20	532.5	65.3	5691	11	US-09-897-511A-11	Sequence 11, Appl
21	531.5	65.1	482	9	US-09-881-823-19	Sequence 19, Appl
22	531	65.1	478	13	US-10-040-739-911	Sequence 911, App
23	530	65.0	418	11	US-09-269-921-2	Sequence 2, Appli
24	530	65.0	418	11	US-09-509-098-3	Sequence 3, Appli
25	530	65.0	418	15	US-10-218-253-2	Sequence 2, Appli
26	528	64.7	418	11	US-09-269-921-75	Sequence 75, Appl
27	528	64.7	418	11	US-09-509-098-97	Sequence 97, Appl
28	528	64.7	418	15	US-10-218-253-75	Sequence 75, Appl
29	522.5	64.0	420	11	US-09-905-928-5	Sequence 5, Appli
30	522.5	64.0	420	14	US-10-096-964-5	Sequence 5, Appli
31	521.5	63.9	1518	14	US-10-207-655-304	Sequence 304, App
32	521.5	63.9	1572	14	US-10-207-655-298	Sequence 298, App
33	521.5	63.9	1584	14	US-10-207-655-285	Sequence 285, App
34	520.5	63.8	420	10	US-09-911-703-9	Sequence 9, Appli
35	520.5	63.8	420	12	US-10-238-681-10	Sequence 10, Appl
36	520.5	63.8	453	11	US-09-911-692-9	Sequence 9, Appli
37	518	63.5	1524	12	US-10-053-530-5	Sequence 5, Appli
38	518	63.5	1524	14	US-10-207-655-5	Sequence 5, Appli
39	518	63.5	1536	14	US-10-207-655-283	Sequence 283, App
40	517	63.4	1521	14	US-10-207-655-351	Sequence 351, App
41	516.5	63.3	474	12	US-09-226-157-1	Sequence 1, Appli
42	516.5	63.3	4191	14	US-10-176-380-18	Sequence 18, Appl
43	514.5	63.1	1515	14	US-10-207-655-380	Sequence 380, App
44	514.5	63.1	1515	14	US-10-207-655-382	Sequence 382, App
45	514.5	63.1	1515	14	US-10-207-655-383	Sequence 383, App

ALIGNMENTS

RESULT 1
US-09-861-294-3
; Sequence 3, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE OF INVENTION: 30414200620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(461)

OTHER INFORMATION: 4D4 Heavy chain V region, plus leader
US-10-006-773-12

Alignment Scores:		
Pred. No.:	1,498-65	Length:
Score:	\$39.00	Matches:
Percent Similarity:	86.67%	Mismatches:
Best Local Similarity:	77.33%	Indels:
Query Match:	73.41%	Gaps:
DB:	13	
		Conservative:
		2
		2
		736

US-08-836-455-4 (1-153) x US-10-006-773-12 (1-736)

QY	5	TrpValPheLeuPheLeuSerIleThrThrGlyValHisSerGlnAlaTyLeuGln	24
Db	26	TGGATCTTTCTTTCTCTCTCTGAGGAACGCGAGGTCTCCATTGCCAGGTTCCAGCTGCAG	85
QY	25	GlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSerCysLysAlaSer	44
Db	86	CAGTCTGGACCTGAGCTGGTGAAGCCTGGGCGCTTTAGTGAAGATATCTTCGAAGGCTTCT	145
QY	45	GlyTyThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeu	64
Db	146	GGTTACACCTTCACAAAGCTACGATATAAAGCTGGGTGAAGCAGACAGGCGCTGGACAGGCATT	205
QY	65	GluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyraSnGlnLysPheLys	84
Db	206	GAGTGGATGGATGGATTTATTCCTGGAGATGGTGGTACTAATTACAAATGAGAAATTCAG	265
QY	85	GlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyMetGlnIleSerSer	104
Db	266	GCGAGGCCACACTGACTGCAGACAAATCTCCAGCACACGCCTACATGACGCTCAGTAGC	325
QY	105	LeuThrSerGluAspSerAlaValItyrPheCysAlaArg---GlyAsnTrpGluGly---	122
Db	326	CTGACTTCTGAGAACTCTGCAGTCTATTCTCTGTGCAAGAGGGGTAACTTCCCTTCTTAT	385
QY	123	AlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThrPro	142
Db	386	GCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAACGACACCC	445
QY	143	ProProValTyrProLeuValProGlySer	152
Db	446	CCATCTGTCTATCCACTGGCCCTGGATCT	475

RESULT 4

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US-09-795-515-6
; Sequence 6, Application US/09795515
; Publication NO. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Ahtwal, Diljeet S.
; APPLICANT: Entage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1r1s
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658

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QY 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethHisTrpValLysGlnThrPro 60
Db 2521 TGCAGGCTTCTGGCTACACATTTACAGTTTACAAATATGACCTGGGTAAACACACACCT 2580
QY 61 GlyClnGlyLeuGluTrpLleGlyAsnLlePheProGlyAsnGlyAspThrTyrTyrAsn 80
Db 2581 GGTCTGGGGCTGGAATGGATTTGGAGCTATTATTCCTGGGAAATGGTGATCTTCTACAAT 2640
QY 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet 100
Db 2641 CACAAGTTCAAGCAAGGCCATTTGACTGCGACAAATCTCCAGCACAGCTCATG 2700
QY 101 GlnLysSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
Db 2701 CAGCTCAGCAGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTAC 2760
QY 121 GluGlyAla-----LeuAspTyrTrpGlyClnGlyThrSerValThrValSer 137
Db 2761 TACGGCGGTGACTGGTACTTCAATGCTGGGGCGCAGGGACACGCTCACCCTCTGCA 2820
QY 138 AlaLysThrThrProProValTyrProLeuValProGlySer 152
Db 2821 GCTAGCACCAAGGCCCATCGGCTTCCCGCTGGCACCTCCTCC 2865
RESULT 10
US-10-109-853-2
; Sequence 2, Application US/10109853
; Publication No. US20020192820A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; BARNETT, Richard Spence
; MCLACHLAN, Karen Retta
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
; SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
; RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,853
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,715
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/819,866
; FILING DATE: 14-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-352
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1896 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-109-853-2
Alignment Scores:
Pred. No.: 5,99e-59 Length: 1896
Score: 561.50 Matches: 109
Percent Similarity: 80.00% Conservative: 15
Best Local Similarity: 70.32% Mismatches: 28
Query Match: 68.81% Indels: 3
DB: 13 Gaps: 1

US-08-836-455-4 (1-153) x US-10-109-853-2 (1-18986)
QY 1 MetGluCysSerTrpValPheLeuPheLeuSerIleThrThrGlyValHisSerGln 20
Db 9433 ATGGGTGGAGCCTCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 9492
QY 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
Db 9493 GTCAACTGCAGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCTCAGTGAAGATGTCC 9552
QY 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethHisTrpValLysGlnThrPro 60
Db 9553 TGAAGGCTTCTGGCTACACATTTACCAATATGACCTGGGTAAACACACACCT 9612
QY 61 GlyClnGlyLeuGluTrpLleGlyAsnLlePheProGlyAsnGlyAspThrTyrTyrAsn 80
Db 9613 GGTCTGGGGCTGGAATGGATTTGGAGCTATTATTCCTGGGAAATGGTGATCTTCTACAAT 9672
QY 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet 100
Db 9673 CAGAAGTTCAAGCAAGGCCATTTGACTGCGACAAATCTCCAGCACAGCTCATG 9732
QY 101 GlnLysSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
Db 9733 CAGCTCAGCAGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTAC 9792
QY 121 GluGlyAla-----LeuAspTyrTrpGlyClnGlyThrSerValThrValSer 137
Db 9793 TACGGCGGTGACTGGTACTTCAATGCTGGGGCGCAGGGACACGCTCACCCTCTGCA 9852
QY 138 AlaLysThrThrProProValTyrProLeuValProGlySer 152
Db 9853 GCTAGCACCAAGGCCCATCGGCTTCCCGCTGGCACCTCCTCC 9897
RESULT 11
US-10-216-484-8
; Sequence 8, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 8
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (58)..(1392)
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Score: 554.50 Matches: 106
Percent Similarity: 80.26% Conservative: 16
Best Local Similarity: 69.74% Mismatches: 25
Query Match: 67.95% Indels: 5
DB: 10 Gaps: 1

US-08-836-455-4 (1-153) x US-09-903-327A-1 (1-1516)

QY 1 MetGluCysSerTrpValPheLeuPheLeuSerIleThrThrGlyValHisSerGln 20
   ||| |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 28 ATGGGATGGAGCTGGATCTTCTCTCTCCTCAGGAACCTGCAGGCGTCCACTGTAG 87
   ||| |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 21 AlaTyrLeuGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 88 GTCCAGCTTCAGCAGTCAGGACCTGAGCTGGTGAACCTGGGCGCTCAGTGAAGATCC 147
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro 60
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 148 TGCAGGCTTCGATACACATCTCAGTACACATGCTGAGTGGGTGAAGCAGGCCAT 207
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 61 GlyGlnGlyLeuGlnTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 208 GGAAGAGCGCTTCAGTGGATGGATATATTATCTTACAAAGGTGGTACTGGCTACAAC 267
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet 100
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 268 CAGAAGTTCAAGAGCAAGGCCACATTGACAACAGACAGTCTCCCAACACAGCCTACATG 327
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 328 GAGCTCCGAGCCTGCATCTGATGCTCTGCACTCTATTACTGTCCAGAGGG----- 381
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 121 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr 140
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 382 -----ATTGCTTACTGGGCGCAAGGAGCTGTGCTCAGTCTCTCTGCAGCAAAACG 432
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 141 ThrProProValTyrProLeuValProGlySer 152
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 433 ACACCCCATCTGTCTATCCACTGGCCCTGGATCT 468

RESULT 14
US-10-160-232-7
; Sequence 7, Application US/10160232
; Publication No. US20030088075A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/10/160,232
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; NAME/KEY: CDS
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; LOCATION: (1)..(408)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(57)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (58)..(408)
US-10-160-232-7

Alignment Scores:
Pred. No.: 4,5e-60 Length: 409
Score: 552.50 Matches: 108
Percent Similarity: 86.13% Conservative: 10
Best Local Similarity: 78.83% Mismatches: 18
Query Match: 67.71% Indels: 1
DB: 14 Gaps: 1

US-08-836-455-4 (1-153) x US-10-160-232-7 (1-409)

QY 1 MetGluCysSerTrpValPheLeuPheLeuSerIleThrThrGlyValHisSerGln 20
   ||| |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 1 ATGGGATTCAGCAGGATCTTCTCTCTCCTCCTCAGTACTAGGTGTCCACTCCAG 60
   ||| |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 21 AlaTyrLeuGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 61 GCTTTCTACAGCAGCTGGGGCTGAGCTGGTGAGCGCTCGGGCCCTCAGTGAAGATGTC 120
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro 60
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 121 TGCAGGCTTCGCTACACATTTATCAATTACAAATATGCATGGGTGAAGCAGACCT 180
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 61 GlyGlnGlyLeuGlnTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 181 AGACAGGCGCTGGAATGGATGGAGCTATTTTCCAGGAATGGTTTACTTCTCATAAT 240
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet 100
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 241 CAGAAGTTCAAGGCGCAAGGCCACACTGACTGTAGACAAATCTCCAGCAGCTACATG 300
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 301 CAGCTCCGCGAGCTGCATCTGAGACTCTGCGGTCTATTCTTCTGTCAAGA---GATGGT 357
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 121 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 137
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 358 GACTATTACTTTGACTACTGGGCGCAAGGCCACTCTCAGACTCTCCTCA 408
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 15
US-10-244-821-85
; Sequence 85, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultiz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-244-821-85

Alignment Scores:
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Pred. No.:	1.64e-58	Length:	406
Score:	540.00	Matches:	104
Percent Similarity:	81.75%	Conservative:	8
Best Local Similarity:	75.91%	Mismatches:	23
Query Match:	66.18%	Indels:	2
DB:	12	Gaps:	1

US-08-836-455-4 (1-153) x US-10-244-821-85 (1-406)

1	MetGluCysSerTrpValPheLeuPheLeuSerIleThrGlyValHisSerGln	20
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Qy		
21	AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer	40
Db		
61	GTCCAGCTTTCAGCAGCTCTGGGCTGAACTGGCAAAACCTGGGGCCCTCAGTGAAGATGCC	120
Qy		
41	CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro	60
Db		
121	TGCAAGGCTTCTGGCTACACCTTTACTAGCTACAGGATGCACCTGGGTAACACAGAGGCCT	180
Qy		
61	GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn	80
Db		
181	GCACAGGCTCTGGAAATGGATTGGATATATTAATCTCAGCACCTGGGTATATCAATACAA	240
Qy		
81	GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet	100
Db		
241	CAGAAGTTCAGGACAAAGGCCCATGTACTGCAGACAAATCTCCAGACACAGCCTTACATG	300
Qy		
101	GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp	120
Db		
301	CAACTGACGACCTGCATTTGAGGACTCTGCAGTCTATTACTGTGCAAGAGGGGGG---	357
Qy		
121	GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer	137
Db		
358	---GGGCTCTTTGACTACTGGGGCCCAAGAACCACTCTCACAGTCTCTCTCA	405

Search completed: August 31, 2003, 01:08:53
Job time : 209.802 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 30, 2003, 22:11:21 ; Search time 1841.13 Seconds
(without alignments)
2019.725 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 816
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delep 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vrt: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rod: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gss1: *

29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	603	73.9	739	10	BE284158	BE284158 601099428
2	600	73.5	637	14	BY724721	BY724721 BY724721
3	596	72.0	644	10	BE281961	BE281961 601099518
4	589.5	72.2	1576	11	AK007918	AK007918 Mus muscu
5	588.5	72.1	767	10	BF165456	BF165456 60177347
6	585	71.7	892	10	EG518664	EG518664 602578528
7	578.5	70.9	941	10	BF138189	BF138189 601781314
8	577.5	70.8	794	12	BI150371	BI150371 602915205
9	575	70.5	771	10	BF140551	BF140551 601787584
10	570.5	69.9	529	14	CA576389	CA576389 K0644A12-
11	570.5	69.9	546	14	CA576594	CA576594 K0647B06-
12	570	69.9	896	13	BUS24012	BUS24012 AGENCOURT
13	567	69.5	847	10	BF165486	BF165486 601777393
14	562.5	68.9	616	10	BF136295	BF136295 601781413
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16	559	68.5	885	10	BF162852	BF162852 601767129
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18	548.5	67.2	507	10	BF015548	BF015548 uy23a08.y
19	548.5	67.2	793	10	BF136093	BF136093 601783539
20	548	67.2	519	14	CA580087	CA580087 K0746G01-
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25	544	66.7	700	10	BF540088	BF540088 602050325
26	543.5	66.6	538	14	CA578968	CA578968 K0731A04-
27	543.5	66.6	604	10	BF140035	BF140035 601791175
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29	542.5	66.5	469	14	CA574907	CA574907 K0622H02-
30	541	66.2	477	14	CA570382	CA570382 K0505G11-
31	540	66.2	745	12	BG871607	BG871607 602790090
32	539	66.1	1012	10	BF579009	BF579009 602096127
33	538.5	66.0	598	12	BI104341	BI104341 602889919
34	537.5	65.9	685	10	BF136104	BF136104 601783550
35	537	65.8	464	10	BE368025	BE368025 601221914
36	536.5	65.7	429	14	CA579143	CA579143 K0733D01-
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39	535.5	65.6	516	14	CA579084	CA579084 K0732F03-
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ALIGNMENTS

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LOCUS BE284158 739 bp mRNA linear EST 13-JUL-2000
DEFINITION 601099428F1 NCI_CGAP_Lu29 Mus musculus cdna clone IMAGE:3491766 5', mRNA sequence.
ACCESSION BE284158
VERSION BE284158.1 GI:9160900
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 739)


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455 AACACAGCCCATCGTCTATCCACTGGCCCT 488

Db      80 nGlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrIatYrMe 100
      273 TGAAGATTCAAGGCAAGGCCACTGACTGACAGACAAATCTCCAGCACACGCTACAT 332

RESULT 6
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LOCUS      892 bp      mRNA      linear      EST 02-APR-2001
DEFINITION 602578528F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491766 5',
mRNA sequence.
ACCESSION  BG518664
VERSION     BG518664.1 GI:13513763
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 892)
NTH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabp@remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM8536 row: h column: 07
High quality sequence stop: 771.
Location/Qualifiers
FEATURES             source
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        /lab_host="DH10B"
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        Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
        Library constructed by Life Technologies. Investigator
        providing samples: Gilbert Smith, NIH"
BASE COUNT  217 a 266 c 211 g 198 t
ORIGIN
Alignment Scores:
Pred. No.:      7,43e-51      Length:      892
Score:          585.00        Matches:    113
Percent Similarity: 82.35%    Conservative: 13
Best Local Similarity: 73.86%  Mismatches: 26
Query Match:    71.69%      Indels:     1
DB:             10          Gaps:       0

US-08-836-455-4 (1-153) x BG518664 (1-892)

QY      1 MetGluCysSerTrpValPheLeuPheLeuSerIleThrThrGlyValHisSerGln 20
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      33 ATGAATGGATCTGGATCTTCTCTCATCTCTCAGGAACCTGCAAGTGTCCACTCCAG 92

Db      21 AlaTyrLeuGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLys-MetSe 40
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      93 GTTCAGCTGCAGCAGCTGTGAGCTGAGCTGGCGCTGGCGCTTCAGTGAACGATGTC 152

QY      40 rCysLysAlaSerGlyTyrThrLeuThrSerTyrAspMetHisTrpValLysGlnThrPr 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      153 CTGCAAGCTCTGGTTACTCATTCACAGCTATGTAAGCTGGGTGAAGCAGAAAC 212

Db      60 oGlyGlnGlyLeuLurPrIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTras 80
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
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/clone_lib="NCI-CCAP_Lu30"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site:1: NotI;
Site 2: SalI; transgenic model WNT-1, expression driven by
MTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 179 a 215 c 195 g 182 t
ORIGIN

Alignment Scores:
Pred. No.: 6.8e-50 Length: 771
Score: 575.00 Matches: 110
Percent Similarity: 82.00% Conservative: 13
Best Local Similarity: 73.33% Mismatches: 25
Query Match: 70.47% Indels: 2
DB: 10 Gaps: 1

US-08-836-455-4 (1-153) x BFL40551 (1-771)
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Qy 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
Db 75 GTTCAGTGAAGCAGCTCTGGAGCTGAGCTGGTGAAGCTGGGCTTCAGTGAAGCTGCC 134
Qy 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro 60
Db 135 TGCAGGCTCTGGCTACACCTTCAACAGCTATATATGCTGGTGAAGCAGGCGCT 194
Qy 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
Db 195 GCACAGGGCCCTGAGTGGTAGGATACCTTTCTCTTACATGATGATACATAATGCAAT 254
Qy 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet 100
Db 255 GAGAAGTCAAAAGGCAAGGCCACACTGACTGACAGACAAATCTCCAGCAGCGCTACATG 314
Qy 101 GlnIleSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
Db 315 GAGCTCAGCAGCCTGACCTCTGAGGACTCTGCCCTCTATTACTGTGCAAGGGGTACTAC 374
Qy 121 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr 140
Db 375 -----GTATTGTACTACTGGGGCCAAAGGCACCACTATCATCAGTCTCTCTCAGCCAAAACA 428
Qy 141 ThrProProValTyrProLeuValPro 150
Db 429 ACAGCCCATCGGCTATCCACTGGCCCT 458

RESULT 10
CA576389
LOCUS CA576389.1 GI:25121091
DEFINITION K0644A12-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+)
cDNA Library (Long) Mus musculus cDNA clone NIA:K0644A12
IMAGE:30072971 5', mRNA sequence.
ACCESSION CA576389
VERSION CA576389.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 529)

AUTHORS Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G.,
Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.
TITLE Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Jin-/c-Kit-/Sca-1+) cDNA Library (Long)
JOURNAL Unpublished
COMMENT Other_ESTS: K0644A12-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0644 row: A column: 12
Seq primer: M13 Reverse
High quality sequence stop: 529
POLYA=No.
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Location/Qualifiers
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(Lin-/c-Kit-/Sca-1+) cDNA Library (Long)"
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NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Drs. Dennis Taub, Dan Longo (National
Institute on Aging, USA), Jonathan Keller (National Cancer
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) primer [invitrogen:
5'-PGACTAGTCTAGTCGCGAGCGCCGCTTTTCTTTT-3'] from
1.1 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lona-linker LL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and NotI enzymes
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.2 kb. The library was constructed
by Yulan Piao (NIA)."
BASE COUNT 125 a 138 c 136 g 130 t
ORIGIN

Alignment Scores:
Pred. No.: 1.22e-49 Length: 529
Score: 570.50 Matches: 110
Percent Similarity: 84.11% Conservative: 17
Best Local Similarity: 72.85% Mismatches: 24
Query Match: 69.91% Indels: 2
DB: 14 Gaps: 0

US-08-836-455-4 (1-153) x CA576389 (1-529)
Qy 1 MetGluCysSerTrpValPheLeuLeuSerIleThrThrGlyValHisSerGln 20
Db 25 ATGGAATGGACCTGGGCTTCTCTCTCTCTGTCAGTAAGTGGGTCACCTCCAGC 84
Qy 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
Db 85 GTTCAGCTGCAGCAGCTCTGGAGCTGAGCTGATGAAGCTGGGCTTCAGTGAAGCTTTC 144
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QY	81	GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyMet	100
Db	254	GAGAAGTTCAAAGGAGCCACACTGACTGCAGACAAATCCTCCAGCAGCGCTACATG	313
QY	101	GlnLysSerLeuThrSerGluAspSerAlaValTyPheCysAlaAsgGlyAsnTrp	120
Db	314	GAGTCAGCAGCGCTGACTCTGAGGACACTGCGCGTCTATTACTGTGCAAGG---GACTAC	370
QY	121	GluGlyAlaLeuAspTyTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr	140
Db	371	ACTGGTAGCCTTGACTACTGGGCAAGCACCACACTATCAGAGTCTCCTCAGAGCTGCG	430
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VERSION	BF136295.1	GI:10975335	
KEYWORDS	EST.		
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ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 616)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9245 row: j column: 04 High quality sequence stop: 613.		
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	/lab_host="DH10B"		
	/clone_lib="NCI CGAP Lu30"		
	/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; transgenic model WNF-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.		
	Investigator providing samples: Gilbert Smith, NIH"		
BASE COUNT	138 a 170 c 160 g 148 t		
ORIGIN			
Alignment Scores:			
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Score:	562.50	Matches:	113
Percent Similarity:	83.12%	Conservative:	15
Best Local Similarity:	73.38%	Mismatches:	22
Query Match:	68.93%	Indels:	4
DB:	10	Gaps:	1
US-08-836-455-4 (1-153) x BF136295 (1-616)			
QY	1	MetGluCysSerTrpValPheLeuPheLeuSerLeuThrGlyValHisSerGln	20

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 31, 2003, 00:02:06 ; Search time 3130.85 Seconds
(without alignments)
1999.191 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 153
Sequence: 1 MECSWFLFLLSITGVHQS.....TVSSAKTTPPPVPLVPGSL 153

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
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Searched: 2888711 seqs, 20454813386 residues

Word size: 1
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2noli.rge -MINMATCH=0_1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
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-NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08836455_@CGN_1_1_3608_@runat_29082003_132953_23045 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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16: em.fun.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	153	100.0	461	6	AR164506 Sequence
2	153	100.0	461	6	BD085738 Methods o
3	135	88.2	411	10	AF124720 Mus muscu
4	38	24.8	471	10	AB050080 Mus muscu
5	31	20.3	458	6	AR083801 Sequence
6	31	20.3	458	6	AR198720 Sequence
7	31	20.3	458	6	AR275320 Sequence
8	29	19.0	294	10	AF303872 Mus muscu
9	27	17.6	735	12	AJ250760 Mus muscu
10	22	14.4	357	10	MMIG07
11	22	14.4	357	10	MMIG09
12	22	14.4	484	10	MUSIGH4C11
13	22	14.4	490	10	MUSIGAC11A
14	21	13.7	390	10	AF433159 Mus muscu
15	21	13.7	390	10	MUSL77IGHV
16	21	13.7	444	10	MUSIGHEB
17	21	13.7	631	10	XMU90237
18	21	13.7	902	12	XXU49832
19	20	13.1	279	10	MMIGGCVRG
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21	20	13.1	285	10	MMIGGCVRC
22	20	13.1	290	10	MMIGGCVRF
23	20	13.1	294	10	AF303873
24	20	13.1	297	10	AY172396
25	20	13.1	302	10	MMIGGCVRI
26	20	13.1	303	10	MMIGGCVRD
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32	20	13.1	352	10	MMMD50C
33	20	13.1	355	10	MMMD47C
34	20	13.1	356	10	AY247151
35	20	13.1	357	10	AF178586
36	20	13.1	358	10	MMMD01C
37	20	13.1	358	10	MMMD52C
38	20	13.1	360	10	AY229957
39	20	13.1	360	12	AF277091
40	20	13.1	366	10	MMU16182
41	20	13.1	387	10	AY058907
42	20	13.1	405	10	AB069863
43	20	13.1	453	10	MMU24114
44	20	13.1	457	10	AY178830
45	20	13.1	469	10	MUSIGHAAE

ALIGNMENTS

1. (bases 1 to 461)
Chatterjee,M. and Foon,K.A.
Methods of delaying development of HMFG-associated tumors using
anti-Idiotypic antibody 11b10
Patent: JP 2001523269-A 20-NOV-2001;
THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
OS Unidentified

PF 2001032009 RY2
 PD 12-NOV-1998
 PF 12-JUN-1998 JP 1999503252
 PR 13-JUN-1997 US 60/049540, 11-JUN-1998 US 09/096244 PI
 MALAYA CHATERJEE, KENNETH A FOON
 PC A61K39/395, A61K39/39/C07K16/42
 CC Strandedness: Single;

CC
CC
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CC

strangeness: single,
Topology: Linear;
Methods of delaying development of HMFG-associated tumors CC

CC	anti-idiotypic antibody 11D10	Location/Qualifiers
FH	Key	
CC	using	

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cbs      peptide      58      453
FT mat      Location/Qualifiers
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112 a 121 c 119 q 109 t

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cores:
3.98e-155      Length: 461
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Similarity:	100.00%	Conservative:	0
Mismatch:	100.00%	Mismatches:	0

Indels:	0
Cons:	0
100.00%	

apps: 0

55-4 (1-153) x BD085738 (1-461)

1 MetGluCysSerTrpValPheLeuPheLeuSerIleThrThrGlyValHisSerGln 20

A vertical ruler with markings from 1 to 50 cm. The markings are in centimeters, with major ticks every 10 units and minor ticks every 1 unit. The numbers 1, 10, 20, 30, 40, and 50 are printed along the right side of the ruler.

I ATGGAAATGCAGCTGCGGTCCTTCTCTCCCTCCTGTCATTAACCTACAGGGTGTCCTCACGCCCAAG 90

221 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40

661 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCTCAGTGAAGATGTC 120

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41 CÝSLÝA LASER GYŤYŤM LEUTAR SERŤYASMECHISTRIPVALLÝSGINIM FIO 60

221 TCGAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACCTGGGTAAAGCAGACACCT 180

661 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

81 GGACAGGCCTGGAATGGAATGGAATATTTTCCTGGAAATGGTGATCTTACTACAAAT 240

881 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet 100

41 CAGAACTTTAAGGGCAAGGCTCATTTGACTGCAGACACATCTCTCCAGCACAGCCTACATG 300

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UI GINleSerSerLeuthrSerGluAspSerAlaValIYFPncysAlaAARGLYAsnTrp I20

001 CAGATCAGCAGCCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACCTGG 360

21 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr 140

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61 GAGGGTGCTCTGGACTACTGGGTC AAGGAACCTCAGTCACCGTCGCCAGCCAAAACG 420

41 ThrProProValTyrProLeuValProGlySerLeu 153

21 ACACCCGCCACCCGTCCTATCCACCTGGTCCCTGGAGCTTG 459

THE ECONOMIC EFFECTS OF THE 1990S

LOCUS	AF124720	411 bp	mRNA	linear	ROD 22-MAY-2000			
DEFINITION	Mus musculus immunoglobulin heavy chain mRNA, partial cds.							
ACCESSION	AF124720							
VERSION	AF124720.1	GI:14164544						
KEYWORDS								
SOURCE	Mus musculus (house mouse)							
ORGANISM	Mus musculus							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
	1 (bases 1 to 411)							
	Tripathi,P.K., Qin,H., Bhattacharya-Chatterjee,M., Ceriani,R.L., Foon,K.A. and Chatterjee,S.K.							
TITLE	Construction and characterization of a chimeric fusion protein consisting of an anti-idiotypic antibody mimicking a breast cancer-associated antigen and the cytokine GM-CSF							
	Hybridoma 18 (2), 193-202 (1999)							
	99306687							
JOURNAL	MEDLINE							
PUBMED	10380019							
AUTHORS	2 (bases 1 to 411)							
	Chatterjee,S.K. and Tripathi,P.K.							
	Direct Submission							
TITLE	Submitted (29-JAN-1999)							
	Internal Medicine, University of Kentucky,							
	800 Rose Street, Lexington, KY 40536, USA							
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	67 CTACACAGCTCTGGGCGCTGAGCTGGTGGAGGTCTGGGGCCCTCAGTGAAGATGCTCCTCGAAG 136							
Qy	43 AlaSerGlyTyrThrLeuThr							

Db 307 AGACGCTGCATCTGAAGACTTCGGCGTCTATTTCGTCAAGAGGAACCTGGGAGGT 366
Qy 123 AlaLeuAspYrrpGlyGInGlyThrSerValThrValSerSer 137
Db 367 GCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGCTCCCTCA 411

RESULT 4
ABO50080 471 bp mRNA linear ROD 02-APR-2002
LOCUS Mus musculus VH9H8 mRNA for anti-A/U antibody, partial cds.
DEFINITION
ACCESSION ABO50080
VERSION ABO50080.1 GI:19909935
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Kitagawa,Y. and Okuhara,E.
TITLE The separation of three antibody populations from
anti-poly(A).poly(U) antibodies elicited in mice or rabbits and
antigenic features of poly(A).poly(U)
Mol. Immunol. 19 (2), 257-266 (1982)
JOURNAL Mol. Immunol. 19 (2), 257-266 (1982)
MEDLINE 82245325
PUBMED 6178956
REFERENCE 2
AUTHORS Kitagawa,Y.
TITLE anti-dsrNA (A/U) Ab VH region VH9H8
JOURNAL Published Only in Database (2002)
REFERENCE 3 (bases 1 to 471)
AUTHORS Kitagawa,Y.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural
University, Biotechnology Institute; Minami 2-2, Ogata, Akita
010-0444, Japan (E-mail:kitagawa@agri.akita-u.ac.jp,
URL:www.akita-pu.ac.jp/, Tel:81-185-45-2026(ex.400),
Fax:81-185-45-2678)

FEATURES source
Location/Qualifiers
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/translations="MGWTGVFLILSIITTHVHSQAYLQQSGAEIVRSAGSVKMSCKAS
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BASE COUNT 114 a 126 c 121 g 110 t
ORIGIN

Alignment Scores:
Pred. No.: 2,65e-31 Length: 471
Score: 38.00 Matches: 38
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.84% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-4 (1-153) x ABO50080 (1-471)

Qy 10 LeuLeuSerIleThrThrGlyValHisSerGlnAlaTyrLeuGlnSerGlyAlaGlu 29
Db 38 CTCCTGTCAATACTACAGGTGTCCACTCCAGCGTTATCTACAGCAGTCTGGGCTGAA 97

QY 30 LeuValArgSerGlyAlaSerValLysMetSerCysLysAlaSerGlyTyrThr 47
|||||
Db 98 CTGTGAGGCTGGGGCTCAGTGAAGATCTCTGCAAGGCTTCTGGCTACACA 151
RESULT 5
AR083801
LOCUS AR083801 458 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 3 from patent US 5977316.
ACCESSION AR083801
VERSION AR083801.1 GI:10010572
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 458)
AUTHORS Chatterjee,M., Foon,K.A. and Chatterjee,S.K.
TITLE Monoclonal antibody 1A7 and related polypeptides
JOURNAL Patent: US 5977316-A 3 02-NOV-1999;
FEATURES Location/Qualifiers
source
BASE COUNT 106 a 131 c 114 g 107 t
ORIGIN
Alignment Scores:
Pred. No.: 8.89e-24 Length: 458
Score: 31.00 Matches: 31
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.26% Indels: 0
DB: 6 Gaps: 0
US-08-836-455-4 (1-153) x AR083801 (1-458)
QY 123 AlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerAlaLysThrPro 142
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Db 364 GCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCAAAAGACACCC 423
QY 143 ProProValTyrProLeuValProGlySerLeu 153
|||||
Db 424 CCACCCGCTATCCATTGGTCCCTGGAAGCTTG 456
RESULT 6
AR198720
LOCUS AR198720 458 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 3 from patent US 6355244.
ACCESSION AR198720
VERSION AR198720.1 GI:20248794
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 458)
AUTHORS Foon,K.A. and Chatterjee,M.
TITLE Methods and compositions for the treatment of psoriasis
JOURNAL Patent: US 6355244-A 3 12-MAR-2002;
FEATURES Location/Qualifiers
source
BASE COUNT 106 a 131 c 114 g 107 t
ORIGIN
Alignment Scores:
Pred. No.: 8.89e-24 Length: 458
Score: 31.00 Matches: 31
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.26% Indels: 0
DB: 6 Gaps: 0
US-08-836-455-4 (1-153) x AR198720 (1-458)
QY 123 AlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerAlaLysThrPro 142

|||||
Db 364 GCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCAAAAGACACCC 423
QY 143 ProProValTyrProLeuValProGlySerLeu 153
|||||
Db 424 CCACCCGCTATCCATTGGTCCCTGGAAGCTTG 456
RESULT 7
AR275320
LOCUS AR275320 458 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 3 from patent US-6509016.
ACCESSION AR275320
VERSION AR275320.1 GI:29708411
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 458)
AUTHORS Chatterjee,M., Foon,K.A. and Chatterjee,S.K.
TITLE Monoclonal antibody 1A7 and use for the treatment of melanoma and small cell carcinoma
JOURNAL Patent: US 6509016-A 3 21-JAN-2003;
FEATURES Location/Qualifiers
source
BASE COUNT 106 a 131 c 114 g 107 t
ORIGIN
Alignment Scores:
Pred. No.: 8.89e-24 Length: 458
Score: 31.00 Matches: 31
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.26% Indels: 0
DB: 6 Gaps: 0
US-08-836-455-4 (1-153) x AR275320 (1-458)
QY 123 AlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerAlaLysThrPro 142
|||||
Db 364 GCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCAGCAAAAGACACCC 423
QY 143 ProProValTyrProLeuValProGlySerLeu 153
|||||
Db 424 CCACCCGCTATCCATTGGTCCCTGGAAGCTTG 456
RESULT 8
AF303872
LOCUS AF303872 294 bp mRNA linear ROD 25-SEP-2001
DEFINITION Mus musculus clone J558.41 immunoglobulin heavy chain variable region mRNA, partial cds.
ACCESSION AF303872
VERSION AF303872.1 GI:11612050
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 294)
AUTHORS Haines,B.B., Angeles,C.V., Parmelee,A.P., McLean,P.A. and Brodeur,P.H.
TITLE Germline diversity of the expressed BALB/c VHJ558 gene family
JOURNAL Mol. Immunol. 38 (1), 9-18 (2001)
MEDLINE 21376477
PUBMED 11483206
REFERENCE 2 (bases 1 to 294)
AUTHORS Haines,B.B., Angeles,C.V., Parmelee,A.P., McLean,P.A. and Brodeur,P.H.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Pathology, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
FEATURES Location/Qualifiers
source
1. .294

/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/cBYJ"
/db_xref="taxon:10090"
/chromosome="12"
/clone="J558.41"
/tissue_type="spleen"
/note="isolated from IGM mRNA from
lipopolysaccharide-stimulated cells"
<1..>294
/note="VhJ558 family"
/codon_start=1
/product="immunoglobulin heavy chain variable region"
/protein_id="AAG39153.1"
/db_xref="GI:11612051"
/translation="QAYLQSGAELVRSGASVKMSCKASGYTFYSSSYAYMQISLTSSEDSAVYFCAR"

CDS

BASE COUNT 79 a 69 c 77 g 69 t
ORIGIN
Alignment Scores:
Pred. No.: 8.33e-22 Length: 294
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.95% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-4 (1-153) x AF303872 (1-294)

Qy 89 LeuThrAlaSpThrSerSerThrAlaTyrMetGlnIleSerSerLeuThrSerGlu 108
|||||
Db 208 TTGACTGCAGACATCTCCAGCACACGCTACATGCAGATCAGACGCTGACATCTGAA 267

Qy 109 AspSerAlaValTyrPheCysAlaArg 117
|||||
Db 268 GACTCTCGGGTCTATTCTGTGCAAGA 294

RESULT 9

SC0250760 735 bp mRNA linear SYN 11-MAY-2000
LOCUS
DEFINITION Mus musculus synthetic construct for anti-guinea pig C5 ScFv antibody, clone E10.

ACCESSION AJ250760.1 GI:6272272

VERSION AJ250760.1 GI:6272272
KEYWORDS antibody; heavy chain; immunoglobulin superfamily; light chain; ScFv; variable region.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE

1 Link,C., Hawlisch,H., Meyer zu Wilsendorf,A., Gylerez,S., Nagel,E. and Koehl,J.
Selection of phage-displayed anti-guinea pig C5 or C5a antibodies and their application in xenotransplantation

JOURNAL Mol. Immunol. 38, 1235-1247 (1999)
REFERENCE 2 (bases 1 to 735)

TITLE

Link,C.

Direct Submission

Submitted (01-NOV-1999) Link C., Medizinische Mikrobiologie,

Medizinische Hochschule Hannover, Carl-Neuberg-Str. 1, 30625.

Hannover, GERMANY

Location/Qualifiers

1..735

/organism="synthetic construct"

/mol_type="mRNA"

/db_xref="taxon:32630"

/clone="E10"

/focus

1..366

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

source

source

412..735
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
<1..>735
/note="synthetic"
/codon_start=1
/transl_table=11
/product="anti-guinea pig C5 ScFv antibody"
/protein_id="CAB60133.1"
/db_xref="GI:6272273"
/translation="EVOLOQSGAELVRSGASVKMSCKASGYTFYRYNNHWKTPPGG
LEWIGYIPRGDGTNYNOKFKGKATLTADTSSSYAYMQISLTSSEDSAVYFCRSRDA
YYVGAMDFWGGTGVTVSSGGGGGGGGSDIVMTQSQKFMSTVGDVRSVTC
KASQNVCTNWAVYQOKPGQPKALIYASVRYSGVDPDRFTGSGSGTDTLTISNVQSE
DLARYFCQYNSYPYTFGGGTNLEKR"

CDS

V_region

1..366
/product="immunoglobulin heavy chain variable region"
367..411
/note="(Gly4Ser)3 linker sequence"
412..735
/product="immunoglobulin light chain variable region"

misc_feature

194 a 170 c 206 g 155 t
ORIGIN

Alignment Scores:
Pred. No.: 2.82e-19 Length: 735
Score: 27.00 Matches: 27
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 17.65% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-4 (1-153) x SC0250760 (1-735)

Qy 89 LeuThrAlaSpThrSerSerThrAlaTyrMetGlnIleSerSerLeuThrSerGlu 108
|||||

Db 208 TTGACTGCAGACATCTCCAGCACACGCTACATGCAGATCAGACGCTGACATCTGAA 267

Qy 109 AspSerAlaValTyrPheCys 115
|||||

Db 268 GACTCTCGGGTCTATTCTGT 288

RESULT 10

MMIG07

LOCUS

DEFINITION

Mouse hybridoma 12s18 mRNA for immunoglobulin heavy chain V region.

ACCESSION X58580 Y00794

VERSION X58580.1 GI:51591

KEYWORDS Ig heavy chain; Ig variable region; immunoglobulin.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 357)

Meek,K., Euthesia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Urban,J. and Capra,J.D.

Pollok,B., Alkan,S.S., Brait,M., Slaoui,M.,

Meek,K., Haseemann,C.,

Structural characterization of antiidiotypic antibodies. Evidence

that Ab2s are derived from the germline differently than Ab1s

J. Exp. Med. 169 (2), 519-533 (1989)

89094248

PUBMED 2492056

REFERENCE 2 (bases 1 to 357)

Meek,K.

Direct Submission

Submitted (09-JAN-1989) K. Meek, University of Texas Southwestern

Medical School, 5323 Harry Hines Blvd. Microbiology, Dallas Texas

75235, USA

Location/Qualifiers

1..357

/organism="Mus musculus"

/mol_type="mRNA"

/strain="A/J"

source

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/db_xref="taxon:10090"
/cell_line="Hybridoma 12S18-G"
1. .357
/gene="IG heavy chain"
/mRNA
<1. .>357
/gene="IG heavy chain"
/note="variable region"
/evidence-experimental
<1. .>357
/gene="IG heavy chain"
/note="variable region"
/codon_start=1
/product="IG heavy chain"
/protein_id="CAA41456.1"
/db_xref="GI:930150"
/translation="QVQLQEPGAEVVKPGASVKMSCKASGYTFTNYMHVYKQPGQG
LEWGNITPGSDTYNNEKPKSKATLVDTSSSYAYMQISLTSSEDSAVYYCARNEG
AWYFDVNGXGTTVAXS"
<1. .>357
/gene="IG heavy chain"
/product="IG heavy chain"
/note="variable region"
78 t 9 others
BASE COUNT 88 a 87 c 95 g
ORIGIN
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Alignment Scores:
Pred. No.: 3.44e-14 Length: 357
Score: 22.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.38% Indels: 0
DB: 10 Gaps: 0
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US-08-836-455-4 (1-153) x MMIG07 (1-357)

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Qy 92 AspThrSerSerThrAlaTyrMetGlnIleSerSerLeuThrSerGluAspSerAla 111
|||||
Db 217 GACACATCTCCAGACAGCCCTACATGCGATGACAGCCCTGACATCTGAGACTCTGCG 276
|||||
Qy 112 ValTyr 113
|||||
Db 277 GTCTAT 282
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RESULT 11
MMIG09
LOCUS Mouse hybridoma 12S18 mRNA 357 bp mRNA linear ROD 05-AUG-1995
DEFINITION Mouse hybridoma 12S18 mRNA for immunoglobulin heavy chain V region.
ACCESSION X58582 Y00794
VERSION X58582.1 GI:51593
KEYWORDS Ig heavy chain; Ig variable region; immunoglobulin.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Meek, K., Hasemann, C., Pollok, B., Alkan, S.S., Brait, M., Slaoui, M.,
Urban, J., and Capra, J.D.
TITLE Structural characterization of antiidiotypic antibodies. Evidence
that Ab2s are derived from the germline differently than Ab1s
J. Exp. Med. 169 (2), 519-533 (1989)
JOURNAL 89094248
MEDLINE
PUBMED 2492056
REFERENCE 2 (bases 1 to 357)
AUTHORS Meek, K.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-1989) K. Meek, University of Texas Southwestern
Medical School, 5323 Harry Hines Blvd. Microbiology, Dallas Texas
75235, USA
FEATURES Location/Qualifiers
source
1. .357
/organism="Mus musculus"
/mol_type="mRNA"
/strain="A/J"
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/db_xref="taxon:10090"
/cell_line="Hybridoma 12S28-G"
1. .357
/gene="IG heavy chain"
/mRNA
<1. .>357
/gene="IG heavy chain"
/note="variable region"
/evidence-experimental
<1. .>357
/gene="IG heavy chain"
/note="variable region"
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/product="IG heavy chain"
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/translation="QVQLQEPGAEVVKPGASVKMSCKASGYTFTNYMHVYKQPGQG
LEWGNITPGSDTYNNEKPKSKATLVDTSSSYAYMQISLTSSEDSAVYYCARNEG
AWYFDVNGXGTTVAXS"
<1. .>357
/gene="IG heavy chain"
/product="IG heavy chain"
/note="variable region"
80 t 6 others
BASE COUNT 89 a 86 c 96 g
ORIGIN
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Alignment Scores:
Pred. No.: 3.44e-14 Length: 357
Score: 22.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.38% Indels: 0
DB: 10 Gaps: 0
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US-08-836-455-4 (1-153) x MMIG09 (1-357)

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Qy 92 AspThrSerSerThrAlaTyrMetGlnIleSerSerLeuThrSerGluAspSerAla 111
|||||
Db 217 GACACATCTCCAGACAGCCCTACATGCGATGACAGCCCTGACATCTGAGACTCTGCG 276
|||||
Qy 112 ValTyr 113
|||||
Db 277 GTCTAT 282
```

```
RESULT 12
MUSIGH4C11
LOCUS Mus musculus immunoglobulin heavy chain precursor (IGH) mRNA,
partial cds.
ACCESSION M54977
VERSION M54977.1 GI:194528
KEYWORDS C-region; V-region; immunoglobulin heavy chain.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 484)
AUTHORS Sood, A.K., Cheng, H.D. and Kohler, H.
TITLE An efficient and general method for sequencing immunoglobulin mRNAs
J. Immunol. Methods 95 (2), 227-235 (1986)
JOURNAL 87084812
MEDLINE
PUBMED 2432131
COMMENT Original source text: Mouse anti-idiotypic hybridoma cell line
4C11, cdna to mRNA.
FEATURES Location/Qualifiers
source
1. .484
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/map="chromosome 12"
/cell_line="4C11"
/tissue_type="anti-idiotypic hybridoma"
1. .484
/gene="Igh"
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CDS
37..>484
/gene="IGH"
/codon_start=1
/product="immunoglobulin heavy chain precursor"
/protein_id="AA51051.1"
/db_xref="GI:553945"
/translation="MGWSWIFLELLSGTAGVLSEVLOQSGPELLKPGASVKISCRAS
GYFTDTHHWKQSKGLEWIGGDPNYDNTFYNEKFKDKATLVDRSSSTAYMEL
RSITSDESAVYCYASYDYGALDYWGQGTSTVTSASKTTPPSVYPLAP"
37..93
/gene="IGH"
/mat_peptide
94..>484
/gene="IGH"
/product="immunoglobulin heavy chain"
445..>484
/gene="IGH"

BASE COUNT 120 a 134 c 112 g 118 t
ORIGIN

Alignment Scores:
Pred. No.: 4.59e-14 Length: 484
Score: 22.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.38% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-4 (1-153) x MUSIGH4C11 (1-484)
QY 122 GYALALEUASPTyrTrpGlyGlnGlyThrSerValThrValSerAlaLysThrThr 141
|||||
Db 397 GGTGCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGCTCTCCTCAGCCAAACGACA 456

QY 142 ProPro 143
|||||
Db 457 CCCCCA 462

RESULT 13
MUSIG4C11A
LOCUS
DEFINITION
Mouse anti-idotype immunoglobulin heavy chain variable, constant,
and complementarity determining regions 1-3 (4C11) mRNA.
ACCESSION M24785.1 GI:194133
VERSION M24785.1
KEYWORDS C-region; V-region; anti-idiotypic antibody; complementarity
determining region; immunoglobulin heavy chain.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 490)
AUTHORS Cheng,H.L., Sood,A.K., Ward,R.E., Kieber-Emmons,T. and Kohler,H.
TITLE Structural basis of stimulatory anti-idiotypic antibodies
JOURNAL Mol. Immunol. 25 (1), 33-40 (1988)
MEDLINE 88142863
PUBMED 3125424
COMMENT Original source text: Mus musculus (strain BALB/c, sub_species
domesticus) cDNA to mRNA.
FEATURES
source
Location/Qualifiers
1..490
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/sub_species="domesticus"
/db_xref="taxon:10090"
1..490
/gene="4C11"
V_region 1..441
/gene="4C11"
184..198
/gene="CDR1"
misc_feature 184..198
/gene="CDR1"

CDS
37..>484
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/product="immunoglobulin heavy chain precursor"
/protein_id="AA51051.1"
/db_xref="GI:553945"
/translation="MGWSWIFLELLSGTAGVLSEVLOQSGPELLKPGASVKISCRAS
GYFTDTHHWKQSKGLEWIGGDPNYDNTFYNEKFKDKATLVDRSSSTAYMEL
RSITSDESAVYCYASYDYGALDYWGQGTSTVTSASKTTPPSVYPLAP"
37..93
/gene="IGH"
/mat_peptide
94..>484
/gene="IGH"
/product="immunoglobulin heavy chain"
445..>484
/gene="IGH"

BASE COUNT 120 a 134 c 116 g 120 t
ORIGIN

Alignment Scores:
Pred. No.: 4.64e-14 Length: 490
Score: 22.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.38% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-4 (1-153) x MUSIG4C11A (1-490)
QY 122 GYALALEUASPTyrTrpGlyGlnGlyThrSerValThrValSerAlaLysThrThr 141
|||||
Db 397 GGTGCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGCTCTCCTCAGCCAAACGACA 456

QY 142 ProPro 143
|||||
Db 457 CCCCCA 462

RESULT 14
AF433159
LOCUS
DEFINITION
Mus musculus monoclonal antibody K1-11 heavy chain variable region
mRNA, partial cds.
ACCESSION AF433159
VERSION AF433159.1 GI:17016945
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 390)
AUTHORS Ho,M. and Segre,M.
TITLE Mimicry of cocaine by anti-idiotypic antibodies
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 390)
AUTHORS Ho,M. and Segre,M.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-2001) Pathobiology, University of Illinois at
Urbana-Champaign, 2001 South Lincoln Avenue, Urbana, IL 61802, USA
FEATURES
source
Location/Qualifiers
1..390
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="1A:D5:A5:C5"
/sex="female"
/cell_type="hybridoma"
/tissue_type="hyperimmunized spleen"
/dev_stage="adult"
<1..>390
/note="anti-idiotypic antibody; K1-11 VH"
/codon_start=1
/product="monoclonal antibody K1-11 heavy chain variable
region"
/protein_id="AAL33541.1"
/db_xref="GI:17016946"

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/translation="EVOLQSGGLVLPSPOTMSLTCTVTGISTITGNRYRNWIRQPPG
NKLEWGIYIYISGTIYNPISLTITRTISKNQFLEMLSLIAEDTATYICARDPI
GLYALDYWGQGSTVIVSSAKTTPPSVY"
BASE COUNT 108 a 113 c 78 g 91 t
ORIGIN

Alignment Scores:
Pred. No.: 4.47e-13 Length: 390
Score: 21.00 Matches: 21
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.73% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-4 (1-153) x AF433159 (1-390)

Qy 123 AlaleuAspYtrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrPro 142
Db 319 GCTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGCTCTCCAGCAAAACGACACCC 378
Qy 143 Pro 143
Db 379 CCA 381

RESULT 15

MUSL77IGHV 390 bp mRNA linear ROD 29-OCT-1994
DEFINITION Mouse hybridoma Ig rearranged H-chain mRNA V-region, partial cds.
ACCESSION M97876

VERSION M97876.1 GI:198678

KEYWORDS V-region; immunoglobulin heavy chain; processed gene.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 390)

TITLE Lohman,K.L., Buck,D.W., Carrillo,M.A. and Kennedy,R.C.

JOURNAL Characterization of murine monoclonal anti-CD4; epitope

COMMENT recognition, idiotope expression, and variable gene sequence

Unpublished (1992)

Original source text: Mus musculus (strain BALB/c, sub-species

domesticus) SP20-BALB/c fusion hybridoma CDNA to mRNA.

FEATURES Location/Qualifiers

source

1..390

/organism="Mus musculus"

/mol_type="mRNA"

/strain="BALB/c"

/sub_species="domesticus"

/db_xref="taxon:10090"

/map="Chromosome 12"

/tissue_type="SP20-BALB/c fusion hybridoma"

1..390

/gene="Igh"

1..390

/gene="Igh"

/standard_name="L77; monoclonal antibody (CD4 antigen

specificity)"

BASE COUNT 98 a 100 c 102 g 90 t

ORIGIN

Alignment Scores:
Pred. No.: 4.47e-13 Length: 390
Score: 21.00 Matches: 21
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.73% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-4 (1-153) x MUSL77IGHV (1-390)

Qy 123 AlaleuAspYtrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrPro 142
Db 316 GCGTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGCTCTCCAGCAAAACGACACCC 375

Qy 143 Pro 143
Db 376 CCA 378

Search completed: August 31, 2003, 03:58:14
Job time : 3132.85 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 30, 2003, 22:12:36 ; Search time 230.013 Seconds
(without alignments)
1795.608 Million cell updates/sec

Title: US-08-836-455-4

Perfect score: 153

Sequence: 1 MECSWFLLSITGVHSQ.....TVSSAKTTPPPVPLPGSL 153

Scoring table:

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
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Searched: 2552756 seqs, 1349719017. residues

Word size: 1

Total number of hits satisfying chosen parameters: 5103490

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters: -DEV=xlh
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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
- 16: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
- 17: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000IA.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
- 25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	153	100.0	461	18	AAT85150	Murine monoclonal
2	153	100.0	461	20	AAV83773	Antibody 11D10 hea
3	153	100.0	461	25	AA151274	Mouse 11D10 antiho
4	31	20.3	458	17	AAT31333	Anti-idiotypic mono
5	31	20.3	458	20	AAZ31366	MAB 1A7 heavy chain
6	31	20.3	458	20	AAZ89553	Heavy chain variab
7	30	19.6	458	20	AAZ60630	Monoclonal antibod
8	27	17.6	366	20	AAZ82028	Anti-5TX1 heavy ch
9	22	14.4	861	16	AAQ81500	sfv anti-rev seque
10	22	14.4	861	16	AAZ45347	Single chain sfv a
11	20	13.1	765	22	AAZ85590	DNA encoding a fus
12	20	13.1	765	22	AAZ85591	DNA encoding a fus
13	20	13.1	1239	22	AAZ85593	DNA encoding a fus
14	20	13.1	1280	22	AAZ85564	Anti-CD20 single c
15	20	13.1	1925	21	AAZ15019	DNA encoding a CD-
16	19	12.4	360	18	AAZ96345	CDNA for Ig heavy
17	19	12.4	373	15	AAZ71395	Anti-carcinoembryo
18	19	12.4	373	15	AAZ71396	Anti-carcinoembryo
19	19	12.4	399	16	AAZ90425	DNA encoding anti-
20	19	12.4	402	14	AAZ37471	Sequence encoding
21	19	12.4	402	16	AAZ90426	DNA encoding anti-
22	19	12.4	402	17	AAZ47894	MAB NM-01 heavy ch
23	19	12.4	420	22	AAZ81910	Anti-CA125 bifunct
24	19	12.4	447	20	AAZ57786	Anti-HCV Ser/Thr p
25	19	12.4	458	10	AAZ91146	2H7 Vh sequence.
26	19	12.4	459	20	AAZ82357	Mouse antibody 2H7
27	19	12.4	459	22	AAZ22070	2H7 heavy chain va
28	19	12.4	470	16	AAZ99892	Mouse VIA-4 antibo
29	19	12.4	470	18	AAZ74760	Alpha-4 integrin m
30	19	12.4	474	18	AAZ70808	Mouse anti-idiotyp
31	19	12.4	474	18	AAZ70810	Mouse anti-idiotyp
32	19	12.4	477	18	AAZ70806	Mouse anti-idiotyp
33	19	12.4	486	18	AAZ59339	MH1 monoclonal ant
34	19	12.4	491	18	AAZ70868	2H7 heavy chain va
35	19	12.4	491	19	AAZ18557	Mouse 2H7 antibody
36	19	12.4	491	19	AAZ03926	Mouse 2H7 antibody
37	19	12.4	491	19	AAZ18593	Mouse 2H7 antibody
38	19	12.4	518	18	AAZ36316	2H7 antibody heavy
39	19	12.4	520	18	AAZ51042	Coding sequence fo
40	19	12.4	588	14	AAZ43385	H-chain V-region o
41	19	12.4	626	25	ACC44926	TSH receptor antib
42	19	12.4	626	25	ACC44927	TSH receptor antib
43	19	12.4	636	17	AAZ87815	Antibody 7G12 heav
44	19	12.4	642	25	ACC44914	TSH receptor antib
45	19	12.4	642	25	ACC44915	TSH receptor antib

ALIGNMENTS

RESULT 1
AAT85150
ID AAT85150 standard; cDNA; 461 BP.
XX AAT85150;
AC AAT85150;
XX
DT 25-MAR-2003 (updated).
DT 04-JAN-1998 (first entry)
XX
DE Murine monoclonal anti-idiotypic antibody 11D10 VH cDNA.
XX
KW Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
KW human milk fat globule; HMF; tumour; breast cancer; vaccine; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers

ID AAT31333 standard; cDNA; 458 BP.
 AC AAT31333;
 XX 25-MAR-2003 (updated)
 XX 26-FEB-1997 (first entry)
 DE Anti-idiotype monoclonal antibody 1A7 variable heavy chain, cDNA.
 XX Murine; mouse; anti-idiotype; monoclonal antibody; MAb; 1A7;
 XX variable heavy chain; ganglioside 2; GD2; 14G2a; neuroblastoma;
 KW glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;
 KW malignant melanoma; soft tissue sarcoma; small cell carcinoma;
 KW vaccine; treatment; palliate; detection; diagnosis;
 KW recombinant production; purification; probe; primer; assay;
 KW amplification; gene therapy; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 1..456
 FT /*tag= a
 FT /*transl_except= pos:373..375, aa:Trp
 XX
 PN W09622373-A2.
 XX
 XX 25-JUL-1996.
 XX
 XX 17-JAN-1996; 96WO-US00882.
 XX
 XX 17-JAN-1995; 95US-0372676.
 XX 16-JAN-1996; 96US-0591196.
 XX 17-JAN-1995; 95US-0372676.
 XX 16-JAN-1996; 96US-0591196.
 XX
 XX (KENT) UNIV KENTUCKY.
 XX
 XX Chatterjee M, Chatterjee SK, Foon KA;
 XX WPI; 1996-354530/35.
 XX P-PSDB; AAW03200.
 XX
 XX Monoclonal antibody 1A7 and related polynucleotide(s) and
 XX polypeptide(s) - useful to treat or palliate a GD2-associated
 XX disease, e.g. melanoma and glioma
 XX
 XX Claim 11; Fig 2; 141pp; English.
 XX
 CC The present sequence encodes the murine anti-idiotype monoclonal
 CC antibody (MAb) 1A7 variable heavy chain. MAb 1A7 was raised against
 CC the anti-ganglioside 2 (GD2) MAb 14G2a, which binds an unique
 CC epitope of GD2. As the glycosphingolipid GD2 is expressed at high
 CC density by human neuroectodermal tumours, e.g. malignant melanoma,
 CC neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma
 CC of the lung, MAb 1A7, or its cDNA can be used in a vaccine to treat
 CC or palliate such diseases. They can also be used to reduce the
 CC risk of recurrence of a clinically detectable tumour, and detect an
 CC anti-GD2 Ab bound to a tumour cell.
 CC MAb 1A7 overcomes immune tolerance and induces an immune response
 CC against GD2, which comprises anti-GD2 Ab (humoral response) and
 CC GD2-specific cells (cellular response). It can be used to purify
 CC anti-1A7 (AB3), anti-GD2 (AB1') or 14G2a (AB1), detect anti-1A7 or
 CC anti-GD2 in a sample or measure the level of cellular anti-1A7 or
 CC anti-GD2 activity.
 CC The cDNA can be used in expression systems for 1A7 prodn., and in
 CC the prepn. of probes and primers to respectively assay for 1A7
 CC cDNA, and amplify desired polynucleotides for use in gene therapy.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 458 BP; 106 A; 131 C; 114 G; 107 T; 0 other;
 Alignment Scores: 7.77e-20 Length: 458
 Pred. No.: 7.77e-20 Length: 458

Score: 31.00 Matches: 31
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 20.26% Indels: 0
 DB: 17 Gaps: 0
 US-08-836-455-4 (1-153) x AAT31333 (1-458)
 QY 123 AlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrPro 142
 Db 364 GCTCTGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCCAGCAAAACGACACC 423
 QY 143 ProProValTyrProLeuValProGlySerLeu 153
 Db 424 CCACCGGTCTATCCATTGGTCCCTGGAAGCTTG 456
 RESULT 5
 AAZ31366
 ID AAZ31366 standard; cDNA; 458 BP.
 XX
 XX AAZ31366;
 XX 07-FEB-2000 (first entry)
 XX
 XX MAb 1A7 heavy chain variable region encoding cDNA.
 XX
 KW Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma;
 KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
 KW tumor-associated antigen; ss.
 XX
 XX Synthetic.
 XX OS Mus sp.
 XX
 XX US5977316-A.
 XX
 XX 02-NOV-1999.
 XX
 XX 16-JAN-1996; 96US-0591196.
 XX
 XX 17-JAN-1995; 95US-0372676.
 XX
 XX (KENT) UNIV KENTUCKY.
 XX
 XX Foon KA, Chatterjee SK, Chatterjee M;
 XX WPI; 1999-619711/53.
 XX P-PSDB; AAY49210.
 XX
 XX Monoclonal antibody 1A7 which elicits an anti-GD2 immunological
 XX response, useful for the development of products for the detection and
 XX treatment of cancers -
 XX Disclosure; Fig 2; 74pp; English.
 XX
 CC The invention provides a monoclonal antibody (MAb) designated 1A7, which
 CC elicits an anti-GD2 (tumor-associated antigen) immunological response in
 CC humans. MAb 1A7 has defined light and heavy chain variable region
 CC sequences. The MAb 1A7 and polypeptides can be used for eliciting an
 CC anti-GD2 immune response. The polypeptides can also be used for detecting
 CC or purifying anti-GD2 antibody. The products can be used for treating GD2
 CC -associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue
 CC carcinoma, and small cell carcinoma. They can be used for palliating the
 CC disease or for reducing the risk of recurrence. The present sequence
 CC represents the cDNA encoding the heavy chain variable region of MAb 1A7.
 XX
 SQ Sequence 458 BP; 106 A; 131 C; 114 G; 107 T; 0 other;
 Alignment Scores: 7.77e-20 Length: 458
 Pred. No.: 31.00 Matches: 31
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 20.26% Indels: 0

DB: 20 Gaps: 0

US-08-836-455-4 (1-153) x AAX231366 (1-458)

QY 123 AlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThrPro 142
 |||||
 Db 364 GCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCCTCAGCCAAAGACACCC 423

QY 143 ProProValTyrProLeuValProGlySerLeu 153
 |||||
 Db 424 CCACCGCTATCCATTGTCCTCGGAGCTTG 456

RESULT 6
 ID AAX89553
 XX AAX89553 standard; cDNA; 458 BP.
 AC AAX89553;
 XX
 DT 06-OCT-1999 (first entry)
 XX
 DE Heavy chain variable region of MAb 1A7.
 XX
 DE heavy chain variable region; antibody 1A7; T cell response; melanoma;
 KW ganglioside GD2; CDR; complementarity determining region; carcinoma; ss.
 KW
 XX Mus musculus.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..456
 FT /*tag= a
 FT /product= "vh chain MAb 1A7
 FT /note= "No stop codon given"
 FT sig_peptide 1..57
 FT /*tag= b
 FT mat_peptide 58..456
 FT /*tag= c
 XX
 PN US5935821-A.
 XX
 PD 10-AUG-1999.
 XX
 PF 21-NOV-1996; 96US-0752844.
 XX
 PR 21-NOV-1996; 96US-0752844.
 PR 17-JAN-1995; 95US-0372676.
 PR 16-JAN-1996; 96US-0591196.
 XX
 PA (KENT) UNIV KENTUCKY.
 XX
 PI Chatterjee M, Chatterjee SK, Foon KA;
 XX
 DR WPI; 1999-457600/38.
 DR P-PSDB; AAV28469.
 XX
 PT Anti-GD2 immunological peptides useful for the treatment of tumours
 PT especially melanomas and small cell carcinomas
 PS
 PS Claim 7; Fig 2; 84pp; English.
 XX
 CC The sequence is the variable heavy chain region of monoclonal
 CC anti-idiotypic antibody 1A7. The polypeptide encoded by this sequence has
 CC three CDRs (complementarity determining regions). When administered to
 CC an individual the 1A7 antibody induces an immune response against
 CC ganglioside GD2. The light chain variable region of the 1A7 antibody
 CC (AAV28469) is also capable of eliciting an anti GD2 response in mammals.
 CC Both the heavy and light chain variable regions of the 1A7 antibody
 CC produce anti-GD2 T cell and antibody responses. The peptides and
 CC antibodies may be useful for the modulation of ganglioside GD2, and
 CC particularly for the treatment of GD2-associated tumours (e.g. melanoma,
 CC neuroblastoma, glioma, soft tissue sarcoma, and small cell carcinoma
 CC (including small cell lung cancer)).
 XX
 SQ Sequence 458 BP; 106 A; 131 C; 114 G; 107 T; 0 other;

Alignment Scores:
 Pred. No.: 7.77e-20 Length: 458
 Score: 31.00 Matches: 31
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 20.26% Indels: 0
 DB: 20 Gaps: 0

US-08-836-455-4 (1-153) x AAX89553 (1-458)

QY 123 AlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThrPro 142
 |||||
 Db 364 GCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCCTCAGCCAAAGACACCC 423

QY 143 ProProValTyrProLeuValProGlySerLeu 153
 |||||
 Db 424 CCACCGCTATCCATTGTCCTCGGAGCTTG 456

RESULT 7
 AAX60630
 ID AAX60630 standard; cDNA; 458 BP.
 XX
 AC AAX60630;
 XX
 DT 03-AUG-1999 (first entry)
 XX
 DE Monoclonal antibody 1A7 heavy chain variable region encoding cDNA.
 DE
 XX
 KW Psoriasis; immunological response; anti-idiotypic antibody; glutamate;
 KW chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis;
 KW monoclonal antibody; 1A7; ss.
 XX
 OS Unidentified.
 XX
 PN WO9925380-A2.
 XX
 PD 27-MAY-1999.
 XX
 PF 17-NOV-1998; 98WO-US24607.
 XX
 PR 16-NOV-1998; 98US-0192838.
 PR 17-NOV-1997; 97US-0065774.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 PI Chatterjee M, Foon KA;
 XX
 DR WPI; 1999-347407/29.
 DR P-PSDB; AAV21546.
 XX
 PT Treatment of psoriasis
 XX
 PS Disclosure; Fig 3; 48pp; English.
 XX
 CC The invention provides a method of treating of psoriasis by administering
 CC an antigen which has similar immunogenic properties to an antigen
 CC expressed on cells of psoriatic tissue so that an immunological response
 CC is elicited in the individual. The antigen stimulates the generation of
 CC anti-idiotypic antibodies that neutralize the aberrant immune response
 CC causing the psoriasis. The method is used to treat psoriasis, especially
 CC chronic plaque, glutamate, pustular, plaque-type psoriasis or psoriatic
 CC arthritis. The compositions allow the individual's own immune system to
 CC act against psoriatic tissue. The present sequence represents a cDNA
 CC encoding the heavy chain variable region of monoclonal antibody 1A7.
 XX
 SQ Sequence 458 BP; 106 A; 132 C; 113 G; 107 T; 0 other;

Alignment Scores:
 Pred. No.: 6.67e-19 Length: 458
 Score: 30.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 19.61% Indels: 0
 DB: 20 Gaps: 0

US-08-836-455-4 (1-153) x AAX60630 (1-458)

Qy 123 AlaLeuAspYrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrPro 142
 Db 364 GCTGTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCCTCAGCAAAACGACACCC 423

Qy 143 ProProValTyrProLeuValProGlySer 152
 Db 424 CCACCCGTCATCCATTGGTCCCTGGGAGC 453

RESULT 8
 AAX82028
 ID AAX82028 standard; DNA; 366 BP.
 XX
 AC AAX82028;
 XX
 DT 10-SEP-1999 (first entry)
 XX
 DE Anti-STX1 heavy chain variable region encoding DNA.
 XX
 KW Humanised; monoclonal antibody; MAb; Shiga toxin; immunoglobulin;
 KW Ig constant region; enterohemorrhagic Escherichia coli; EHEC; uremia;
 KW edema; bloody diarrhoea; hemorrhagic colitis; hemolytic uremic syndrome;
 KW thrombocytopenia; EHEC-mediated disease; anti-STX1; ss.
 XX
 OS Shigella dysenteriae.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..366
 FT /*tag= a
 FT /transl_except= (pos;67..60, aa:Asp)
 FT /note= "the start and stop codons are not indicated"

WO9932645-A1.
 XX
 PD 01-JUL-1999.
 XX
 PF 22-DEC-1998; 98WO-US27267.
 XX
 PR 18-DEC-1998; 98US-0215163.
 PR 23-DEC-1997; 97US-0086635.
 XX
 PA (MELT/) MELTON-CELSA A.
 PA (OBRI/) O'BRIEN A D.
 PA (SCHM/) SCHMITT C K.
 PA (STIN/) STINSON J L.
 PA (WONG/) WONG H.
 XX
 PI Melton-Celsa A, O'Brien AD, Schmitt CK, Stinson JL;
 PI Wong H;
 XX
 DR WPI: 1999-418935/35.
 DR P-PSDB: AAY21816.
 XX
 PT Humanized monoclonal antibodies against Shiga toxins, useful for
 PT protection against enterohemorrhagic Escherichia coli or other Shiga
 PT toxin producing bacteria
 XX
 PS Claim 11; Fig 3; 75pp; English.
 XX

The invention relates to humanised monoclonal antibodies (MAb) against Shiga toxins. The humanised MAb that binds to Shiga toxin comprises a constant and a variable region, where: (a) the constant region contains at least part of a human immunoglobulin (Ig) constant region; and (b) the variable region contains at least part of a non-human Ig variable region. Host cells transformed with vectors encoding a humanised MAb against Shiga toxin type 2 is useful for treating a patient with an infection caused by enterohemorrhagic Escherichia coli (EHEC) or other Shiga toxin producing bacteria. The humanised MAb can also be used to reduce illness caused by EHEC or other Shiga toxin producing bacteria. EHEC are

CC associated with food-borne outbreaks of bloody diarrhoea (hemorrhagic colitis) and the hemolytic uremic syndrome. In particular, the humanised MAb ameliorate edema, thrombocytopenia and uremia associated with EHEC-mediated disease. The present sequence represents a DNA encoding an anti-STX1 heavy chain variable region.

XX
 SQ Sequence 366 BP; 94 A; 92 C; 92 G; 88 T; 0 other;

Alignment Scores:
 Pred. No.: 3.42e-16 Length: 366
 Score: 27.00 Matches: 27
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 17.65% Indels: 0
 DB: 20 Gaps: 0

US-08-836-455-4 (1-153) x AAX82028 (1-366)

Qy 89 LeuThrAlaAspThrSerSerSerThrAlaTyrMetGlnIleSerSerLeuThrSerGlu 108
 Db 208 TTGACTCGACACATCTCCAGCACAGCCTACATGATCATGACATCTGACATCTGAA 267

Qy 109 AspSerAlaValTyrPheCys 115
 Db 268 GACTCTCGGTCTATTCTGT 288

RESULT 9
 AAO81500
 ID AAO81500 standard; cDNA; 861 BP.
 XX
 AC AAO81500;
 XX
 DT 25-MAR-2003 (updated)
 DT 30-AUG-1995 (first entry)
 XX
 DE sfv anti-rev sequence.
 XX
 KW HIV-1; human immunodeficiency virus type 1; AIDS; Rev protein;
 KW intracellular immunization; gene therapy; single chain antibody; Fv;
 KW sfv; antibody engineering; resistance; cell immunity; HeLa; ss.
 XX
 OS Synthetic.
 XX
 PN WO9503832-A1.
 XX
 PD 09-FEB-1995.
 XX
 PF 28-JUL-1994; 94WO-US08448.
 XX
 PR 30-JUL-1993; 93US-0099870.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Duan L, Pomerantz R;
 XX
 DR WPI: 1995-082039/11.
 XX
 PT Method for conducting gene therapy - comprises using recombinant
 PT gene encoding antibody binding antigen associated with a disease;
 PT useful for providing cell immunity.
 XX
 PS Example 4; Page 23; 62pp; English.
 XX

The sequence given in AAO81500 encodes an sfv anti-rev antibody consisting of the variable domains of the heavy and light chains of a mouse MAb against HIV-1 IIIB rev. The sfv specifically binds a highly conserved Rev domain. HeLa T4 cells expressing the sfv were resistant to all HIV-1 clinical isolates tested.
 (Updated on 25-MAR-2003 to correct PN field.)

XX
 SQ Sequence 861 BP; 199 A; 234 C; 230 G; 198 T; 0 other;

Alignment Scores:

Pred. No.: 3.53e-11 Length: 861
 Score: 22.00 Matches: 22
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 14.38% Indels: 0
 DB: 16 Gaps: 0

US-08-836-455-4 (1-153) x AAQ81500 (1-861)

QY 126 TyrTrpGlyGlnGlyThrValSerSerAlaLysThrThrProProVal 145
 DB 794 TACTGGGTCAGGAACCTCAGTCACCGTCTCTCAGCCAAACGACACCCCGTC 853
 QY 146 TyrPro 147
 DB 854 TATCCT 859

RESULT 10

AA45347

ID AAT45347 standard; cDNA; 861 BP.

XX AC AAT45347;

DT 08-AUG-1997 (first entry)

XX Single chain sfv anti-rev antibody encoding cDNA.

KW Gene therapy; antibody; immunisation; human immunodeficiency virus;
 KW HIV; human T-cell leukaemia virus; ss.

XX Mus musculus.

XX WO9637234-A1.

XX 28-NOV-1996.

XX 23-MAY-1996; 96WO-US07393.

XX 23-MAY-1995; 95US-0447610.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Duan L, Pomerantz RJ;

XX WPI; 1997-020948/02.

XX Improved gene therapy using recombinant gene coding for an antibody
 PT - for intracellular immunisation against pathogens recognised by the
 PT antibody, esp. human immunodeficiency virus HIV-1

PS Example 4; Page 54; 213pp; English.

XX The present sequence encodes a single chain sfv anti-rev antibody
 CC constructed using variable domains of the heavy and light chains of a
 CC murine monoclonal antibody against (HIV-1/IIIB) rev (the parent
 CC antibody). This is incorporated into a viral vector where
 CC expression of the anti-rev gene causes inhibition of the rev function
 CC and so affects replication of the other virus (HIV). Rev is one of the
 CC essential regulatory proteins of HIV, it binds to rev responsive element
 CC (RRE) and promotes the nuclear export, stabilisation and utilisation of
 CC the viral mRNA's containing RRE. A novel gene therapy method has been
 CC produced, where a recombinant (rev) gene is introduced into the cells of
 CC a mammal. The method is improved by using a rec gene encoding an
 CC antibody (Ab) that is selectively specific for an intracellular (IC)
 CC antigen associated with a disease. The method is used to prevent or
 CC halt the progress of a disease by IC immunisation. Specifically, the Ab
 CC can be used to inhibit the replication of a virus, such as human T-cell
 CC leukaemia virus or especially HIV-1, or of other pathogens, e.g.
 CC bacteria, fungi. The method provides immunity before or after the
 CC development of the disease and can be used to control the severity of
 CC the disease.

XX Sequence 861 BP; 199 A; 234 C; 230 G; 198 T; 0 other;

Alignment Scores:

Pred. No.: 3.53e-11 Length: 861
 Score: 22.00 Matches: 22
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 14.38% Indels: 0
 DB: 18 Gaps: 0

US-08-836-455-4 (1-153) x AAT45347 (1-861)

QY 126 TyrTrpGlyGlnGlyThrValSerSerAlaLysThrThrProProVal 145
 DB 794 TACTGGGTCAGGAACCTCAGTCACCGTCTCTCAGCCAAACGACACCCCGTC 853

QY 146 TyrPro 147

DB 854 TATCCT 859

RESULT 11

AA86590

ID AAC86590 standard; DNA; 765 BP.

XX AC AAC86590;

DT 02-APR-2001 (first entry)

XX DNA encoding a fusion of a single chain antibody and streptavidin.

XX Streptavidin; tumour cell; cancer; adenocarcinoma;

XX hematological malignancy; ss.

XX Synthetic.

XX Streptomyces avidinii.

XX Unidentified.

XX WO200075333-A1.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000WO-US15595.

XX 07-JUN-1999; 99US-0137900.

XX 03-DEC-1999; 99US-0168976.

XX (NEOR-) NEORX CORP.

XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;

XX WPI; 2001-091213/10.

XX New vector constructs for expressing genomic streptavidin fusion
 PT proteins which are useful for targeting tumour cells associated with
 PT cancer, e.g. adenocarcinomas -

PS Example 5; Page 95; 100pp; English.

XX The present sequence encodes a fusion of an anti-CD20 single chain
 CC antibody and streptavidin. The fusion protein is expressed using
 CC vectors of the invention. The specification describes vector constructs
 CC for expressing streptavidin fusion proteins. The vector comprises a
 CC nucleic acid encoding streptavidin or its functional variant operatively
 CC linked to a promoter, and a cloning site for insertion of a second
 CC nucleic acid sequence encoding a polypeptide to be fused with
 CC streptavidin, interposed between the promoter and the first nucleic
 CC acid sequence. Alternatively, the vector construct comprises a nucleic
 CC acid, operatively linked to a promoter, encoding a polypeptide to be
 CC fused with streptavidin, and a cloning site for insertion of a second
 CC nucleic acid encoding at least 129 amino acids of streptavidin or its
 CC functional variant. The fusion proteins are useful for targeting tumour
 CC cells, particularly tumour cells associated with cancer.
 CC e.g. adenocarcinomas or hematological malignancies. The vector construct
 CC is useful for expressing of streptavidin fusion proteins. In particular,

CC these are useful as tools for medical diagnostics and therapeutic
CC purposes, e.g. for detecting the presence or absence of, or treating, a
CC target site within a mammalian host.

XX
SQ Sequence 765 BP; 169 A; 201 C; 230 G; 165 T; 0 other;

Alignment Scores:
Pred. No.: 2.33e-09 Length: 765
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 22 Gaps: 0

US-08-836-455-4 (1-153) x AAC86590 (1-765)

QY 49 ThrSerTyrAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
Db 88 ACCAGTTACAAATGCACTGGGTAAAGCAGACACCTGGACAGGCCCTGGGATGGATTGGA 147

RESULT 12

AAC86591
ID AAC86591 standard; DNA; 765 BP.

XX AAC86591;

XX 02-APR-2001 (first entry)

XX DNA encoding a fusion of a single chain antibody and streptavidin.

XX Streptavidin; tumour cell; cancer; adenocarcinoma;
KW hematological malignancy; ss.

XX Synthetic.
OS Streptomyces avidinii.
OS Unidentified.

XX WO200075333-Al.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000WO-US15595.

XX 07-JUN-1999; 99US-0137900.

XX 03-DEC-1999; 99US-0168976.

XX (NEOR-) NEORX CORP.

XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;

XX WPI; 2001-091213/10.

XX New vector constructs for expressing genomic streptavidin fusion
XX proteins which are useful for targeting tumour cells associated with
XX cancer, e.g. adenocarcinomas -

XX Example 5; Page 95; 100pp; English.

XX The present sequence encodes a fusion of an anti-CD20 single chain
XX antibody and streptavidin. The fusion protein is expressed using
XX vectors of the invention. The specification describes vector constructs
XX for expressing streptavidin fusion proteins. The vector comprises a
XX nucleic acid encoding streptavidin or its functional variant operatively
XX linked to a promoter, and a cloning site for insertion of a second
XX nucleic acid sequence encoding a polypeptide to be fused with
XX streptavidin, interposed between the promoter and the first nucleic
XX acid sequence. Alternatively, the vector construct comprises a nucleic
XX acid, operatively linked to a promoter, encoding a polypeptide to be
XX fused with streptavidin, and a cloning site for insertion of a second
XX nucleic acid encoding at least 129 amino acids of streptavidin or its
XX functional variant. The fusion proteins are useful for targeting tumour
XX cells, particularly tumour cells associated with cancer,
XX e.g. adenocarcinomas or hematological malignancies. The vector construct

CC is useful for expressing of streptavidin fusion proteins. In particular,
CC these are useful as tools for medical diagnostics and therapeutic
CC purposes, e.g. for detecting the presence or absence of, or treating, a
CC target site within a mammalian host.

XX
SQ Sequence 765 BP; 170 A; 201 C; 231 G; 163 T; 0 other;

Alignment Scores:
Pred. No.: 2.33e-09 Length: 765
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 22 Gaps: 0

US-08-836-455-4 (1-153) x AAC86591 (1-765)

QY 49 ThrSerTyrAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
Db 88 ACCAGTTACAAATGCACTGGGTAAAGCAGACACCTGGACAGGCCCTGGGATGGATTGGA 147

RESULT 13

AAC86563

ID AAC86563 standard; DNA; 1239 BP.

XX AAC86563;

XX 02-APR-2001 (first entry)

XX DNA encoding a fusion of anti-CD20 single chain antibody/streptavidin.

XX Streptavidin; tumour cell; cancer; adenocarcinoma;
KW hematological malignancy; ss.

XX Synthetic.
OS Streptomyces avidinii.
OS Homo sapiens.

XX WO200075333-Al.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000WO-US15595.

XX 07-JUN-1999; 99US-0137900.

XX 03-DEC-1999; 99US-0168976.

XX (NEOR-) NEORX CORP.

XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;

XX WPI; 2001-091213/10.

XX P-PSDB; AAB30694.

XX New vector constructs for expressing genomic streptavidin fusion
XX proteins which are useful for targeting tumour cells associated with
XX cancer, e.g. adenocarcinomas -

XX Example 2; Fig 11A; 100pp; English.

XX The present sequence encodes a fusion of an anti-CD20 single chain
XX antibody (B9E9) streptavidin. The fusion protein is expressed using
XX vectors of the invention. The specification describes vector constructs
XX for expressing streptavidin fusion proteins. The vector comprises a
XX nucleic acid encoding streptavidin or its functional variant operatively
XX linked to a promoter, and a cloning site for insertion of a second
XX nucleic acid sequence encoding a polypeptide to be fused with
XX streptavidin, interposed between the promoter and the first nucleic
XX acid sequence. Alternatively, the vector construct comprises a nucleic
XX acid, operatively linked to a promoter, encoding a polypeptide to be
XX fused with streptavidin, and a cloning site for insertion of a second
XX nucleic acid encoding at least 129 amino acids of streptavidin or its
XX functional variant. The fusion proteins are useful for targeting tumour

CC cells, particularly tumour cells associated with cancer,
 CC e.g. adenocarcinomas or hematological malignancies. The vector construct
 CC is useful for expressing of streptavidin fusion proteins. In particular,
 CC these are useful as tools for medical diagnostics and therapeutic
 CC purposes, e.g. for detecting the presence or absence of, or treating, a
 CC target site within a mammalian host.

XX Sequence 1239 BP; 270 A; 392 C; 356 G; 221 T; 0 other;

Alignment Scores:
 Pred. No.: 3.64e-09 Length: 1239
 Score: 20.00 Matches: 20
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 13.07% Indels: 0
 DB: 22 Gaps: 0

US-08-836-455-4 (1-153) x AAC86563 (1-1239)

QY 49 ThrSerTyAsnMethIstTpVallySGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
 |||||
 Db 469 ACCAGTTACAATATGCTGGTAAAGCAGACACCTGGACAGGCGCTGGGAATGGATTGGA 528

RESULT 14

AAC86564
 ID AAC86564 standard; DNA; 1280 BP.

XX AAC86564;

XX 02-APR-2001 (first entry)

XX Anti-CD20 single chain antibody/streptavidin fusion protein cassette.

XX Streptavidin; tumour cell; cancer; adenocarcinoma;
 XX hematological malignancy; ss.

XX Synthetic.

XX Streptomyces avidinii.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 3..1274

FT /tag- a
 FT /product- "anti-CD20 scFv and streptavidin fusion"

XX WO200075333-A1.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000WO-US15595.

XX 07-JUN-1999; 99US-0137900.

XX 03-DEC-1999; 99US-0168976.

XX (NEOR-) NEORX CORP.

XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;

XX WPI: 2001-091213/10.

XX P-PSDB; AAB30695.

XX New vector constructs for expressing genomic streptavidin fusion
 PT proteins which are useful for targeting tumour cells associated with
 PT cancer, e.g. adenocarcinomas -

XX Example 2; Fig 11C; 100pp; English.

XX The present sequence encodes a fusion of an anti-CD20 single chain
 CC antibody (B9E9) streptavidin. The fusion protein is expressed using
 CC vectors of the invention. The specification describes vector constructs
 CC for expressing streptavidin fusion proteins. The vector comprises a
 CC nucleic acid encoding streptavidin or its functional variant operatively
 CC linked to a promoter, and a cloning site for insertion of a second

CC nucleic acid sequence encoding a polypeptide to be fused with
 CC streptavidin, interposed between the promoter and the first nucleic
 CC acid sequence. Alternatively, the vector construct comprises a nucleic
 CC acid operatively linked to a promoter, encoding a polypeptide to be
 CC fused with streptavidin, and a cloning site for insertion of a second
 CC nucleic acid encoding at least 129 amino acids of streptavidin or its
 CC functional variant. The fusion proteins are useful for targeting tumour
 CC cells, particularly tumour cells associated with cancer,
 CC e.g. adenocarcinomas or hematological malignancies. The vector construct
 CC is useful for expressing of streptavidin fusion proteins. In particular,
 CC these are useful as tools for medical diagnostics and therapeutic
 CC purposes, e.g. for detecting the presence or absence of, or treating, a
 CC target site within a mammalian host.

XX Sequence 1280 BP; 267 A; 397 C; 388 G; 228 T; 0 other;

Alignment Scores:

Pred. No.: 3.75e-09 Length: 1280
 Score: 20.00 Matches: 20
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 13.07% Indels: 0
 DB: 22 Gaps: 0

US-08-836-455-4 (1-153) x AAC86564 (1-1280)

QY 49 ThrSerTyAsnMethIstTpVallySGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
 |||||
 Db 96 ACCAGTTACAATATGCTGGTAAAGCAGACACCTGGACAGGCGCTGGGAATGGATTGGA 155

RESULT 15

AAA15019

ID AAA15019 standard; DNA; 1925 BP.

XX AAA15019;

XX 21-AUG-2000 (first entry)

XX DNA encoding a CD-20 specific chimeric receptor.

XX CD20-specific receptor; CD-20 specific redirected T cell; leukemia;

XX CD20+ malignancy; non-Hodgkin's lymphoma; myeloablative chemotherapy;

XX stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis; ss.

XX Synthetic.

XX Mus sp.

XX Key Location/Qualifiers

XX CDS 27..1928

XX /*tag= a

XX WO200023573-A2.

XX 27-APR-2000.

XX 20-OCT-1999; 99WO-US24484.

XX 20-OCT-1998; 98US-0105014.

XX (CITY) CITY OF HOPE.

XX Raubitschek A, Jensen MC, Wu AM;

XX WPI: 2000-339676/29.

XX P-PSDB; AAY84965.

XX Genetically engineered CD20-specific redirected T cells useful for

XX treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+

XX acute or chronic leukemia, and autoimmune disease -

XX Example 1; Page 50-53; 58pp; English.

XX The present sequence encodes a synthetic CD20-specific chimeric

CC receptor. The specification describes CD-20 specific redirected T cells
CC which express and bear on the cell surface membrane a CD20-chimeric
CC receptor comprising an intracellular signalling domain, a transmembrane
CC domain and an extracellular domain, the extracellular domain comprising
CC a CD20-specific receptor. The genetically engineered CD20-specific
CC redirected T cells are useful for treating a CD20+ malignancy, such
CC as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, in a
CC human patient having previously undergone myeloablative chemotherapy and
CC stem cell rescue. The genetically engineered CD20-specific redirected
CC T cells are also useful for abrogating an untoward B cell function, such
CC as autoimmune disease (lupus or rheumatoid arthritis) in a patient.
XX
SQ Sequence 1925 BP; 471 A; 554 C; 541 G; 359 T; 0 other;

Alignment Scores:
Pred. No.: 5.48e-09 Length: 1925
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 21 Gaps: 0
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Qy 49 ThrSerTyrAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
Db 546 ACCAGTTACAATATGCACCTGGTAAAGCAGACACCTGGACAGGCGCTGGATGGATTGGA 605

Search completed: August 31, 2003, 01:16:26
Job time : 232.013 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 31, 2003, 01:02:06 ; Search time 202.802 Seconds
(without alignments)
1730.853 Million cell updates/sec

Title: us-08-836-455-4

Perfect score: 153

Sequence: 1 MNCWVFLLSITTVGHVSQ.....TVSSAKTTPPPVPLVPGSL 153

Scoring table:

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1533700 seqs, 1147125425 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3063161

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-DB=Published_Applications_NA_QFMT-fastap -SUFFIX=p2noli.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=PCO -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US08836455 @CGN_1.1_271 @runat_29082003_132954_23062
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -XGAPOP=60 -XGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Published_Applications_NA:*
1: /cgn2.6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2.6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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10: /cgn2.6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2.6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2.6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	153	100.0	461	9 US-09-861-294-3 Sequence 3, Appli

2	153	100.0	461	12 US-10-367-506-3 Sequence 3, Appli
3	31	20.3	458	10 US-09-990-205-3 Sequence 3, Appli
4	31	20.3	458	14 US-10-153-401-3 Sequence 3, Appli
5	20	13.1	765	12 US-10-244-821-44 Sequence 44, Appl
6	20	13.1	765	12 US-10-244-821-45 Sequence 45, Appl
7	20	13.1	765	14 US-10-013-173-44 Sequence 44, Appl
8	20	13.1	765	14 US-10-013-173-45 Sequence 44, Appl
9	20	13.1	765	14 US-10-150-762-44 Sequence 44, Appl
10	20	13.1	765	14 US-10-150-762-45 Sequence 45, Appl
11	20	13.1	1239	14 US-10-244-821-5 Sequence 5, Appli
12	20	13.1	1239	14 US-10-013-173-5 Sequence 5, Appli
13	20	13.1	1280	12 US-10-150-762-5 Sequence 5, Appli
14	20	13.1	1280	14 US/10/244 Sequence 7, Appli
15	20	13.1	1280	14 US/10/013 Sequence 7, Appli
16	20	13.1	1280	14 US/10/150 Sequence 7, Appli
17	19	12.4	736	13 US-10-006-773-12 Sequence 12, Appl
18	19	12.4	786	12 US-10-244-821-37 Sequence 37, Appl
19	19	12.4	786	14 US-10-013-173-37 Sequence 37, Appl
20	19	12.4	786	14 US-10-150-762-37 Sequence 37, Appl
21	17	11.1	414	13 US-10-146-305-6 Sequence 6, Appli
22	17	11.1	454	10 US-09-797-941A-1 Sequence 1, Appli
23	17	11.1	518	9 US-09-881-823-17 Sequence 17, Appl
24	16	10.5	360	10 US-09-910-059-10 Sequence 10, Appl
25	16	10.5	408	9 US-09-564-329A-10 Sequence 10, Appl
26	16	10.5	408	10 US-09-855-153-10 Sequence 10, Appl
27	16	10.5	408	10 US-09-854-811-10 Sequence 10, Appl
28	16	10.5	408	10 US-09-934-773-10 Sequence 10, Appl
29	16	10.5	408	10 US-09-963-620-10 Sequence 10, Appl
30	16	10.5	408	11 US-09-855-632-10 Sequence 10, Appl
31	16	10.5	408	12 US-10-224-720-10 Sequence 10, Appl
32	16	10.5	408	12 US-10-225-779-10 Sequence 10, Appl
33	16	10.5	408	14 US-10-225-784-10 Sequence 10, Appl
34	16	10.5	478	13 US-10-040-739-911 Sequence 911, App
35	16	10.5	765	10 US-09-910-059-18 Sequence 18, Appl
36	16	10.5	1173	12 US-10-075-947A-4 Sequence 4, Appli
37	15	9.8	339	10 US-09-924-099-12 Sequence 12, Appl
38	15	9.8	412	10 US-09-924-099-28 Sequence 28, Appl
39	15	9.8	436	11 US-09-967-719C-7 Sequence 7, Appli
40	15	9.8	462	11 US-09-967-719C-1 Sequence 1, Appli
41	15	9.8	690	10 US-09-995-693-4 Sequence 4, Appli
42	15	9.8	690	14 US-10-232-408-4 Sequence 4, Appli
43	15	9.8	711	10 US-09-924-099-19 Sequence 19, Appl
44	15	9.8	714	8 US-08-940-544-4 Sequence 4, Appli
45	15	9.8	714	12 US-10-075-947A-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-861-294-3
; Sequence 3, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(461)

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; NAME/KEY: sig_peptide
; LOCATION: (1)...(57)
; NAME/KEY: mat_peptide
; LOCATION: (58)...(461)
US-09-861-294-3

Alignment Scores:
Pred. No.: 6,85e-146 Length: 461
Score: 153.00 Matches: 153
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-08-836-455-4 (1-153) x US-09-861-294-3 (1-461)
Qy 1 MetGluCysSerTrpValPheLeuLeuSerIleThrThrGlyValHisSerGln 20
Db 1 ATGAATGCAGCTGGGCTTCTCTCTCTGTCATAACTACAGGTGTCCACTCCAG 60
Qy 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
Db 61 GCTTATCTACAGCAGCTGGGGCTGAGCTGGTGGGCTCAGTGAAGATGTC 120
Qy 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethIstPValLysGlnThrPro 60
Db 121 TGCAAGGCTTCTGGCTACACATTGACCAGTACAAATATGCACTGGGTAAAGCAGACAC 180
Qy 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
Db 181 GGACAGGCTTGGATGGATGGAAATATTTCTCTGGAATATTTCTCTGGAATGTTACTTAC 240
Qy 81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet 100
Db 241 CAGAAGTTTAAAGGCAAGGCTCATTCACCTGCAGACACATCCTCCAGCAGCCTACATG 300
Qy 101 GlnIleSerSerLeuThrSerGluAspSerAlaValPheCysAlaArgGlyAsnTrp 120
Db 301 CAGATCAGACGCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGAACTGG 360
Qy 121 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr 140
Db 361 GAGGTGCTCTGGACTACTGGGTCAAGAACTCAGTCACTCCCTCTCTCTCAGCCAAAACG 420

RESULT 2
US-10-367-506-3
; Sequence 3, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMGF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (1)...(461)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(57)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (58)...(461)
US-10-367-506-3

Alignment Scores:
Pred. No.: 6,85e-146 Length: 461
Score: 153.00 Matches: 153
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-4 (1-153) x US-10-367-506-3 (1-461)
Qy 1 MetGluCysSerTrpValPheLeuLeuSerIleThrThrGlyValHisSerGln 20
Db 1 ATGAATGCAGCTGGGCTTCTCTCTCTGTCATAACTACAGGTGTCCACTCCAG 60
Qy 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
Db 61 GCTTATCTACAGCAGCTGGGGCTGAGCTGGTGGGCTCAGTGAAGATGTC 120
Qy 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMethIstPValLysGlnThrPro 60
Db 121 TGCAAGGCTTCTGGCTACACATTGACCAGTACAAATATGCACTGGGTAAAGCAGACAC 180
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Db 241 CAGAAGTTTAAAGGCAAGGCTCATTCACCTGCAGACACATCCTCCAGCAGCCTACATG 300
Qy 101 GlnIleSerSerLeuThrSerGluAspSerAlaValPheCysAlaArgGlyAsnTrp 120
Db 301 CAGATCAGACGCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGAACTGG 360
Qy 121 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr 140
Db 361 GAGGTGCTCTGGACTACTGGGTCAAGAACTCAGTCACTCCCTCTCTCTCAGCCAAAACG 420

RESULT 3
US-09-990-205-3
; Sequence 3, Application US/09990205
; Patent No. US20020150572A1
; GENERAL INFORMATION:
; APPLICANT: FOON, Kenneth A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000501
; CURRENT APPLICATION NUMBER: US/09/990,205
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: U.S. 09/192,838
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/065,774
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Mus Musculus
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(456)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(456)
US-09-990-205-3

Alignment Scores:
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Score: 31.00 Matches: 31
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.26% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-4 (1-153) x US-09-990-205-3 (1-458)
QY 123 AlaLeuAspTyrTrpGlnGlyThrSerValThrValSerSerAlaLysThrThrPro 142
Db 364 GCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCCAGCAAAAGACACCC 423
QY 143 ProProValTyrProLeuValProGlySerLeu 153
Db 424 CCACCCGTCTATCCATTTGGTCCCTGGAAGCTTG 456

RESULT 4
US-10-153-401-3
; Sequence 3, Application US/10153401
; Publication No. US20030114398A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malay A
; Foon, Kenneth A.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,401
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/293,533
; FILING DATE: 1999-04-15
; APPLICATION NUMBER: US 08/372,676
; FILING DATE: 1995-01-17
; APPLICATION NUMBER: US 08/591,196
; FILING DATE: 1996-01-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine M. Polizzi
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 304142000202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
;
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..456
; NAME/KEY: mat_peptide
; LOCATION: 58
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-153-401-3

Alignment Scores:
Pred. No.: 2,46e-22 Length: 458
Score: 31.00 Matches: 31
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.26% Indels: 0
DB: 14 Gaps: 0

US-08-836-455-4 (1-153) x US-10-153-401-3 (1-458)
QY 123 AlaLeuAspTyrTrpGlnGlyThrSerValThrValSerSerAlaLysThrThrPro 142
Db 364 GCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCCAGCAAAAGACACCC 423
QY 143 ProProValTyrProLeuValProGlySerLeu 153
Db 424 CCACCCGTCTATCCATTTGGTCCCTGGAAGCTTG 456

RESULT 5
US-10-244-821-44
; Sequence 44, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-244-821-44

Alignment Scores:
Pred. No.: 5.37e-11 Length: 765
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-4 (1-153) x US-10-244-821-44 (1-765)
QY 49 ThrSerTyrAsnMethIstTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIlegly 68
Db 88 ACCAGTTACAATATGCACTGGTAAAGACACACCTGGACGGCCTCGAATGATGGA 147

RESULT 6
US-10-244-821-45
; Sequence 45, Application US/10244821
```

```

; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C2B8 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-244-821-45

Alignment Scores:
Pred. NO.: 5.37e-11 Length: 765
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-4 (1-153) x US-10-244-821-45 (1-765)

QY 49 ThrSerTyrAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
Db 88 ACCAGTTACAATATGCACTGGTAAAGCAGACACCTGGAGGCGCTGGATGATGGA 147

RESULT 7
US-10-013-173-44
; Sequence 44, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-013-173-44

Alignment Scores:
Pred. No.: 5.37e-11 Length: 765
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 14 Gaps: 0

US-08-836-455-4 (1-153) x US-10-013-173-44 (1-765)

QY 49 ThrSerTyrAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
Db 88 ACCAGTTACAATATGCACTGGTAAAGCAGACACCTGGAGGCGCTGGATGATGGA 147

RESULT 8
US-10-013-173-45
; Sequence 45, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C2B8 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-013-173-45

Alignment Scores:
Pred. No.: 5.37e-11 Length: 765
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 14 Gaps: 0

US-08-836-455-4 (1-153) x US-10-013-173-45 (1-765)

QY 49 ThrSerTyrAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
Db 88 ACCAGTTACAATATGCACTGGTAAAGCAGACACCTGGAGGCGCTGGATGATGGA 147

RESULT 9
US-10-150-762-44
; Sequence 44, Application US/10150762
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150,762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-013-173-44

Alignment Scores:
Pred. No.: 5.37e-11 Length: 765
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 14 Gaps: 0

```

```

US-08-836-455-4 (1-153) x US-10-013-173-44 (1-765)

QY 49 ThrSerTyrAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
Db 88 ACCAGTTACAATATGCACTGGTAAAGCAGACACCTGGAGGCGCTGGATGATGGA 147

RESULT 8
US-10-013-173-45
; Sequence 45, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C2B8 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-013-173-45

Alignment Scores:
Pred. No.: 5.37e-11 Length: 765
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 14 Gaps: 0

US-08-836-455-4 (1-153) x US-10-013-173-45 (1-765)

QY 49 ThrSerTyrAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
Db 88 ACCAGTTACAATATGCACTGGTAAAGCAGACACCTGGAGGCGCTGGATGATGGA 147

RESULT 9
US-10-150-762-44
; Sequence 44, Application US/10150762
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150,762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-013-173-44

```



```
; OTHER INFORMATION: fusion construct
US-10-150-762-44
Alignment Scores:
Pred. No.: 5.37e-11 Length: 765
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 14 Gaps: 0

US-08-836-455-4 (1-153) x US-10-150-762-44 (1-765)
QY 49 ThrSerTyAsnMethIstRpVallysGlnThrProGlycInGlyLeuGluTrpIleGly 68
Db 88 ACCAGTTACAATATGCACTGGTAAAGACAGACACCTGGAGCGGCTGGAATGGATTGGA 147
RESULT 10
US-10-150-762-45
; Sequence 45, Application US/10150762
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150,762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C2B8 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
US-10-150-762-45
Alignment Scores:
Pred. No.: 5.37e-11 Length: 765
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 14 Gaps: 0

US-08-836-455-4 (1-153) x US-10-150-762-45 (1-765)
QY 49 ThrSerTyAsnMethIstRpVallysGlnThrProGlycInGlyLeuGluTrpIleGly 68
Db 88 ACCAGTTACAATATGCACTGGTAAAGACAGACACCTGGAGCGGCTGGAATGGATTGGA 147
RESULT 11
US-10-244-821-5
; Sequence 5, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; OTHER INFORMATION: fusion construct
US-10-150-762-44
Alignment Scores:
Pred. No.: 5.37e-11 Length: 765
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 14 Gaps: 0

US-08-836-455-4 (1-153) x US-10-150-762-44 (1-765)
QY 49 ThrSerTyAsnMethIstRpVallysGlnThrProGlycInGlyLeuGluTrpIleGly 68
Db 88 ACCAGTTACAATATGCACTGGTAAAGACAGACACCTGGAGCGGCTGGAATGGATTGGA 147
RESULT 12
US-10-013-173-5
; Sequence 5, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion
US-10-013-173-5
Alignment Scores:
Pred. No.: 8.25e-11 Length: 1239
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.07% Indels: 0
DB: 14 Gaps: 0

US-08-836-455-4 (1-153) x US-10-013-173-5 (1-1239)
QY 49 ThrSerTyAsnMethIstRpVallysGlnThrProGlycInGlyLeuGluTrpIleGly 68
Db 469 ACCAGTTACAATATGCACTGGTAAAGACAGACACCTGGAGCGGCTGGAATGGATTGGA 528
RESULT 13
US-10-150-762-5
; Sequence 5, Application US/10150762
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
```

```
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; GENERAL INFORMATION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150,762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion
US-10-150-762-5

Alignment Scores:
Pred. No.:      8.25e-11      Length:      1239
Score:          20.00        Matches:      20
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    13.07%       Indels:        0
DB:             14          Gaps:          0

US-08-836-455-4 (1-153) x US-10-150-762-5 (1-1239)

Qy 49 ThrSerTyraAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
|||||
Db 469 ACCAGTTACAATATGCACCTGGGTAAGACACACACCTGGACAGGCGCTGGATGGATTGGA 528

RESULT 14
US/10/244
; Sequence 7, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; GENERAL INFORMATION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1280
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion construct
US/10/244,821-7

Alignment Scores:
Pred. No.:      8.5e-11      Length:      1280
Score:          20.00        Matches:      20
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    13.07%       Indels:        0
DB:             12          Gaps:          0

US-08-836-455-4 (1-153) x US/10/244 (1-1280)

Qy 49 ThrSerTyraAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
```

```
|||||
Db 96 ACCAGTTACAATATGCACCTGGGTAAGACACACACCTGGACAGGCGCTGGATGGATTGGA 155

RESULT 15
US/10/013
; Sequence 7, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; GENERAL INFORMATION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1280
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion constru
US/10/013,173-7

Alignment Scores:
Pred. No.:      8.5e-11      Length:      1280
Score:          20.00        Matches:      20
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    13.07%       Indels:        0
DB:             14          Gaps:          0

US-08-836-455-4 (1-153) x US/10/013 (1-1280)

Qy 49 ThrSerTyraAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
|||||
Db 96 ACCAGTTACAATATGCACCTGGGTAAGACACACACCTGGACAGGCGCTGGATGGATTGGA 155

Search completed: August 31, 2003, 04:05:01
Job time : 205.802 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 30, 2003, 22:20:21 ; Search time 1841.13 Seconds
(without alignments)
2019.725 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 153
Sequence: 1 MECSWVFLLSITGVHSQ.....TVSSAKTTPPPVPLVPGSL 153

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 1

Total number of hits satisfying chosen parameters: 45562604

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q/cqn2.1/USPTO_spool/US08836455/runat_29082003_132953_23055/app_query.fasta_1.654
-DB=EST -QEXT=fastap -SUFFIX=p2noli.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08836455.ecgn_1.1_3596@runat_29082003_132953_23055 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mus:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	15.7	745	12	BG871607	BG871607 602790090
2	23	15.0	958	13	B0523796	B0523796 AGENCOURT
3	21	13.7	749	12	B1096997	B1096997 602884553
4	19	12.4	676	10	BE369087	BE369087 601221765
5	18	11.8	903	12	BG963063	BG963063 602828076
6	17	11.1	724	12	BG962137	BG962137 602826902
7	17	11.1	802	10	B137216	B137216 601784466
8	17	11.1	861	12	B1455668	B1455668 603173862
9	17	11.1	862	10	B143948	B143948 601786493
10	17	11.1	883	12	B1151077	B1151077 602917012
11	17	11.1	914	10	B163883	B163883 601772396
12	17	11.1	1012	10	B142302	B142302 601791844
13	16	10.5	393	10	BG095410	BG095410 mac28d12.
14	16	10.5	439	10	BE136816	BE136816 ug56601.y
15	16	10.5	529	14	CA577954	CA577954 K0716F08-
16	16	10.5	639	10	BE371136	BE371136 601218628
17	16	10.5	829	10	B144014	B144014 601791270
18	16	10.5	861	12	BG962366	BG962366 602827176
19	16	10.5	979	10	BF578874	BF578874 602095434
20	15	9.8	124	13	BQ358790	BQ358790 MK1-HT106
21	15	9.8	136	12	B1043088	B1043088 QV1-OT017
22	15	9.8	176	10	BF822838	BF822838 MR1-SN007
23	15	9.8	212	13	BQ364985	BQ364985 MR4-SN007
24	15	9.8	379	10	AW908776	AW908776 uf57d02.y
25	15	9.8	389	9	AI555192	AI555192 UI-R-C2p-
26	15	9.8	417	14	CA577519	CA577519 K0710F01-
27	15	9.8	462	14	CA578969	CA578969 K0731A05-
28	15	9.8	481	14	CA576938	CA576938 K0702C06-
29	15	9.8	509	14	CA578347	CA578347 K0722D09-
30	15	9.8	517	10	BF545108	BF545108 UI-R-C2p-
31	15	9.8	598	12	B1149725	B1149725 602848572
32	15	9.8	607	9	AV259014	AV259014 AV259014
33	15	9.8	616	10	B136295	B136295 601781413
34	15	9.8	637	14	BY724721	BY724721 BY724721
35	15	9.8	644	10	BE281961	BE281961 601099518
36	15	9.8	689	11	AK007163	AK007163 Mus muscu
37	15	9.8	718	10	B136279	B136279 601780988
38	15	9.8	739	10	BE284158	BE284158 601099428
39	15	9.8	748	10	B136397	B136397 601783927
40	15	9.8	794	12	B1150371	B1150371 602915205
41	15	9.8	801	13	B0946353	B0946353 AGENCOURT
42	15	9.8	853	12	B1249876	B1249876 602995978
43	15	9.8	891	10	B138460	B138460 601782916
44	15	9.8	892	10	BG518664	BG518664 602578528
45	15	9.8	896	12	B1149320	B1149320 602848859

ALIGNMENTS

RESULT 1
BG871607
LOCUS
DEFINITION BG871607 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4921295 5',
745 bp mRNA linear EST 29-MAY-2001
ACCESSION BG871607
VERSION BG871607.1 GI:14222147
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 745)

AUTHORS
TITLE NIH-MGC <http://mgc.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LHAM10839 row: c column: 24
 High quality sequence stop: 582.
FEATURES
 source
 1. .745
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clones="IMAGE:4921295"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_SG2"
 /note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 179 a 222 c 181 g 163 t
ORIGIN
 Alignment Scores:
 Pred. No.: 1.37e-12 Length: 745
 Score: 24.00 Matches: 24
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 15.69% Indels: 0
 DB: 12 Gaps: 0
 US-08-836-455-4 (1-153) x BG871607 (1-745)
 Qy 94 SerSerThrAlaTyrMetGlnIleSerSerLeuThrSerGluAspSerAlaValTyr 113
 Db 315 TCCTCCAGCAGCGCTACATGCAGATCAGCAGCCCTGACCTCTGAGGACTCTGCGGTCTAT 374
 Qy 114 PheCysalaArg 117
 Db 375 TTCTGTGCAAGA 386
RESULT 2
LOCUS BU523796 958 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT_10123257 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:6530504 5', mRNA sequence.
ACCESSION BU523796
VERSION BU523796.1 GI:22834235
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 958)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LHAM14132 row: f column: 08
 High quality sequence stop: 608.
FEATURES
 source
 1. .958
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clones="IMAGE:6530504"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Co24"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 233 a 285 c 231 g 208 t
ORIGIN
 Alignment Scores:
 Pred. No.: 1.57e-11 Length: 958
 Score: 23.00 Matches: 23
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 15.03% Indels: 0
 DB: 13 Gaps: 0
 US-08-836-455-4 (1-153) x BU523796 (1-958)
 Qy 94 SerSerThrAlaTyrMetGlnIleSerSerLeuThrSerGluAspSerAlaValTyr 113
 Db 318 TCCTCCAGCAGCGCTACATGCAGATCAGCAGCCCTGACCTCTGAGGACTCTGCGGTCTAT 377
 Qy 114 PheCysala 116
 Db 378 TTCTGTGCA 386
RESULT 3
LOCUS BU099697 749 bp mRNA linear EST 26-JUN-2001
DEFINITION 60288453F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5040084 5', mRNA sequence.
ACCESSION BU099697
VERSION BU099697.1 GI:14550590
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 749)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LHAM1110 row: i column: 13
 High quality sequence stop: 741.
FEATURES
 source
 1. .749
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clones="IMAGE:5040084"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Kid14"
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. I"

BASE COUNT 183 a 214 c 185 g 167 t
ORIGIN

Alignment Scores:
Pred. No.: 9.92e-10 Length: 749
Score: 21.00 Matches: 21
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.73% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-4 (1-153) x BT099697 (1-749)

Qy 97 ThrAlaTyrMetGlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAla 116
|||||
Db 118 ACAGCCTACATGAGATCAGACGCTGACCTCTGAGACTCTGCGGTCTATTTCTGTGCG 177
|||||

Qy 117 Arg 117
117
Db 178 AGA 180

RESULT 4
BE369087
LOCUS
DEFINITION BE369087 676 bp mRNA linear EST 21-JUL-2000
mRNA sequence.

ACCESSION BE369087
VERSION BE369087.1 GI:9314450

KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/

JOURNAL
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabps-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LHAM8758 row: b column: 17
High quality sequence stop: 580.

Location/Qualifiers

1. .676
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clones="IMAGE:3590320"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin.
/lab_host="DH10B"

/clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 161 a 188 c 173 g 154 t
ORIGIN

Alignment Scores:
Pred. No.: 7.2e-08 Length: 676
Score: 19.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.42% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-4 (1-153) x BE369087 (1-676)

Qy 125 AspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThrProPro 143
|||||
Db 392 GACTACTGGGTCAAGGAAGCTCAGTCACCGTCTCCCTCAGCCAAAGACACCCCA 448
|||||

RESULT 5

BE363063

LOCUS

DEFINITION BE363063 903 bp mRNA linear EST 12-JUN-2001

ACCESSION BE363063.1 GI:14350700

VERSION BE363063.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE NIH-MGC http://mgc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabps-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LHAM10986 row: g column: 20

High quality sequence stop: 875.

Location/Qualifiers

1. .903

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clones="IMAGE:4982827"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 208 a 266 c 229 g 200 t

ORIGIN

Alignment Scores:

Pred. No.: 8.55e-07 Length: 903

Score: 18.00 Matches: 18

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 11.76% Indels: 0

DB: 12 Gaps: 0

US-08-836-455-4 (1-153) x BE363063 (1-903)

Qy 101 GlnIleSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGly 118

|||||

Db 50 CAGATCAGACGCTGACCTCTGAGACTCTGCGGTCTATTTCTGTGCAAGAGGC 103

|||||

RESULT 6

BE362137

LOCUS

DEFINITION BE362137 724 bp mRNA linear EST 12-JUN-2001

ACCESSION BE362137

LOCUS

DEFINITION BE362137 724 bp mRNA linear EST 12-JUN-2001

ACCESSION BE362137

VERSION BG962137.1 GI:14349774
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 724)

REFERENCE

NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10983 row: d column: 02
 High quality sequence stop: 713.

FEATURES

source

1..724

/organism="Mus musculus"

/mol_type="mrna"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4981585"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT

183 a 199 c 180 g 162 t

ORIGIN

Alignment Scores:
 Pred. NO.: 6.17e-06 Length: 724
 Score: 17.00 Matches: 17
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 11.11% Indels: 0
 DB: 12 Gaps: 0

US-08-836-455-4 (1-153) x BG962137 (1-724)

QY

94 SerSerThrAlaTyMetGlnSerSerLeuThrSerGluAspSer 110

DB

314 TCCCTCCAGCAGCGCTACATGCAGATCAGCAGCTGAGGACTCT 364

RESULT 7

BF137216

LOCUS

BF137216 802 bp mRNA linear EST 24-OCT-2000
 mRNA sequence.

DEFINITION

601784466F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4012360 5',

ACCESSION

BF137216

VERSION

BF137216.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 802)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLAM9253 row: c column: 17

High quality sequence stop: 697.

FEATURES

source

1..802

/organism="Mus musculus"

/mol_type="mrna"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:4012360"

/tissue_type="tumor, metastatic to mammary"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Lu30"

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; transgenic model WNT-1, expression driven by
 MMV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
 dt. Library constructed by Life Technologies.
 Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 191 a 217 c 211 g 183 t

ORIGIN

Alignment Scores:
 Pred. NO.: 6.82e-06 Length: 802
 Score: 17.00 Matches: 17
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 11.11% Indels: 0
 DB: 10 Gaps: 0

US-08-836-455-4 (1-153) x BF137216 (1-802)

QY

125 AspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThr 141

DB

435 GACTACTGGGTCGAGGAACCTCAGTCACCGCTCTCTCCAGCAACAAACA 485

RESULT 8

BF137216

LOCUS

BF137216 861 bp mRNA linear EST 21-AUG-2001
 mRNA sequence.

ACCESSION

BF137216.1

VERSION

BF137216.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 861)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11639 row: l column: 16

High quality sequence stop: 780.

FEATURES

source

1..861

/organism="Mus musculus"

/mol_type="mrna"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:5253279"

/tissue_type="tumor, gross tissue"

/dev_stage="7 months"

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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
BASE COUNT 205 a 239 c 211 g 206 t
ORIGIN

Alignment Scores:
Pred. No.: 7,31e-06 Length: 861
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.11% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-4 (1-153) x BI45568 (1-861)

QY 125 AsptYrTpGlyGlnGlyThrSerValThrValSerSerAlalysThrThr 141
|||||
Db 443 GACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCCACCAACAACA 493

RESULT 9
BF143948 862 bp mRNA linear EST 24-OCT-2000
LOCUS 601786493F1 NCI_CGAP_Lu30 Mus musculus cdna clone IMAGE:4014430 5',
DEFINITION mRNA sequence.
ACCESSION BF143948 GI:10982988
VERSION BF143948.1
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 862)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9258 row: i column: 23
High quality sequence stop: 671.
FEATURES
Location/Qualifiers
1..862
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4014430"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu30"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dr. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 213 a 236 c 236 g 176 t
ORIGIN

Alignment Scores:
Pred. No.: 7,32e-06 Length: 862
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0

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```

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.11% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-4 (1-153) x BF143948 (1-862)

QY 125 AsptYrTpGlyGlnGlyThrSerValThrValSerSerAlalysThrThr 141
|||||
Db 412 GACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCCACCAACAACA 462

RESULT 10
BF151077 883 bp mRNA linear EST 05-JUL-2001
LOCUS 602917012F1 NCI_CGAP_Lu29 Mus musculus cdna clone IMAGE:5067314 5',
DEFINITION mRNA sequence.
ACCESSION BF151077
VERSION BF151077.1 GI:14611078
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 883)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM11181 row: h column: 03
High quality sequence stop: 719.
FEATURES
Location/Qualifiers
1..883
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5067314"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu29"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 211 a 268 c 217 g 187 t
ORIGIN

Alignment Scores:
Pred. No.: 7,49e-06 Length: 883
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.11% Indels: 0
DB: 12 Gaps: 0

US-08-836-455-4 (1-153) x BF151077 (1-883)

QY 125 AsptYrTpGlyGlnGlyThrSerValThrValSerSerAlalysThrThr 141
|||||
Db 257 GACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCCACCAACAACA 307

RESULT 11
BF163883 914 bp mRNA linear EST 30-OCT-2000
LOCUS 601772396F1 NCI_CGAP_Lu29 Mus musculus cdna clone IMAGE:3991558 5',
DEFINITION

```

```

mRNA sequence.
ACCESSION BF163883
VERSION BF163883.1 GI:11044161
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9204 row: p column: 23
High quality sequence stop: 679.
FEATURES
    source
        1..914
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="CZECH II"
            /db_xref="taxon:10090"
            /clone="IMAGE:3991558"
            /tissue_type="spontaneous tumor, metastatic to mammary.
            Stem cell origin."
            /lab_host="DH10B"
            /clone_lib="NCI_CGAP_Lu29"
            /note="Organ: lung; Vector: pCMV-SPORT6; Site.1: SalI;
            Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
            Library constructed by Life Technologies. Investigator
            providing samples: Gilbert Smith, NIH"
BASE COUNT 220 a 228 c 265 g 201 t
ORIGIN
Alignment Scores:
Pred. No.: 7,75e-06 Length: 914
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.11% Indels: 0
DB: 10 Gaps: 0
US-08-836-455-4 (1-153) x BF163883 (1-914)
Qy 125 AsPTyrrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThr 141
|||||
Db 415 GACTACTGGGGTCAAGGACGTGAGTCACCGTCTCTCTCCAGCAACAAACA 465

RESULT 12
BF142302
LOCUS BF142302
DEFINITION 601791844F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4022459 5',
mRNA sequence.
ACCESSION BF142302
VERSION BF142302.1 GI:10981252
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9204 row: p column: 23
High quality sequence stop: 679.
FEATURES
    source
        1..914
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="CZECH II"
            /db_xref="taxon:10090"
            /clone="IMAGE:3991558"
            /tissue_type="spontaneous tumor, metastatic to mammary.
            Stem cell origin."
            /lab_host="DH10B"
            /clone_lib="NCI_CGAP_Lu29"
            /note="Organ: lung; Vector: pCMV-SPORT6; Site.1: SalI;
            Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
            Library constructed by Life Technologies. Investigator
            providing samples: Gilbert Smith, NIH"
BASE COUNT 220 a 228 c 265 g 201 t
ORIGIN
Alignment Scores:
Pred. No.: 7,75e-06 Length: 914
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.11% Indels: 0
DB: 10 Gaps: 0
US-08-836-455-4 (1-153) x BF163883 (1-914)
Qy 125 AsPTyrrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThr 141
|||||
Db 415 GACTACTGGGGTCAAGGACGTGAGTCACCGTCTCTCTCCAGCAACAAACA 465

RESULT 13
BG095410
LOCUS BG095410
DEFINITION mac28d12.y1 Soares mouse 3NbMS Mus musculus cDNA clone
IMAGE:400967 5' similar to SW:DTCM_MOUSE P01882 IG DELTA CHAIN C
REGION MEMBRANE-BOUND FORM. ;, mRNA sequence.
ACCESSION BG095410
VERSION BG095410.1 GI:12577973
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1498695
Seq primer: -40RP from Gibco
High quality sequence stop: 334.
FEATURES
    source
        1..393
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="IMAGE:400967"
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9279 row: h column: 12
High quality sequence stop: 711.
FEATURES
    source
        1..1012
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="CZECH II"
            /db_xref="taxon:10090"
            /clone="IMAGE:4022459"
            /tissue_type="tumor, metastatic to mammary"
            /lab_host="DH10B"
            /clone_lib="NCI_CGAP_Lu30"
            /note="Organ: lung; Vector: pCMV-SPORT6; Site.1: NotI;
            Site.2: SalI; transgenic model WNT-1, expression driven by
            MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
            dt. Library constructed by Life Technologies.
            Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 273 a 271 c 267 g 201 t
ORIGIN
Alignment Scores:
Pred. No.: 8,56e-06 Length: 1012
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.11% Indels: 0
DB: 10 Gaps: 0
US-08-836-455-4 (1-153) x BF142302 (1-1012)
Qy 125 AsPTyrrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThr 141
|||||
Db 413 GACTACTGGGGTCAAGGACGTGAGTCACCGTCTCTCTCCAGCAACAAACA 463

```



```

/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mouse 3NDMS"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TCTTACCAATCTGAAGTGGAGCGCGCGCTGTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(AATTGGGATCTTG), digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT73 vector.
Source: irradiated bowel harvested 72 hours after
irradiation (1400 Gys). Library constructed by Bob
Barstead."
BASE COUNT 108 a 95 c 93 g 97 t
ORIGIN

Alignment Scores:
Pred. No.: 3,04e-05 Length: 393
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.46% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-4 (1-153) x BG095410 (1-393)

QY 103 SerSerLeuthrSerGluAspSerAlaValTyrPheCysAlaArgGly 118
|||||
Db 40 AGCAGCCTGACATCTGAGGACTCTGGGTCGTATTCTGTGCCAGGGGT 87

RESULT 14
BE136816
LOCUS
DEFINITION
u55b01.y1 Barstead bowel MPLRB9 Mus musculus cDNA clone
IMAGE:1546345 5' similar to gb:M12376 Mouse immunoglobulin H-chain
V-region pseudogene mRNA, complete (MOUSE);, mRNA sequence.
BE136816
BE136816.1 GI:8599316
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 439)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R., and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LILNL; contact the
IMAGE Consortium (info@image.lilnl.gov) for further information.
MGI:951693
Seq primer: -40RP from Gibco.
FEATURES
source
1. .439
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:1546345"
/tissue_type="bowel"
/dev_stage="8 weeks"
/lab_host="DH10B"

/clone_lib="Barstead bowel MPLRB9"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TCTTACCAATCTGAAGTGGAGCGCGCGCTGTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Bonaldo."
BASE COUNT 110 a 108 c 106 g 115 t
ORIGIN

Alignment Scores:
Pred. No.: 3,39e-05 Length: 439
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.46% Indels: 0
DB: 10 Gaps: 0

US-08-836-455-4 (1-153) x BE136816 (1-439)

QY 103 SerSerLeuthrSerGluAspSerAlaValTyrPheCysAlaArgGly 118
|||||
Db 367 AGCAGCCTAACATCTGAGGACTCTGGGTCGTATTCTGTGCAAGAGGA 414

RESULT 15
CA577954
LOCUS
DEFINITION
CA577954 529 bp mRNA linear EST 19-NOV-2002
K0716F08-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-kit-/Sca-1-)
cDNA Library (Long) Mus musculus cDNA clone NIA:K0716F08
IMAGE:30075139 5', mRNA sequence.
CA577954
CA577954.1 GI:25126345
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 529)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,
Aiba, K., Raub, D., Longo, D.L., Keiler, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/c-kit-/Sca-1-) cDNA Library (Long)
Unpublished
Other ESTs: K0716F08-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0716 row: F column: 08
Seq primer: M13 Reverse
High quality sequence stop: 529
POLYA=No.
FEATURES
source
1. .529
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6NCr"
/db_xref="niaEST:K0716F08-5N"
/db_xref="taxon:10090"
/clone="NIA:K0716F08 IMAGE:30075139"
/tissue_type="Hematopoietic Stem Cell (Lin-/c-kit-/Sca-1-)"
/dev_stage="Age approx.10 weeks old"
/lab_host="DH10B"
/clone_lib="NIA Mouse Hematopoietic Stem Cell
(Lin-/c-kit-/Sca-1-) cDNA Library (Long)"
/notes="Vector: pSPORT1 (Invitrogen); Site_1: Salt; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,"

```

National Institute on Aging (NIA), Intramural Research Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]. Total RNAs were obtained from Drs. Dennis Taub, Dan Longo (National Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized with an oligo(dT) primer [Invitrogen: 5'-pgactatgttcagatcgagcgccgctttttttttttt-3'] from 0.9 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Lb-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.1 kb. The library was constructed by Yulan Piao (NIA)."

BASE COUNT 113 a 146 c 139 g 131 t
ORIGIN

Alignment Scores:
Pred. No.: 4.07e-05 Length: 529
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.46% Indels: 0
DB: 14 Gaps: 0

US-08-836-455-4 (1-153) x CA577954 (1-529)

Qy 103 SerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGly 118
Db 329 AGCAGCCTGACCTCTGAGGACTCGCGGCTCTATTCTGTGCAAGAGGG 376

Search completed: August 31, 2003, 02:16:28
Job time : 1845.13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2003, 19:50:30 ; Search time 36.453 Seconds
(without alignments)
666.204 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 816
Sequence: 1 MCSWVFLPILLSITGVHSQ.....TVSSAKTTPPVYPLVPGSL 153

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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3:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
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24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	816	100.0	153	18	AAW27120 Murine monoclonal
2	816	100.0	153	20	AAW87594 Antibody 11D10 hea
3	816	100.0	153	24	AAO16293 Mouse 11D10 antibo
4	621	76.1	465	16	AAW86758 Anti-tobacco mosai
5	602	73.8	159	10	AAW93079 Heavy chain of mon
6	574.5	70.4	468	12	AAW13061 Monoclonal antibod
7	568	69.6	561	20	AAV17415 Mouse immunoglobul
8	565	69.2	140	10	AAW94780 2 H7 VH gene. Syn
9	565	69.2	140	18	AAW10588 2H7 antibody heavy

10	565	69.2	140	18	AAW16343	2H7 heavy chain va
11	565	69.2	140	18	AAW10242	Heavy chain variab
12	565	69.2	140	19	AAW41070	Mouse 2H7 antibody
13	565	69.2	140	19	AAW47513	Mouse 2H7 antibody
14	565	69.2	140	19	AAW47520	Mouse 2H7 antibody
15	565	69.2	140	20	AAW89540	Mouse antibody 2H7
16	565	69.2	140	22	AAW98092	2H7 heavy chain va
17	563	69.0	463	18	AAW14939	3F4 (Chimeric) hum
18	563	69.0	463	18	AAW14940	3F4 (Chimeric) hum
19	563	69.0	464	18	AAW14941	3F4 Human IgG4 exp
20	563	69.0	464	18	AAW14938	Murine anti-porcine
21	563	69.0	469	14	AAW40384	Monoclonal antibod
22	561.5	68.8	360	23	AAE27924	Human CH2 domain d
23	561.5	68.8	360	24	ABB82833	Antibody C2B8 CH2
24	561.5	68.8	470	21	AAW80826	A dimeric anti-CD2
25	561.5	68.8	470	23	AAE27923	Human C2B8 antibod
26	561.5	68.8	470	24	ABB82832	Antibody C2B8 heav
27	561	68.8	140	8	AAW70627	Sequence encoded b
28	560.5	68.7	464	19	AAW83041	Anti-Fas MAb HFE7A
29	560.5	68.7	464	21	AAW14747	Mouse anti-Fas ant
30	560.5	68.7	464	21	AAW90897	Murine anti-Fas an
31	560.5	68.7	464	23	ABB74866	Humanised anti-Fas
32	560.5	68.7	464	23	ABB74912	Humanised anti-Fas
33	554.5	68.0	438	23	AAE18372	Human penton base
34	554.5	68.0	438	24	ABG76347	Portion of mouse D
35	554.5	68.0	456	23	AAE18370	Human penton base
36	554.5	68.0	456	24	ABG76345	Mouse DAV-1 heavy
37	554.5	68.0	464	16	AAW76088	MAB 55.1 heavy cha
38	554.5	68.0	493	23	AAE18379	Human N-terminal D
39	554.5	68.0	493	24	ABG76354	Mouse DAV-1 heavy
40	554.5	68.0	510	23	AAE18378	Human N-terminal D
41	554.5	68.0	510	24	ABG76353	Mouse DAV-1 heavy
42	554.5	68.0	597	23	AAE18377	Human N-terminal D
43	554.5	68.0	597	24	ABG76352	Mouse DAV-1 heavy
44	554.5	68.0	613	23	AAE18380	Human N-terminal D
45	554.5	68.0	613	24	ABG76355	Mouse DAV-1 heavy

ALIGNMENTS

RESULT 1
AAW27120
ID AAW27120 standard; Protein; 153 AA.
XX AC AAW27120;
XX DT 25-MAR-2003 (updated)
XX DE 04-JAN-1998 (first entry)
XX Murine monoclonal anti-idiotyp antibody 11D10 VH region.
XX Monoclonal antibody 11D10; anti-idiotyp antibody; mucin;
XX human milk fat globule; HMF; tumour; breast cancer; vaccine.
XX OS Mus musculus.
XX Key Location/Qualifiers
XX Peptide 1..19
XX Protein /label= Sig_peptide
XX Region /label= Mat_protein
XX Region /label= PR1
XX Region /note= "framework region 1"
XX Region /label= CDR1
XX Region /note= "complementarity determining region 1"
XX Region /label= PR2
XX Region /note= "framework region 2"
XX Region /label= CDR2

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FT      Region      /note= "complementarity determining region 2"
FT      86..117
FT      /label= FR3
FT      AC          /note= "framework region 3"
FT      118..126
FT      /label= CDR3
FT      /note= "complementarity determining region 3"
FT      127..137
FT      /label= FR1
FT      /note= "framework region 4"
FT      138..153
FT      /label= Constant
XX
XX      WO9722699-A2.
XX      PN
XX      PD      26-JUN-1997.
XX      PF      19-DEC-1996; 96WO-US20757.
XX      PR      20-DEC-1995; 95US-0575762.
XX      PR      26-JAN-1996; 96US-0591965.
XX      PR      13-DEC-1996; 96US-0766350.
XX
XX      (KENT ) UNIV KENTUCKY.
XX      PA
XX      PI      Chatterjee M, Chatterjee SK, Foon KA;
XX      PN      WPI; 1997-341690/31.
XX      DR      N-PSDB; AAT85150.
XX
XX      Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
XX      PT      against human milk fat globule disease associated tumours,
XX      PT      especially breast cancer.
XX
XX      Claim 10; Page 94-95; 130pp; English.
XX
XX      This polypeptide sequence comprises the heavy chain variable region
XX      CC      (VH) of monoclonal anti-idiotypic antibody 11D10 produced by
XX      CC      hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
XX      CC      naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotypic
XX      CC      response. It elicits an immune response against a specific epitope
XX      CC      of a high mol.wt. mucin of human milk fat globule (HMFG). It
XX      CC      induces an immunological response to HMFG in mice, rabbits, monkeys
XX      CC      and patients with advanced HMFG-associated tumours. Pharmaceutical
XX      CC      compositions and vaccines comprising 11D10, 11D10 polypeptides
XX      CC      and/or 11D10 polynucleotides (see also AAT85149-50) are claimed.
XX      CC      Also claimed are diagnostic kits and methods of using 11D10, 11D10
XX      CC      polypeptides and/or 11D10 polynucleotides, including methods of
XX      CC      treating HMFG-associated tumours. 11D10 is also used in a claimed
XX      CC      method of palliating HMFG-associated disease and in claimed kits to
XX      CC      detect or quantify anti-HMFG antibody.
XX      CC      (Updated on 25-MAR-2003 to correct PR field.)
XX
XX      SQ      Sequence 153 AA;
XX
XX      Query Match      100.0%; Score 816; DB 18; Length 153;
XX      Best Local Similarity 100.0%; Pred. No. 3.7e-55;
XX      Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY      1      MECSWFLFLSITGVHQAAYLQOAGAEVRSASVMSCKASGYTLTSTNMHWKQTP 60
DB      1      MECSWFLFLSITGVHQAAYLQOAGAEVRSASVMSCKASGYTLTSTNMHWKQTP 60
OY      61      GQGLEWIGNTPPGNDYYNQKFKGASLTADTSSSTAYMQISLTSEDSAVYFCARGNW 120
DB      61      GQGLEWIGNTPPGNDYYNQKFKGASLTADTSSSTAYMQISLTSEDSAVYFCARGNW 120
OY      121      EGALDYWGQGSVTVSSAKTTPPPVPLVPGSL 153
DB      121      EGALDYWGQGSVTVSSAKTTPPPVPLVPGSL 153
XX
XX      RESULT 2

```

```

AAW87594
ID      AAW87594 standard; Protein; 153 AA.
XX
XX      AAW87594;
XX
DT      16-MAR-1999 (first entry)
DE      Antibody 11D10 heavy chain variable region.
XX
XX      Murine; mouse; antibody; heavy chain; variable region; anti-idiotypic;
XX      KW      human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
XX      OS      Mus sp.
XX
XX      Key      Location/Qualifiers
XX      FT      1..19
XX      FT      /note= "signal peptide"
XX      FT      20..153
XX      FT      /note= "mature protein"
XX      FT      20..49
XX      FT      /label= framework_1
XX      FT      50..54
XX      FT      /label= CDR1
XX      FT      /note= "complementarity determining region 1"
XX      FT      55..68
XX      FT      /label= framework_2
XX      FT      69..85
XX      FT      /label= CDR2
XX      FT      /note= "complementarity determining region 2"
XX      FT      86..117
XX      FT      /label= framework_3
XX      FT      118..126
XX      FT      /label= CDR3
XX      FT      /note= "complementarity determining region 3"
XX      FT      127..137
XX      FT      /label= framework_4
XX
XX      WO9856419-A1.
XX      PN
XX      PD      17-DEC-1998.
XX      PF      12-JUN-1998; 98WO-US12250.
XX      PR      11-JUN-1998; 98US-0096244.
XX      PR      13-JUN-1997; 97US-0049540.
XX
XX      (KENT ) UNIV KENTUCKY RES FOUND.
XX      PI      Chatterjee M, Foon KA;
XX      DR      WPI; 1999-060029/05.
XX      DR      N-PSDB; AAV83773.
XX
XX      Delaying development of, or treating, HMFG-associated tumours -
XX      PT      using anti-idiotypic antibody 11D10 raised against antibodies to
XX      PT      human milk fat globule protein
XX
XX      Disclosure; Fig 2; 54pp; English.
XX
XX      This sequence represents the heavy chain variable region of the murine
XX      CC      antibody 11D10. This anti-idiotypic antibody is used to delay the
XX      CC      development of, or treat, a human milk fat globule (HMFG) associated
XX      CC      tumour in an individual having low tumour burden. The antibody 11D10
XX      CC      is used to prevent the recurrence of HMFG-associated tumours e.g.
XX      CC      ovarian, non-small cell lung and pancreatic carcinoma, especially for
XX      CC      treating breast tumours.
XX
XX      SQ      Sequence 153 AA;
XX
XX      Query Match      100.0%; Score 816; DB 20; Length 153;
XX      Best Local Similarity 100.0%; Pred. No. 3.7e-55;
XX      Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MECSWVFLFLISITTVHVSQAYLQOQSGAELVRSYGASVKMSCKASGYTLTSTYNMHWKQTP 60
 Db |||||||
 1 MECSWVFLFLISITTVHVSQAYLQOQSGAELVRSYGASVKMSCKASGYTLTSTYNMHWKQTP 60
 QY 61 GQGLEWIGNIFPGNGDYIYNQKFKGKASLTADTSSSTAYMIOISLTSEDSAVYFCARGNW 120
 Db |||||||
 61 GQGLEWIGNIFPGNGDYIYNQKFKGKASLTADTSSSTAYMIOISLTSEDSAVYFCARGNW 120
 QY 121 EGALDYGQGTSTVTSSAKTTPPPVPLVPGSL 153
 Db |||||||
 121 EGALDYGQGTSTVTSSAKTTPPPVPLVPGSL 153

RESULT 3
 AA016293
 ID AA016293 standard; Protein; 153 AA.
 AC AA016293;
 XX
 DT 20-MAR-2003 (first entry)
 XX
 DE Mouse 11D10 antibody heavy chain variable region.
 XX
 KW Mouse; murine; vaccine; tumour; human milk fat globules; HMFG;
 KW carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour;
 KW CEA-associated tumour; anti-idiotypic antibody.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal_peptide
 FT Protein 20..153
 FT /note= "Mature murine 11D10 antibody heavy chain variable
 FT region"
 XX
 PN W0200292012-A2.
 XX
 XX 21-NOV-2002.
 XX
 XX 17-MAY-2002; 2002WO-US15840.
 XX
 XX 17-MAY-2001; 2001US-0861294.
 XX
 XX (KENT) UNIV KENTUCKY RES FOUND.
 XX
 XX Chatterjee M, Foon KA;
 PI
 XX WPI; 2003-129216/12.
 DR N-PSDB; AAL51274.
 XX
 XX Use of anti-idiotypic antibodies for human milk fat globules (HMFG)- or
 PT carcinoembryonic antigen (CEA)-associated tumor for delaying the
 PT development of, or treating a HMFG- or CEA-associated tumor (e.g.
 PT breast tumor) in humans
 XX
 XX Claim 2; Fig 2; 98pp; English.
 PS
 XX The invention comprises a method for delaying the development of, or
 CC treating a tumour that is associated with human milk fat globules (HMFG)
 CC or carcinoembryonic antigen (CEA). The method of the invention involves
 CC administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an
 CC anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for
 CC delaying the development, of or treating HMFG/CEA-associated tumours. The
 CC present amino acid sequence represents the heavy chain variable region of
 CC the mouse 11D10 anti-idiotypic antibody.
 XX
 XX Sequence 153 AA;

Query Match 100.0%; Score 816; DB 24; Length 153;
 Best Local Similarity 100.0%; Pred. No. 3.7e-55;
 Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECSWVFLFLISITTVHVSQAYLQOQSGAELVRSYGASVKMSCKASGYTLTSTYNMHWKQTP 60
 Db |||||||
 1 MECSWVFLFLISITTVHVSQAYLQOQSGAELVRSYGASVKMSCKASGYTLTSTYNMHWKQTP 60
 QY 61 GQGLEWIGNIFPGNGDYIYNQKFKGKASLTADTSSSTAYMIOISLTSEDSAVYFCARGNW 120
 Db |||||||
 61 GQGLEWIGNIFPGNGDYIYNQKFKGKASLTADTSSSTAYMIOISLTSEDSAVYFCARGNW 120
 QY 121 EGALDYGQGTSTVTSSAKTTPPPVPLVPGSL 153
 Db |||||||
 121 EGALDYGQGTSTVTSSAKTTPPPVPLVPGSL 153

RESULT 4
 AAR66758
 ID AAR66758 standard; Protein; 465 AA.
 AC AAR66758;
 XX
 DT 01-SEP-1995 (first entry)
 XX
 DE Anti-tobacco mosaic virus monoclonal Ab heavy chain.
 XX

KW Tobacco mosaic virus; TMV; monoclonal antibody;
 KW heavy chain; virus-resistant plants; biofarming.
 XX
 OS Synthetic.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= leader
 FT Peptide 20..465
 FT /label= mat_peptide
 FT Domain 20..128
 FT /note= "variable heavy domain"
 FT Domain 129..141
 FT /note= "J heavy 4 domain"
 FT Domain 142..465
 FT /note= "constant heavy domain"
 XX

PN JP06319396-A.
 XX
 XX 22-NOV-1994.
 XX
 XX 07-MAY-1993; 93JP-0131208.
 XX
 XX 07-MAY-1993; 93JP-0131208.
 XX
 XX (NIBS) JAPAN TOBACCO INC.
 XX (KURS) KURARAY CO LTD.
 XX
 XX WPI; 1995-040220/06.
 DR N-PSDB; AAQ79930.
 XX
 XX Transformed plant producing animal-derived anti-virus antibody -
 PT esp. tobacco plants producing anti-tobacco mosaic virus
 PT monoclonal antibody
 XX
 XX Example 2; Pages 14-15; 26pp; Japanese.

PS
 XX AAQ79929 and AAQ79930 encode AAR66757 and AAR66758, the light and heavy
 CC chains of an animal derived anti-tobacco mosaic virus (TMV)
 CC monoclonal antibody. The cDNAs were incorporated into a T1
 CC plasmid vector, which was incorporated into A. tumefaciens.
 CC The resultant plant expression vector was used to transform
 CC tobacco plants, making them TMV resistant, the plants could
 CC also be biofarmed for the prodn. of anti-virus antibodies.
 XX
 XX Sequence 465 AA;

Query Match 76.1%; Score 621; DB 16; Length 465;
 Best Local Similarity 75.6%; Pred. No. 1e-39;
 Matches 118; Conservative 15; Mismatches 19; Indels 4; Gaps 2;

```

Qy 1 MECSWFLFLSITITGVHSGAYLQOQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTP 60
Db 1 MECNWILPFLSVTSYGYSQVQLQOQSGAELARPGASVKLSCKASGYTFTSYMOWVKQRP 60
Qy 61 GQGLEWIGNIFPGNGDYYNOKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG-- 118
Db 61 GQGLEWIGAIYPGNGDYYNOKFKGKATLTADKSSSTAYMQLSALASEDSAVYFCAREGG 120
Qy 119 -NW-EGALDYWGQGTSTVTSSAKTTPPPVPLVPGS 152
Db 121 YNSDYANDYWGQGTSTVTSSAKTTPPSVPLAPGS 156

RESULT 5
AAP93079 ID AAP93079 standard; peptide: 159 AA.
XX AC AAP93079;
XX 25-MAR-2003 (updated)
DT 31-OCT-2002 (updated)
DT 15-MAR-1990 (first entry)
XX Heavy chain of monoclonal antibody 6A4.
XX Monoclonal antibody 6A4; heavy chain; Pseudomonas aeruginosa; OMP-1.
XX Unidentified.
XX EP338395-A.
XX 25-OCT-1989.
XX 12-APR-1989; 89EP-0106463.
XX 19-APR-1988; 88DE-3813023.
XX (BEHW ) BEHRINGER AG.
XX Domdey H, Marget M, Vonspecht B;
XX WPI; 1989-310861/43.
XX N-PSDB; RAN91645.
XX Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
XX variable antibody regions.
XX Claim 1; page 6; 7pp; german.
XX The peptide is encoded by the heavy chain of monoclonal antibody 6A4.
XX 6A4 reacts with the OMP-1 protein of all 19 known serotypes of
XX P.aeruginosa. It is used for therapy and diagnosis of infection, and as
XX a carrier for drugs. The antibody is IgG2a subclass.
XX (Updated on 31-OCT-2002 to add missing OS field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 159 AA;
Query Match 73.8%; Score 602; DB 10; Length 159;
Best Local Similarity 76.3%; Pred. No. 9.4e-39;
Matches 116; Conservative 9; Mismatches 25; Indels 2; Gaps 1;
Qy 1 MECSWFLFLSITITGVHSGAYLQOQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTP 60
Db 1 MERHWILFLSVTAGVHSGAYLQOQSGAELARPGASVKMSCKASGYTFTSYMOWVKQRP 60
Qy 61 GQGLEWIGNIFPGNGDYYNOKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG-- 118
Db 61 GQGLEWIGYINPNTGYEYINQNFKDKATLTADKSSSTAYMQLSALASEDSAVYCTRSY 120
Qy 119 NWEGALDYWGQGTSTVTSSAKTTPPPVPLV 150

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Db 121 NYEGAMDYWGQGTSTVTSSAKTTPAPSVPLAP 152

RESULT 6
AAR13061 ID AAR13061 standard; Protein: 468 AA.
XX AC AAR13061;
XX 25-MAR-2003 (updated)
DT 03-OCT-1991 (first entry)
XX Monoclonal antibody OK3T heavy chain.
XX OK3T; light chain; humanised antibodies; CDR-grafting.
XX Mus musculus.
XX Key Location/Qualifiers
XX Peptide 1..19
XX FT /label= signal peptide
XX FT 20..468
XX FT /label= light chain
XX W09109967-A.
XX 11-JUL-1991.
XX 21-DEC-1990; 90WO-GB02017.
XX 21-DEC-1990; 90WO-GB02017.
XX 21-DEC-1989; 89GB-0028874.
XX (CLLT ) CELLTech LTD.
XX Adair JR, Athwal DS, Emtage JS;
XX WPI; 1991-222915/30.
XX N-PSDB; AAQ12637.
XX New humanised antibodies comprising CDR grafted antibody - with
XX heavy and light chains, for use in vivo therapy and diagnosis
XX Disclosure; Fig 2b; 91pp; English.
XX The OK3T heavy chain sequence was deduced from the cDNA sequence
XX isolated from a library prepared from OK3T producing cells. The
XX library was screened with a probe complementary to a region in the
XX mouse IgG2a constant domain region. The OK3T sequence was used in
XX CDR-grafting experiments to prepare humanised antibodies.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 468 AA;
Query Match 70.4%; Score 574.5; DB 12; Length 468;
Best Local Similarity 74.8%; Pred. No. 3.7e-36;
Matches 113; Conservative 8; Mismatches 29; Indels 1; Gaps 1;
Qy 1 MECSWFLFLSITITGVHSGAYLQOQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTP 60
Db 1 MERHWILFLSVTAGVHSGAYLQOQSGAELARPGASVKMSCKASGYTFTSYMOWVKQRP 60
Qy 61 GQGLEWIGNIFPGNGDYYNOKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG--GN 119
Db 61 GQGLEWIGYINPSRGYTNQNFKDKATLTADKSSSTAYMQLSALASEDSAVYCYARYD 120
Qy 120 WEGALDYWGQGTSTVTSSAKTTPPPVPLV 150
Db 121 DHYCLDYWGQGTSTVTSSAKTTPAPSVPLAP 151

RESULT 7

```

AAV17415
ID AAY17415 standard; Protein; 561 AA.

XX AC AAY17415;
XX DT 26-JUL-1999 (first entry)
XX DE Mouse immunoglobulin E heavy chain.
XX KW Mouse; immunoglobulin E; IgE; allergy; transgenic animal.
XX OS Mus sp.

Key Location/Qualifiers
FT Peptide 1..19
FT /label= signal
FT Protein 20..561
FT /label= immunoglobulin_E_heavy_chain

XX EP921189-A1.
XX 09-JUN-1999.
XX 13-NOV-1998; 98EP-0309340;
XX 14-NOV-1997; 97JP-0313989.
XX (SANY) SANKYO CO LTD.
XX (TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI.
XX Karasuyama H, Matsuoka K, Taya C, Yonemawa H;
XX WPI; 1999-315404/27.
XX N-PSDB; AAX61084.

Transgenic non-human animal allergy models

Claim 27; Page 24-27; 42pp; English.

The present invention describes a transgenic, non-human animal with its genome altered to constitutively express a molecule having a constant region which can bind an IgE receptor on mast cells in the animals, the molecule having an immunoglobulin structure and being further capable of specifically binding a predetermined antigen. The transgenic animal is useful as a model for evaluating the activity and the ability of substances i.e. with anti-allergic activity, to affect any allergic reaction caused in the animal by the administration of the antigen to the animal, and applying the substance to be evaluated. The present sequence is the mouse immunoglobulin E (IgE) heavy chain, given in the present invention.

XX Sequence 561 AA;

Query Match 69.6%; Score 568; DB 20; Length 561;
Best Local Similarity 72.%; Pred. No. 1.4e-35;
Matches 109; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

QY 1 MECSWFLFLSLTTGVHSGAYLQQSGAELVRGASVKMSCKASGYTLTSYNNHWKQTP 60

DB 1 MELIWFLLSLTAGVHSEVQLQQSGAELVRGSSVKMSCKSGTFTSYGINWVKQRP 60

QY 61 GQGLEWIGNTFPGNGDTYYNQKPKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNW 120

DB 61 GQGLEWIGYIYGYTEYNEKEFGKATLTSDTSRTAYMQLSSLTSEDSAIYFCARWGL 120

QY 121 EGALDYWGQGTSTVTSVSAKTPPTPPVPLVP 150

DB 121 IFANDYWGQGTSTVTSVSSIRNPQLPLKP 150

RESULT 8

AAV17415

ID AAP94780 standard; protein; 140 AA.

XX AAP94780;
XX AC 25-MAR-2003 (updated)
XX DT 06-JUL-1990 (first entry)
XX DE 2 H7 VH gene.
XX KW Antibodies; passive immunisation; pH3-12a; ss.
XX OS Synthetic.
XX Key Location/Qualifiers
XX Peptide 1..19
XX /label=Leader peptide.
XX Domain 20..49
XX /label=FR1.
XX Domain 50..54
XX /label=CDR1
XX Domain 55..68
XX /label=FR2
XX Domain 69..85
XX /label=CDR2.
XX Domain 86..117
XX /label=FR3.
XX Domain 118..130
XX /label=CDR3.
XX Domain 131..140
XX /label=FR4.
XX Domain 108..123
XX /label=JK2
XX WO8900999-A.
XX 09-FEB-1989.
XX 25-JUL-1988; 88WO-US02514.
XX 24-JUL-1987; 87US-0077528.
XX (ITGE-) INT GENETIC ENG INC.
XX (INGE-) INGENE INT GENETIC ENG INC.
XX Robinson RR, Liu AY, Horwitz AH, Wall R, Better M;
XX WPI; 1989-061144/08.
XX N-PSDB; AAN91146.
XX Polynucleotide(s) encoding Immunoglobulin molecules -
XX used for efficient prodn. of chimeric human or non-human or
XX class switched antibodies.
XX Disclosure; Page -; 7pp; English.
XX Sequence carries the variable region of the chimeric immunoglobulin
XX sequence. The antibodies are useful in passive immunisation avoiding
XX negative immune reactions. They are also useful in assaying and in vitro
XX imaging.
XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 140 AA;

Query Match 69.2%; Score 565; DB 10; Length 140;
Best Local Similarity 80.0%; Pred. No. 5.6e-36;
Matches 112; Conservative 6; Mismatches 18; Indels 4; Gaps 1;

QY 1 MECSWFLFLSLTTGVHSGAYLQQSGAELVRGASVKMSCKASGYTLTSYNNHWKQTP 60

DB 1 MGFSRIFLFLSLVTGVHSGAYLQQSGAELVRGASVKMSCKASGYTLTSYNNHWKQTP 60

QY 61 GQGLEWIGNTFPGNGDTYYNQKPKGKASLTADTSSSTAYMQISLTSSEDSAVYFCAR--- 117

DB 61 RQGLEWIGAIYPNGDTSYNQKPKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVY 120

FT /note= "complementarity determining region 3"
 FT 131..140
 FT /label= FR4
 FT /note= "framework region 4"
 XX
 PN US5618920-A.
 XX
 XX 08-APR-1997.
 XX 29-APR-1994; 94US-0235225.
 XX 29-MAR-1990; 90US-0501092.
 PR 01-NOV-1985; 85US-0793980.
 PR 27-OCT-1986; 86WO-US02269.
 PR 24-JUL-1987; 87US-0077528.
 PR 11-JAN-1988; 88US-0142039.
 PR 17-APR-1992; 92US-0870404.
 PR 29-APR-1994; 94US-0235225.
 XX
 PA (XOMA) XOMA CORP.
 XX
 XX Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
 PI Wall R, Wilcox GL;
 PI
 XX WPI: 1997-225473/20.
 DR N-PSDB; AAT70868.
 XX
 XX Secretable immunoglobulin heavy and light chain fragments - capable
 PT of assembling into chimeric antibodies, useful for e.g. passive
 PT immunisation, diagnosis, etc
 XX
 PS Example 4; Fig 21; 96pp; English.
 XX
 CC A polypeptide (AAW16343) comprises the heavy chain variable region of
 CC mouse monoclonal antibody 2H7, which recognises human B-cell surface
 CC antigen Bp35. It is encoded by a cDNA clone (AAT70868) obtd. from a
 CC 2H7 cDNA library by PCR amplification. The 2H7 light chain variable
 CC sequence (AAW16344) is also provided. A novel human-mouse chimaeric
 CC antibody with specificity for the human B-cell antigen has been
 CC constructed.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 XX Sequence 140 AA;
 SQ
 Query Match 69.2%; Score 565; DB 18; Length 140;
 Best Local Similarity 80.0%; Pred. No. 5.6e-36;
 Matches 112; Conservative 6; Mismatches 18; Indels 4; Gaps 1;
 QY 1 MECSWFLFLLSITTTGVHSGAYLQOQSGAELVRSAGSKASGYTLTSYNNHWKQTP 60
 Db 1 MGFSRIFLFLSVTTGVHSGAYLQOQSGAELVRSAGSKASGYTLTSYNNHWKQTP 60
 QY 61 GQGLEWIGNIFPGNGDTYYNQKFGKASLTADTSSSTAYYMQISLTSSEDSAVYFCAR--- 117
 Db 61 RQGLEWIGALYPNGDTSYQKFGKATLTVDSSTAYYMQLSLTSSEDSAVYFCARVY 120
 QY 118 -GNWEGALDYWGQGTSTVTS 136
 Db 121 YSNSYWFYDVGWGTGTTVTS 140
 RESULT 11
 AAW10242
 ID AAW10242 standard; Protein; 140 AA.
 XX
 AC AAW10242;
 XX
 XX 25-MAR-2003 (updated)
 DT 06-AUG-1997 (first entry)
 XX
 XX Heavy chain variable sequence of 2H7.
 XX
 XX Pectate lyase; signal sequence; Gram-negative bacterium; Immunoglobulin;

KW protein production; human; constant region; passive immunisation; toxin;
 KW serum sickness; anaphylaxis; sweetener; thaumatin; cytoplasm; periplasm;
 KW antibody; Ig; heavy-chain; hepatitis; mouse; lung carcinoma; cancer;
 KW myeloma cell.
 XX
 OS Mus musculus.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /note= "leader peptide"
 FT Region 20..49
 FT /note= "framework region 1"
 FT Region 50..54
 FT /note= "complementarity determining region 1"
 FT Region 55..68
 FT /note= "framework region 2"
 FT Region 69..85
 FT /note= "complementarity determining region 2"
 FT Region 86..117
 FT /note= "framework region 3"
 FT Region 118..130
 FT /note= "complementarity determining region 3"
 FT Region 131..140
 FT /note= "framework region 4"
 XX
 XX US5576195-A.
 XX
 XX 19-NOV-1996.
 XX
 PF 09-DEC-1994; 94US-0357234.
 XX
 XX 29-MAR-1990; 90US-0501092.
 PR 01-NOV-1985; 85US-0793980.
 PR 27-OCT-1986; 86WO-US02269.
 PR 24-JUL-1987; 87US-0077528.
 PR 11-JAN-1988; 88US-0142039.
 PR 08-DEC-1992; 92US-0987555.
 PR 22-FEB-1993; 93US-0020671.
 PR 09-DEC-1994; 94US-0357234.
 XX
 PA (XOMA) XOMA CORP.
 XX
 XX Better M, Lei S, Robinson RR, Wilcox GL;
 PI
 XX WPI: 1997-011254/01.
 DR N-PSDB; AAT51042.
 XX
 XX Improved prodn. of protein in Gram -ve bacteria using signal
 PT sequence - from pectate lyase to ensure transport of protein from
 PT the cytoplasm, esp. for prodn. of antibodies
 XX
 PS Example 4; Fig 21; 86pp; English.
 XX
 CC This sequence represents the heavy chain variable region of the 2H7
 CC mouse monoclonal antibody. The 2H7 antibody recognises the human B-cell
 CC surface antigen Bp35, which plays a role in B-cell activation. This
 CC sequence was used in a human-mouse chimeric antibody with human B-cell
 CC antigen specificity, that was produced using the method of the invention.
 CC The method of the invention is for the production of a protein in a
 CC Gram-negative bacterium. The method improves on current techniques, by
 CC using a vector including DNA encoding the pectate lyase signal sequence
 CC (see AAT51034), attached to the sequence encoding the protein for
 CC production. The method is especially used to make immunoglobulins (Ig),
 CC particularly those with a human constant region, suitable for passive
 CC immunisation (without risk of serum sickness or anaphylaxis) or for in
 CC vivo/in vitro diagnosis and imaging. The Ig may also be used
 CC therapeutically, optionally coupled to toxins, etc. Alternatively the
 CC protein to be produced is the sweetener thaumatin. The presence of this
 CC signal sequence means that the protein is exported from the cytoplasm
 CC and can be recovered from the culture medium or periplasm, in active and
 CC correctly folded form. The method allows the class of any antibody to be
 CC switched, e.g. most human-human Ig are of M class, easily reduced and
 CC aggregated, and these can now be changed to G, A or E classes.

CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 140 AA;
 Query Match 69.2%; Score 565; DB 18; Length 140;
 Best Local Similarity 80.0%; Pred. No. 5.6e-36;
 Matches 112; Conservative 6; Mismatches 18; Indels 4; Gaps 1;
 Qy 1 MECSWFLFLLSITTVGHSQAYLQOQSGAELVRGASVKMSCKASGYTLTSYNNHWWKQTP 60
 Db 1 MGFSRIFLFLSVTTGVHSGAYLQOQSGAELVRGASVKMSCKASGYTLTSYNNHWWKQTP 60
 Qy 61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCAR--- 117
 Db 61 GQGLEWIGAIYPGNGDTYYNQKFKGKATLVDRKSSSTAYMQISLTSSEDSAVYFCARVY 120
 Qy 118 -GNWEGALDYWGQTSVTVS 136
 Db 121 YSNSYWFYDWGTTVTVS 140

RESULT 12

AAW41070
 ID AAW41070 standard; Protein; 140 AA.

XX AC AAW41070;

XX DT 01-JUN-1998 (first entry)

XX DE Mouse 2H7 antibody heavy chain variable region.

XX KW Mouse; murine; heavy chain; variable region;
 KW immunoglobulin fragment production; Ig fragment production;
 KW monoclonal antibody 2H7; human B-cell surface antigen.

XX OS Mus sp.

XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Peptide /label= sig_peptide
 FT Peptide 20..140
 FT Peptide /label= mat_peptide

PN US5693493-A.

XX PD 02-DEC-1997.

XX PF 25-MAY-1995; 95US-0450731.

XX PR 29-MAR-1990; 90US-0501092.

XX PR 01-NOV-1985; 85US-0793980.

XX PR 27-OCT-1986; 86WO-US02269.

XX PR 24-JUL-1987; 87US-0077528.

XX PR 11-JAN-1988; 88US-0142039.

XX PR 08-DEC-1992; 92US-0987555.

XX PR 18-AUG-1994; 94US-0299085.

XX PR 25-MAY-1995; 95US-0450731.

XX PA (XOMA) XOMA CORP.

XX PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;

XX PI Wall R, Wilcox GL;

XX XX WPI; 1998-031749/03.

XX DR N-ESDB; AAV03926.

XX PT Production of chimeric antibody fragments - by culturing E. coli

XX PT transformed with dicistronic expression cassette

XX PS Example IV; Fig 21; 98pp; English.

XX CC The present sequence was used in the development of a novel method

CC for the production of an immunoglobulin (Ig) fragment capable of

CC binding an antigen. The method comprises culturing an E. coli host
 CC that has been transformed with a nucleic acid molecule encoding the
 CC Ig fragment, under conditions so that the Ig fragment is produced
 CC and secreted. The nucleic acid molecule comprises DNA sequences
 CC encoding: (a) pectate lyase secretion signal sequence operably
 CC linked to a DNA sequence encoding at least the variable region of
 CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
 CC operably linked to a DNA sequence encoding at least the variable
 CC region of an Ig light chain, where (a) and (b) are operably linked
 CC to a single prokaryotic promoter to form a dicistronic
 CC transcription unit. The method is used to produce chimeric Fab
 CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
 CC against human B-cell surface antigen. The invention provides a
 CC novel approach for producing genetically engineered antibodies of
 CC desired variable region specificity and constant region
 CC properties. The cloned Ig gene products can be produced by
 CC expression in genetically engineered organisms. The application of
 CC chemical gene synthesis, recombinant DNA cloning and production of
 CC specific Ig chains in various organisms provides an effective
 CC solution for the efficient large scale production of human
 CC monoclonal antibodies. The invention also provides a solution to
 CC the problem of class switching antibody molecules.

XX SQ Sequence 140 AA;

Query Match 69.2%; Score 565; DB 19; Length 140;
 Best Local Similarity 80.0%; Pred. No. 5.6e-36;
 Matches 112; Conservative 6; Mismatches 18; Indels 4; Gaps 1;

Qy 1 MECSWFLFLLSITTVGHSQAYLQOQSGAELVRGASVKMSCKASGYTLTSYNNHWWKQTP 60
 Db 1 MGFSRIFLFLSVTTGVHSGAYLQOQSGAELVRGASVKMSCKASGYTLTSYNNHWWKQTP 60
 Qy 61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCAR--- 117
 Db 61 GQGLEWIGAIYPGNGDTYYNQKFKGKATLVDRKSSSTAYMQISLTSSEDSAVYFCARVY 120
 Qy 118 -GNWEGALDYWGQTSVTVS 136
 Db 121 YSNSYWFYDWGTTVTVS 140

RESULT 13

AAW47513
 ID AAW47513 standard; Protein; 140 AA.

XX AC AAW47513;

XX DT 05-JUN-1998 (first entry)

XX DE Mouse 2H7 antibody heavy chain variable region.

XX KW Mouse; murine; heavy chain; variable region;
 KW immunoglobulin fragment production; Ig fragment production;
 KW monoclonal antibody 2H7; human B-cell surface antigen.

XX OS Mus sp.

XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Peptide /label= sig_peptide
 FT Peptide 20..140
 FT Peptide /label= mat_peptide

XX PN US5698435-A.

XX PD 16-DEC-1997.

XX PF 06-JUN-1995; 95US-0467140.

XX PR 29-MAR-1990; 90US-0501092.

XX PR 01-NOV-1985; 85US-0793980.

XX PR 27-OCT-1986; 86WO-US02269.

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PR 24-JUL-1987; 87US-0077528.
PR 11-JAN-1988; 88US-0142039.
PR 08-DEC-1992; 92US-0987555.
PR 18-AUG-1994; 94US-0299085.
PR 06-JUN-1995; 95US-0467140.
XX
XX (XOMA ) XOMA CORP.
XX
XX Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
XX
XX WPI: 1998-051492/05.
DR N-PSDB; AAV18557.
XX
XX DNA encoding secretable immunoglobulin fragments - comprising at
PT least the variable regions of light or heavy chains
XX
XX Example IV; Fig 21; 98pp; English.
XX
XX The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
CC against human B-cell surface antigen. The invention provides a
CC novel approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
XX
XX Sequence 140 AA;
XX
XX Query Match 69.2%; Score 565; DB 19; Length 140;
XX Best Local Similarity 80.0%; Pred. No. 5.6e-36;
XX Matches 112; Conservative 6; Mismatches 18; Indels 4; Gaps 1;
XX
QY 1 MECSWVFLFLSITTGVSQAYLQSGAELVRSGASVKMSCKASGYTLTSYNNHWVKQTP 60
Db 1 MGFSRIFLLSVTTGVHSQAYLQSGAELVRGASVKMSCKASGYTLTSYNNHWVKQTP 60
QY 61 GQGLEWIGNIFPGNGDTYNNQKFKASLTADTSSSTAYMQISLTSEDSAVFYCAR--- 117
Db 61 ROGLEWIGAYIPGNGDTYNNQKFKASLTADTSSSTAYMQISLTSEDSAVFYCARVY 120
QY 118 -GNWEGALDYWGQGTSTVTVS 136
Db 121 YSNWYFEDWVGRTTVTVS 140
XX
XX RESULT 14
XX AAW47520
XX ID AAW47520 standard; Protein; 140 AA.
XX AC AAW47520;
XX
XX 05-JUN-1998 (first entry)
XX
XX Mouse 2H7 antibody heavy chain variable region.
XX

```

```

KW Mouse; murine; heavy chain; variable region;
KW immunoglobulin fragment production; Ig fragment production;
KW monoclonal antibody 2H7; human B-cell surface antigen.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= sig_peptide
FT Peptide 20..140
FT /label= mat_peptide
XX
XX US5698417-A.
XX
XX 16-DEC-1997.
XX
XX 06-JUN-1995; 95US-0466203.
XX
XX 29-MAR-1990; 90US-0501092.
XX 01-NOV-1985; 85US-0793980.
XX 27-OCT-1986; 86WO-US02269.
XX 24-JUL-1987; 87US-0077528.
XX 11-JAN-1988; 88US-0142039.
XX 08-DEC-1992; 92US-0987555.
XX 18-AUG-1994; 94US-0299085.
XX 25-MAY-1995; 95US-0450731.
XX 06-JUN-1995; 95US-0466203.
XX
XX (XOMA ) XOMA CORP.
XX
XX Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
XX
XX WPI: 1998-051487/05.
DR N-PSDB; AAV18593.
XX
XX Production of recombinant immunoglobulin fragment - comprising Fd
XX molecule and light chain
XX
XX Example IV; Fig 21; 98pp; English.
XX
XX The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
CC against human B-cell surface antigen. The invention provides a
CC novel approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
XX
XX Sequence 140 AA;
XX
XX Query Match 69.2%; Score 565; DB 19; Length 140;
XX Best Local Similarity 80.0%; Pred. No. 5.6e-36;
XX Matches 112; Conservative 6; Mismatches 18; Indels 4; Gaps 1;
XX
QY 1 MECSWVFLFLSITTGVSQAYLQSGAELVRSGASVKMSCKASGYTLTSYNNHWVKQTP 60

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2003, 21:57:15 ; Search time 24.6443 Seconds
(without alignments)
849.188 Million cell updates/sec

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Perfect score: 816
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0
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Maximum Match 0%
Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	816	100.0	153	9	US-09-861-294-4
2	816	100.0	153	12	US-10-367-506-4
3	574.5	70.4	468	11	US-09-795-515-7
4	560.5	68.0	468	15	US-10-216-484-9
5	554.5	68.0	438	10	US-09-903-327A-6
6	554.5	68.0	456	10	US-09-903-327A-2
7	554.5	68.0	493	10	US-09-903-327A-13
8	554.5	68.0	510	10	US-09-903-327A-12
9	554.5	68.0	597	10	US-09-903-327A-11
10	554.5	68.0	613	10	US-09-903-327A-14
11	552.5	67.7	136	15	US-10-160-232-88
12	540	66.2	135	12	US-10-244-821-91
13	539.5	66.1	180	9	US-09-748-960-6
14	530	65.0	139	11	US-09-269-921-105
15	530	65.0	139	11	US-09-509-098-4

Sequence 105, App	16	530	65.0	139	16	US-10-218-253-105	Sequence 105, App
Sequence 126, App	17	528	64.7	139	11	US-09-269-921-126	Sequence 126, App
Sequence 98, Appl	18	528	64.7	139	11	US-09-509-098-98	Sequence 98, Appl
Sequence 13, Appl	19	528	64.7	139	14	US-10-006-773-13	Sequence 13, Appl
Sequence 126, App	20	528	64.7	139	16	US-10-218-253-126	Sequence 126, App
Sequence 6, Appl	21	522.5	64.0	140	11	US-09-905-928-6	Sequence 6, Appl
Sequence 6, Appl	22	522.5	64.0	140	15	US-10-096-964-6	Sequence 6, Appl
Sequence 305, App	23	521.5	63.9	502	15	US-10-207-655-305	Sequence 305, App
Sequence 299, App	24	521.5	63.9	516	15	US-10-207-655-299	Sequence 299, App
Sequence 286, App	25	521.5	63.9	520	15	US-10-207-655-286	Sequence 286, App
Sequence 11, Appl	26	520.5	63.8	140	12	US-10-238-681-11	Sequence 11, Appl
Sequence 18, Appl	27	518	63.5	505	12	US-10-053-530-18	Sequence 18, Appl
Sequence 18, Appl	28	518	63.5	505	13	US-10-207-655-18	Sequence 18, Appl
Sequence 284, App	29	517	63.4	500	15	US-10-207-655-284	Sequence 284, App
Sequence 352, App	30	517	63.4	500	15	US-10-207-655-352	Sequence 352, App
Sequence 2, Appl	31	516.5	63.3	150	12	US-09-226-157-2	Sequence 2, Appl
Sequence 16, Appl	32	514.5	63.1	499	12	US-10-053-530-16	Sequence 16, Appl
Sequence 16, Appl	33	514.5	63.1	499	15	US-10-207-655-16	Sequence 16, Appl
Sequence 274, App	34	514.5	63.1	500	15	US-10-207-655-274	Sequence 274, App
Sequence 385, App	35	514.5	63.1	500	15	US-10-207-655-385	Sequence 385, App
Sequence 386, App	36	514.5	63.1	500	15	US-10-207-655-386	Sequence 386, App
Sequence 387, App	37	514.5	63.1	500	15	US-10-207-655-387	Sequence 387, App
Sequence 388, App	38	514.5	63.1	500	15	US-10-207-655-388	Sequence 388, App
Sequence 389, App	39	514.5	63.1	500	15	US-10-207-655-389	Sequence 389, App
Sequence 235, App	40	514	63.0	498	15	US-10-207-655-235	Sequence 235, App
Sequence 4, Appl	41	513.5	62.9	140	9	US-09-748-960-4	Sequence 4, Appl
Sequence 397, App	42	513	62.9	500	15	US-10-207-655-397	Sequence 397, App
Sequence 334, App	43	513	62.9	592	15	US-10-207-655-334	Sequence 334, App
Sequence 398, App	44	512.5	62.8	500	15	US-10-207-655-398	Sequence 398, App
Sequence 236, App	45	512.5	62.8	514	15	US-10-207-655-236	Sequence 236, App

ALIGNMENTS

RESULT 1

US-09-861-294-4
; Sequence 4, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMGF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861.294
; CURRENT FILING DATE: 2001-05-17
; PRIOR FILING DATE: 1997-06-13
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-861-294-4

Query Match	100.0%;	Score 816;	DB 9;	Length 153;
Best Local Similarity	100.0%;	Pred. No. 2.4e-62;		
Matches 153;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Oy	61	GQGLEWIGNFPNGDYYNOKFKGASLTADTSSSTAYMIOISLTSDSAYVFCARGNW	120	
Db	61	GQGLEWIGNFPNGDYYNOKFKGASLTADTSSSTAYMIOISLTSDSAYVFCARGNW	120	

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QY 121 EGALDYGQGTSTVSSAKTTPPVYPLVPGSL 153
DB 121 EGALDYGQGTSTVSSAKTTPPVYPLVPGSL 153

RESULT 2
US-10-367-506-4
; Sequence 4, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/095,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Mus musculus
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; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-367-506-4

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Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MECSWFLFLSITTTGVHSGAYLQOQSGAELVRSGASVKMSCKASGYTLTSTNMHWKQTP 60
QY 61 GQGLEWIGNIPGNGDYNNQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNW 120
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DB 121 EGALDYGQGTSTVSSAKTTPPVYPLVPGSL 153

RESULT 3
US-09-795-515-7
; Sequence 7, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-795-515-7

Query Match 70.4%; Score 574.5; DB 11; Length 468;
Best Local Similarity 74.8%; Pred. No. 3.2e-41;
Matches 113; Conservative 8; Mismatches 29; Indels 1; Gaps 1;

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DB 1 MECSWFLFLSITTTGVHSGAYLQOQSGAELVRSGASVKMSCKASGYTLTSTNMHWKQTP 60
QY 61 GQGLEWIGNIPGNGDYNNQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCAR-GN 119
DB 61 GQGLEWIGNIPGNGDYNNQKFKGKATLTADTSSSTAYMQISLTSSEDSAVYCYARYD 120
QY 120 WEGALDYGQGTSTVSSAKTTPPVYPLVP 150
DB 121 DHYCLDYGQGTTLTVSSAKTTPSVIPLAP 151

RESULT 4
US-10-216-484-9
; Sequence 9, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 9
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-484-9

Query Match 68.7%; Score 560.5; DB 15; Length 464;
Best Local Similarity 71.3%; Pred. No. 4.9e-40;
Matches 112; Conservative 10; Mismatches 28; Indels 7; Gaps 2;

QY 1 MECSWFLFLSITTTGVHSGAYLQOQSGAELVRSGASVKMSCKASGYTLTSTNMHWKQTP 60
DB 1 MGWSCIILFLVATATGVHSGVQLQPGAEVLKPGASVKLSCKASGYTLTSTNMHWKQTP 60
```

```

; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody
US-09-903-327A-2

```

```

Query Match      68.0%; Score 554.5; DB 10; Length 456;
Best Local Similarity 69.7%; Pred. NO. 1.6e-39;
Matches 106; Conservative 16; Mismatches 25; Indels 5; Gaps 1;

1  MECSWVFLLSIITGVHSQAYLQOQSGAELVRSASGVKWSCKASCYTTLTSTNMHWVKTP 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MGWSWIFLFLSGTAGVHSEVOLQOQSGPELVKPGASVKISCKASYTTFTDNMHWKOSH 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

61  CQGLEWICNIIPGNGDITYYNNQKFKKASLTADTSSSTAYMQTSSITSDSASVYFCARGNW 120
      . | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61  GKSLEWICGIYIYPYKGGTCYNNQKFKSKALTTWDSSTNTAYMELRSLTSDASAVYICARG-- 118
      . | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

121  EGALDYWGQGTSTVTVSSAKTTPPPVYPLVPGS 152
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
119  ---IAYWGGTLTYVSAAKTTPPPVYPLAGS 147
      . | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

RESULT 7
US-09-903-327A-13
; Sequence 13, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erguang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARTARIC ACID
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and EGF mature peptide
US-09-903-327A-13

```

```

Query Match      68.0% ; Score 554.5 ; DB 10 ; Length 493 ;
Best Local Similarity 69.7% ; Pred. No. 1.7e-39 ;
Matches 106 ; Conservative 16 ; Mismatches 25 ; Indels 5 ; Gaps 1

```

Qy	1	MECSWFLFLTLSTTGVHSGOAYLQOQGAELVRSGASVKMCKASGYTLTSTNMHWVKTP	60
		:	
Db	1	MGWSWFLFLSLGTAGVSEVQLQOQGPGLVKPQASVKISCKASGYTFDTNMHWVKSH	60
		:	
Qy	61	GCGLEWIGNIFPGNGDTPYNNQKFKGKASLTADTSSSTAYMQISLTSDDSAVYFCARGNW	120
		:	
Db	61	GKSLEWIGYIYPYKGGTGYNNQKFKSKATLTDDSSSNTAYMELRSLTSDASAVYICARG--	118
		:	
Qy	121	EGALDVGWQGTSTVTVSSAKTTPPPVYPLVPGS	152
		:	
Db	119	---IAYWGQGLTVTSAAKTPPPSVYPLAPGS	147

```

RESULT 8
US-09-903-327A-12
; Sequence 12, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:

```


OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-10-160-232-88

Query Match	66.1%	Score 539.5	DB 9:	Length 180:
-------------	-------	-------------	-------	-------------

Db 121 DGWDYIDYWGQGTLTVTSSASTKGPSVFPLAPSS 155

; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
 ; FILE REFERENCE: 35029-20007.00

US-09-269-921-105

S-09-269-921-105

Query Match	65.0%;	Score 530;	DB 11;	Length 139;
Best Local Similarity	71.9%;	Pred. No. 5,28-39;		

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2003, 22:02:45 ; Search time 18.4832 Seconds
(without alignments)
796.063 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 816
Sequence: 1 MECSWVFLFLSITGVHQS.....TVSSAKTTPPPYPLVPGSL 153
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96158682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	568	69.6	475	2 S01321	Ig gamma-2b chain
2	563	69.0	469	2 S37483	Ig gamma-2a chain
3	560	68.6	474	1 G2MS11	Ig gamma-2b chain
4	549	67.3	139	2 PS0024	Ig heavy chain pre
5	548.5	67.2	151	2 PL0011	Ig heavy chain pre
6	547	67.0	150	2 PN0444	Ig heavy chain v r
7	537.5	65.9	246	2 S38950	Ig gamma chain - m
8	537.5	65.9	446	2 S40295	Ig gamma-2a chain
9	533	65.3	178	2 S29594	Ig heavy chain pre
10	529	64.8	137	2 H32513	Ig heavy chain pre
11	527.5	64.6	140	2 PH1482	Ig heavy chain v r
12	523.5	64.2	140	1 HVMSG7	Ig heavy chain pre
13	523.5	64.2	166	2 PL0012	Ig heavy chain pre
14	516.5	63.3	140	2 PH1489	Ig heavy chain v r
15	512	62.7	141	2 A39276	Ig heavy chain pre
16	510.5	62.6	138	2 E32513	Ig heavy chain pre
17	507.5	62.2	138	2 S21810	Ig heavy chain v r
18	507	62.1	133	2 PC1155	Ig heavy chain pre
19	506.5	62.1	140	2 PH1488	Ig heavy chain v r
20	502.5	61.6	135	2 PH1493	Ig heavy chain v r
21	502.5	61.6	140	2 PH1484	Ig heavy chain v r
22	502.5	61.6	140	2 PH1498	Ig heavy chain v r
23	501.5	61.5	135	2 PH1494	Ig heavy chain v r
24	499	61.2	135	2 PS0057	Ig heavy chain pre
25	497	60.9	139	2 A27609	Ig heavy chain pre
26	496.5	60.8	135	2 PH1492	Ig heavy chain v r
27	495	60.7	135	2 A30577	Ig heavy chain pre
28	494.5	60.6	140	2 PH1486	Ig heavy chain v r
29	493	60.4	139	1 MHMS18	Ig heavy chain pre

ALIGNMENTS

RESULT 1

S01321

Ig gamma-2b chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999

C:Accession: S01321

R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fliers, W.

Eur. J. Biochem. 176: 287-295, 1988

A:title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed

A:Reference number: S01320; MUID:88329081; PMID:3138116

A:Accession: S01321

A:Molecule type: mRNA

A:Residues: 1-475

A:Cross-references: EMBL:X13188; NID:q51780; PIDN:CAA31580.1; PID:q51781

A:Note: this sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>

F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 69.6%; Score 568; DB 2; Length 475;

Best Local Similarity 71.2%; Pred. No. 1.1e-37;

Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1;

Qy 1 MECSWVFLFLSITGVHQSQAELVRSASVVKMSCKASGYTLTSYNMHWKQTP 60

Db 1 MEWIFLFLSTAGVQSQVQLQSGAELRPGASVKLSCKASGYTLTSIGISWAKRT 60

Qy 61 GQGLEWIGTGNFPGNGDTYYNQKPKKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNW 120

Db 61 GQGLEWIGEYIPGSGNSYFNEKEKATLTVDKSSSTAYLHLSLTSSEDSAVYFCAGPRQ 120

Qy 121 EGAL--DYWGQGTSTVTVSSAKTTPPPYPLVPG 151

Db 121 VGLLPFGYWGQGTSLVTASAKTTPPSVYPLAPG 153

RESULT 2

S37483

Ig gamma-2a chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37483

R:Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A:Reference number: S37483

A:Accession: S37483

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-469 <DUC>

A:Cross-references: EMBL:X70423; NID:q406252; PIDN:CAA49868.1; PID:q406253

J. Biol. Chem. 269, 12345-12350, 1994

```
db      |          ||| ||||| :||||| :||||| :||||| :||||| :||| :  
61 GQLEWIGYINPTGYTEYNQNFKDKATLTADKSSSTAYMQLSSLTSEDSAVIYG
```

J. Biol. Chem. 269, 12345-12350, 1994


```

Db      134 FGNSLDYWGQGTSVNVSSAKTTPSPVPLAPG 165
          : :::::::::::::::::::: ||||| |||
RESULT 14
PH1489
Ig heavy chain V region (clone X41-2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1489
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1489
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-140 <GID>
A:Experimental source: hybridoma cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMK>

Query Match      63.3%; Score 516.5; DB 2; Length 140;
Best Local Similarity 71.4%; Pred. No. 3.6e-34;
Matches 100; Conservative 14; Mismatches 23; Indels 3; Gaps 1;

Qy      1 MECSWFLFLSITGVHISOAYLQOAGELVRSGASVKMSCKASCYTTLTSYNMHWKQTP 60
Dy      1 MWGSFFILLSVTAGVHSEVQLQOAGELVRAGSSVKMSCKASCYTTFSGMNWVKORP 60
Qy      61 GGLEWIGNIPPGNGDTYYNQFKGKASLTADTSSSTAYMOISSLTSDSAVFCAARGNW 120
Dy      61 GGLEWIGIYINPGNGIATYNEKEKGKTLLTVDKSSSTAYMQLRLGLTSDSAVHFCAARSY 120
Qy      121 EGA---LDYWQGQGTSTVTVSS 137
Dy      121 YGGSYFDYWGQGTTLTVSS 140

RESULT 15
A39276
Ig heavy chain precursor V-D-J region (6-19) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 23-Jul-1999
C:Accession: A39276
R:Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990
A:Title: Cryoglobulinemia induced by a murine IgG3 rheumatoid factor: skin vasculiti
A:Reference number: A39276; MUID:91088540; PMID:2263605
A:Accession: A39276
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-141 <REL>
A:Cross-references: GB:M55312; NID:g196002; PIDN:AAA63337.1; PID:g196003
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMK>

Query Match      62.7%; Score 512; DB 2; Length 141;
Best Local Similarity 71.6%; Pred. No. 8.2e-34;
Matches 101; Conservative 16; Mismatches 20; Indels 4; Gaps 2;

Qy      1 MECSWFLFLSITGVHISOAYLQOAGELVRSGASVKMSCKASCYTTLTSYNMHWKQTP 60
Dy      1 MEWSGFIFLLSVTAGVHSQVLQOAGELVRPGTSVKMSCKASCYTTFNFWIGWKORP 60
Qy      61 GGLEWIGNIPPGNGDTYYNQFKGKASLTADTSSSTAYMOISSLTSDSAVFCAARG-- 118
Dy      61 GHGLEWIGNIYPGGDYNYIEKFKGKATLTADTSSSTAYMQLSSLTSDSAIIYCAREY 120

119 NWEGA--LDYWQGQGTSTVTVSS 137

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2003, 19:57:10 ; Search time 10.7819 Seconds
(without alignments)
667.331 Million cell updates/sec

Title: us-08-836-455-4
Perfect score: 816
Sequence: 1 MECSWVFLFLSITTVGHVSQ.....TVSSAKTTPPPVPLVPGSL 153

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Result No.	Score	Query Match	Length	DB ID	Description
1	523.5	64.2	140	1	HV02_MOUSE
2	493	60.4	139	1	HV07_MOUSE
3	470	57.6	137	1	HV11_MOUSE
4	461	56.5	117	1	HV52_MOUSE
5	459.5	56.3	120	1	HV03_MOUSE
6	458	56.1	117	1	HV14_MOUSE
7	451	55.3	117	1	HV05_MOUSE
8	446	54.7	117	1	HV06_MOUSE
9	445.5	54.6	138	1	HV48_MOUSE
10	443	54.3	117	1	HV04_MOUSE
11	440	53.9	117	1	HV09_MOUSE
12	430	52.7	117	1	HV49_MOUSE
13	429.5	52.6	136	1	HV15_MOUSE
14	426.5	52.3	121	1	HV01_MOUSE
15	425.5	52.1	117	1	HV12_MOUSE
16	421.5	51.7	117	1	HV13_MOUSE
17	418	51.2	117	1	HV10_MOUSE
18	417	51.1	118	1	HV51_MOUSE
19	416	51.0	120	1	HV50_MOUSE
20	389	47.7	117	1	HV16_HUMAN
21	388	47.5	117	1	HV19_HUMAN
22	375	46.0	147	1	HVIC_HUMAN
23	342	41.9	114	1	HV00_MOUSE
24	333	40.8	136	1	HV16_MOUSE
25	321.5	39.4	142	1	HV01_RAT
26	308.5	37.8	121	1	HV30_HUMAN
27	308	37.7	122	1	HV36_HUMAN
28	304.5	37.3	144	1	HV43_MOUSE
29	301.5	36.9	117	1	HV1A_HUMAN
30	301	36.9	117	1	HV3C_HUMAN
31	300.5	36.6	117	1	HV41_MOUSE
32	299	36.6	119	1	HV40_MOUSE
33	299	36.6	126	1	HV3K_HUMAN

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523.5	64.2	140	1	HV02_MOUSE
2	493	60.4	139	1	HV07_MOUSE
3	470	57.6	137	1	HV11_MOUSE
4	461	56.5	117	1	HV52_MOUSE
5	459.5	56.3	120	1	HV03_MOUSE
6	458	56.1	117	1	HV14_MOUSE
7	451	55.3	117	1	HV05_MOUSE
8	446	54.7	117	1	HV06_MOUSE
9	445.5	54.6	138	1	HV48_MOUSE
10	443	54.3	117	1	HV04_MOUSE
11	440	53.9	117	1	HV09_MOUSE
12	430	52.7	117	1	HV49_MOUSE
13	429.5	52.6	136	1	HV15_MOUSE
14	426.5	52.3	121	1	HV01_MOUSE
15	425.5	52.1	117	1	HV12_MOUSE
16	421.5	51.7	117	1	HV13_MOUSE
17	418	51.2	117	1	HV10_MOUSE
18	417	51.1	118	1	HV51_MOUSE
19	416	51.0	120	1	HV50_MOUSE
20	389	47.7	117	1	HV16_HUMAN
21	388	47.5	117	1	HV19_HUMAN
22	375	46.0	147	1	HVIC_HUMAN
23	342	41.9	114	1	HV00_MOUSE
24	333	40.8	136	1	HV16_MOUSE
25	321.5	39.4	142	1	HV01_RAT
26	308.5	37.8	121	1	HV30_HUMAN
27	308	37.7	122	1	HV36_HUMAN
28	304.5	37.3	144	1	HV43_MOUSE
29	301.5	36.9	117	1	HV1A_HUMAN
30	301	36.9	117	1	HV3C_HUMAN
31	300.5	36.6	117	1	HV41_MOUSE
32	299	36.6	119	1	HV40_MOUSE
33	299	36.6	126	1	HV3K_HUMAN

34	296.5	36.3	117	1	HV42_MOUSE
35	296	36.3	119	1	HV37_MOUSE
36	296	36.3	119	1	HV38_MOUSE
37	293.5	36.0	119	1	HV3L_HUMAN
38	291.5	35.7	116	1	HV05_CARAU
39	289	35.4	120	1	HV30_HUMAN
40	289	35.4	122	1	HV3H_HUMAN
41	288.5	35.4	118	1	HV39_MOUSE
42	288	35.3	114	1	HV3B_HUMAN
43	288	35.3	116	1	HV3T_HUMAN
44	285.5	35.0	144	1	HV26_MOUSE
45	285	34.9	111	1	HV35_MOUSE

ALIGNMENTS

RESULT 1

HV02_MOUSE STANDARD; PRT; 140 AA.

AC P01746;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region 93G7 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RC SEQUENCE FROM N.A.

RP STRAIN=A/J;

RX MEDLINE=82152818; PubMed=6801765;

RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,

RA Capra J.D.;

RT "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain.";

RL Science 216:309-311(1982).

CC -!- SIMILARITY: Contains 1 Immunoglobulin-like domain.

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CC -----

EMBL; J00493; AAA38128.1; -.

PIR; A94264; HVMSG7.

DR HSSP; P01810; 2FBJ.

DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
KW	Immunoglobulin V region; Hybridoma; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT	DOMAIN 20 139 IG-LIKE.
FT	NON_TER 140 140
SQ	SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 64.2%; Score 523.5; DB 1; Length 140;

Best Local Similarity 72.1%; Pred. No. 1.9e-40;

Matches 101; Conservative 14; Mismatches 22; Indels 3; Gaps 1;

QY 1 MECSWVFLFLSITTVGHVSQAYLQSQGAELVRSGASVKMSCKASGYTLTSYNHHWVKQTP 60

Db 1 MGHSFIFLLSVTAGVHSEVQLQSQGAELVRSGASVKMSCKASGYTLTSYNHHWVKQTP 60

QY 61 GQGLEWIGNIFPGNGDTYYNQKPKGASLTADTSSSTAYMQISLTSSEDSAVYFCARGNW 120

Db 61 GQGLEWIGINPGNGYINAEKFKGKTLTVDKSSSTAYMQLSLTSSEDSAVYFCARSHY 120
 QY 121 EGA---LDYWGQGTSTVSS 137
 Db 121 YGGSYDFYWGQGTPLTVSS 140

RESULT 2

HV07_MOUSE
 ID HV07_MOUSE STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region B1-8/186-2 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC (NPB ANTIBODIES).
 CC
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 CC
 CC EMBL: J00529; AAA38170.1; -
 DR PIR: A90809; MMS18
 DR PDB: 1A60; 27-MAY-98.
 DR PDB: 1A6W; 15-JUL-98.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Igv; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal; 3D-structure.
 KW SIGNAL 1 19
 FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DOMAIN 118 124 D SEGMENT.
 FT DOMAIN 125 139 JH2 SEGMENT.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 139 139
 SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match
 Best Local Similarity 69.18; Score 493; DB 1; Length 139;
 Matches 96; Conservative 15; Mismatches 26; Indels 2; Gaps 1;
 QY 1 MECSWFLFLSLITTVGHSQAYLQQSGAELVRSGASYKMSCKASGYTLTSTNMHWKQTP 60
 Db 1 MGWSCIMFLAATATGVHSQVQLQPGAEVFKPGASVKLSCKASGYTFTSYNMHWKQRP 60

QY 61 GQGLEWIGINPGNGDYINQKFKKSLTADTSSSTAYMQLSLTSSEDSAVYFCARGNW 120
 Db 61 GRGLEWIGRIDPNSGGTKYNEKPKSKATLVDRFSSSTAYMQLSLTSSEDSAVYCARVDY 120
 QY 121 EGA---LDYWGQGTSTVSS 137
 Db 121 YGGSYDFYWGQGTPLTVSS 139

RESULT 3

HV11_MOUSE
 ID HV11_MOUSE STANDARD; PRT; 137 AA.
 AC P01755;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region S43 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC (NPB ANTIBODIES).
 CC
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 CC
 CC EMBL: J00539; AAA38172.1; -
 DR PIR: A02038; G2MS43.
 DR HSP: P01810; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Igv; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DOMAIN 118 122 D SEGMENT.
 FT DOMAIN 123 137 JH2 SEGMENT.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 137 137
 SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match
 Best Local Similarity 57.6%; Score 470; DB 1; Length 137;
 Matches 91; Conservative 13; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MECSWFLFLSLITTVGHSQAYLQQSGAELVRSGASYKMSCKASGYTLTSTNMHWKQTP 60
 Db 1 MGWSCIMFLAATATGVHSQVQLQPGAEVFKPGASVKLSCKASGYTFTSYLMHWKQRP 60
 QY 61 GQGLEWIGINPGNGDYINQKFKKSLTADTSSSTAYMQLSLTSSEDSAVYFCARGNW 120

```
Db 61 GRGLEMIGRIDNSGGTYNEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVVYCYARYL 120
QY 121 EGALDYWGQGTSTVTVSS 137
Db 121 GRFYDWGQGTTLTVSS 137

RESULT 4
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH58 A1/A4 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments."
RL Cell 40:271-281(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; M13787; AAA38499.1; -
DR PIR; A02029; HVMSAL.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH58 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 56.5%; Score 461; DB 1; Length 117;
Best Local Similarity 77.0%; Pred. No. 6.5e-35;
Matches 87; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 5 WYFLLSTTTGVHQAQLQSGAELVRSGAVKMSCKASGYTLTSYNMHWKQTPGQGL 64
Db 5 WYFLLSTAGVHCVQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKRPGQGL 64
QY 65 EWIGNIFPCNGDYYNKEFKASLTADTSSSTAYMQLSSLTSEDSAVVYFCAR 117
Db 65 EWIGWIPGDGSKYNEKFKGATLTADKSSSTAYMQLSSLTSENSAVYFCAR 117

RESULT 5
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
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AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Geffer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiotypic response of the strain A mouse."
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 56.3%; Score 459.5; DB 1; Length 120;
Best Local Similarity 75.4%; Pred. No. 9.1e-35;
Matches 89; Conservative 10; Mismatches 16; Indels 3; Gaps 1;

QY 23 LQSGAELVRSGAVKMSCKASGYTLTSYNMHWKQTPGQGLWIGNIFPGNDTYNQK 82
Db 3 LQSGAELVRSGAVKMSCKASGYTFTSYGINWVKRPGQGLWIGNIFPGNYTKYNEK 62
QY 83 FRGKASLTADTSSSTAYMQLSSLTSEDSAVVYFCARWEGA---LDYWGQGTSTVTVSS 137
Db 63 FRGKTLTVDKSSSTAYMQLSSLTSEDSAVVYFCARSVYGGSYFYFDYWGQGTTLTVSS 120

RESULT 6
HV14_MOUSE
ID HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 108A precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes."
RL Nature 292:426-430(1981).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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Matches 86; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
QY 1 MECSWFLFLSITGVHSHQAVLQSGAELVSGASVKMSCKASGYTLTSYNNHWKQTP 60
D 1 MWSCILFLVATATGVHSHVQLQPGALVPGASVKVSKASGYTFTSYNNHWKQRP 60
QY 61 GOGLEWIGNIFPGNGDTYNNQKFKASLTADTSSSTAYMQISLTSSEDSAVYFCA 116
D 61 GOGLEWIGRIHPSDSNTYNNQKFKATLTVDKSSSTAYMQISLTSSEDSAVYFCA 116

RESULT 9
HV48_MOUSE
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RL delta in an IgD-secreting plasmacytoma."
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMST7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 FRAMEWORK-3.
FT DOMAIN 86 117 FRAMEWORK-4.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 54.6%; Score 445.5; DB 1; Length 138;
Best Local Similarity 62.9%; Pred. No. 1.9e-33;
Matches 88; Conservative 19; Mismatches 28; Indels 5; Gaps 2;
QY 1 MECSWFLFLSITGVHSHQAVLQSGAELVSGASVKMSCKASGYTLTSYNNHWKQTP 60
D 1 MWSCILFLVATATGVHSHVQLQPGALVPGASVKVSKASGYTFTSYNNHWKQRP 60
QY 61 GOGLEWIGNIFPGNGDTYNNQKFKASLTADTSSSTAYMQISLTSSEDSAVYFCA 120
D 61 GOGLEWIGINPNDGRSNTYNNQKFKATLTVDKSSSTAYMQISLTSSEDSAVYFCA 118

QY 121 EGALD---YWGQTSVTSS 137
D 119 DGYDFVYWGQTLVTFSA 138

RESULT 10
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.

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AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR; A02030; HVM523.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 54.3%; Score 443; DB 1; Length 117;
Best Local Similarity 72.6%; Pred. No. 2.7e-33;
Matches 85; Conservative 9; Mismatches 23; Indels 0; Gaps 0;
QY 1 MECSWFLFLSITGVHSHQAVLQSGAELVSGASVKMSCKASGYTLTSYNNHWKQTP 60
D 1 MWSCILFLVAAANGVHSHVQLQPGALVPGASVKVSKASGYTFTSYNNHWKQRP 60
QY 61 GOGLEWIGNIFPGNGDTYNNQKFKASLTADTSSSTAYMQISLTSSEDSAVYFCA 117
D 61 GOGLEWIGNINPNDGRSNTYNNQKFKATLTVDKSSSTAYQLSSLTSSEDSAVYFCA 117

RESULT 11
HV09_MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."

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RL Cell 24:525-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; D90809; HVMS61.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 53.98; Score 440; DB 1; Length 117;
Best Local Similarity 72.68; Pred. No. 5e-33;
Matches 85; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 MECSWFLFLSLITGVHSGAYLQSGAELVRSGASVKMSCKASGYTLTSTYNMHWVKOTP 60
   I : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MGWSCIMFLAATATGVHSPVQLOPGAEVLKPGASVKLSCKASGYTFTSYNHHWVKORP 60

QY 61 GQGLEWIGNIFPGNDTYNKNQKFGKASLTADTSSSTAYMQISLTSEDSAVYFCAR 117
   I : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDTSSTAYMQLSLTSEDSAVYICAR 117

RESULT 12
HV49_MOUSE STANDARD; PRT; 117 AA.
ID HV49_MOUSE
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH58 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85093340; PubMed=2578321;
RA Yancopoulos G.D.; Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
  unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
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CC -----
CC EMBL; M13788; AAA38506.1; -.
DR PIR; A02035; MHMSB4.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION BCL1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 53.98; Score 440; DB 1; Length 117;
Best Local Similarity 72.68; Pred. No. 5e-33;
Matches 85; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 MECSWFLFLSLITGVHSGAYLQSGAELVRSGASVKMSCKASGYTLTSTYNMHWVKOTP 60
   I : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MGWSCIMFLAATATGVHSPVQLOPGAEVLKPGASVKLSCKASGYTFTSYNHHWVKORP 60

QY 61 GQGLEWIGNIFPGNDTYNKNQKFGKASLTADTSSSTAYMQISLTSEDSAVYFCAR 117
   I : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDTSSTAYMQLSLTSEDSAVYICAR 117

RESULT 13
HV15_MOUSE STANDARD; PRT; 136 AA.
ID HV15_MOUSE
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R.; Liu C.-P.; Newell N.; Ward R.B.; Tucker P.W.; Strober S.;
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
  by a cloned B-cell lymphoma: a single copy of the VH gene is shared
  by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J00494; AAA38130.1; -.
DR PIR; A02042; HVMSB1.
DR HSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT DOMAIN 20 136 IG-LIKE.
FT NON_TER 136 136
FT SEQUENCE 136 AA; 15078 MW; 6827CFBC6B3F35E CRC64;

Query Match 52.68; Score 429.5; DB 1; Length 136;

```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2003, 21:05:00 ; Search time 36.453 Seconds
(without alignments)
1083.094 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 816
Sequence: 1 MCSWVFLPILLSITGVHSQ.....TVSSAKTTPPPVPLVPGSL 153

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriapi:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	589.5	72.2	473	11 Q9D8L4	Q9D8L4 mus musculus
2	581	71.2	463	11 Q99LC4	Q99LC4 mus musculus
3	569	69.7	473	11 Q99L25	Q99L25 mus musculus
4	549.5	67.3	168	11 Q8VDC9	Q8VDC9 mus musculus
5	544	66.7	613	11 Q8VXC7	Q8VXC7 mus musculus
6	526.5	64.5	481	11 Q91WT1	Q91WT1 mus musculus
7	524.5	64.3	474	11 Q8R3H6	Q8R3H6 mus musculus
8	521	63.8	278	11 Q921K1	Q921K1 mus musculus
9	521	63.8	482	11 Q8K172	Q8K172 mus musculus
10	516.5	63.3	489	11 Q8VCX4	Q8VCX4 mus musculus
11	515.5	63.2	468	11 Q99L31	Q99L31 mus musculus
12	506.5	62.1	142	11 Q924Q1	Q924Q1 mus musculus
13	499	61.2	480	11 Q8K0Z4	Q8K0Z4 mus musculus
14	494.5	60.6	481	11 Q8VCV5	Q8VCV5 mus musculus
15	493	60.4	488	11 Q91WR1	Q91WR1 mus musculus
16	489	59.9	488	11 Q8K0F2	Q8K0F2 mus musculus

17	482	59.1	143	11 Q924R0	Q924R0 mus musculus
18	479.5	58.8	481	11 Q91WT3	Q91WT3 mus musculus
19	478	58.6	145	11 Q924R4	Q924R4 mus musculus
20	474	58.1	145	11 Q924P7	Q924P7 mus musculus
21	474	58.1	145	11 Q924R1	Q924R1 mus musculus
22	473.5	58.0	140	11 Q924P8	Q924P8 mus musculus
23	473.5	58.0	146	11 Q924Q3	Q924Q3 mus musculus
24	472	57.8	145	11 Q924Q6	Q924Q6 mus musculus
25	471	57.7	143	11 Q924P9	Q924P9 mus musculus
26	469	57.5	145	11 Q924Q9	Q924Q9 mus musculus
27	467	57.2	145	11 Q924Q7	Q924Q7 mus musculus
28	466.5	57.2	142	11 Q924Q2	Q924Q2 mus musculus
29	466.5	57.2	146	11 Q924R8	Q924R8 mus musculus
30	465	57.0	143	11 Q924Q0	Q924Q0 mus musculus
31	464	56.9	143	11 Q924R7	Q924R7 mus musculus
32	464	56.9	143	11 Q924P6	Q924P6 mus musculus
33	464	56.9	145	11 Q924R3	Q924R3 mus musculus
34	463.5	56.8	140	11 Q924R2	Q924R2 mus musculus
35	463	56.7	137	11 Q924R6	Q924R6 mus musculus
36	459	56.2	143	11 Q91VA2	Q91VA2 mus musculus
37	458	56.1	143	11 Q91V67	Q91V67 mus musculus
38	453	55.5	141	11 Q924Q4	Q924Q4 mus musculus
39	451.5	55.3	497	4 Q8WY24	Q8WY24 homo sapien
40	450	55.1	118	11 Q921C4	Q921C4 mus musculus
41	449	55.0	143	11 Q924Q5	Q924Q5 mus musculus
42	447.5	54.8	146	11 Q924Q8	Q924Q8 mus musculus
43	447.5	54.8	614	4 Q96GA6	Q96GA6 homo sapien
44	446.5	54.7	117	11 Q9QXE9	Q9QXE9 mus musculus
45	445.5	54.6	144	11 Q924P5	Q924P5 mus musculus

ALIGNMENTS

RESULT 1

Q9D8L4	PRELIMINARY;	PRT;	473 AA.
ID	Q9D8L4		
AC	Q9D8L4;		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	1810060009RIK protein.		
OS	IGH-1 OR 1810060009RIK.		
GN	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Famanaka I.,		
RA	Saito T., Matsuda Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadoita K., Katsuma H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,		
RT	Hayashizaki Y.;		
RL	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
DR	EMBL; AK007918; BAB25349.1; -		
DR	HSSP; P01842; 7FAB.		


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DR SMART: SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 168
SQ SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;

Query Match 67.3%; Score 549.5; DB 11; Length 168;
Best Local Similarity 69.5%; Pred. No. 3e-44;
Matches 105; Conservative 16; Mismatches 29; Indels 1; Gaps 1;

QY 1 MECSWVFLFLSITTVGHVSQAYLQOQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTP 60
DB 11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MEWTWVFLFLSVTAGVHVSQVQLQOQSGAELMKPGASVKISCKATGYTFSSYIWDWKQRP 60
QY 61 GQGLEWIGNFPNGDYYNQKFKGASLTADTSSSTAYMQISLTSSEDSAVYFCAR-GN 119
DB 11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 GHGLEWIGELPGSGRTNYNEKFKGTTFTADTSSNTAYIQFSLSLTSSEDSAVYCYANGS: 120
QY 120 WEGALDYWGQGTSTVTVSSAKTTPPPVPLV 150
DB 11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 SRWYFDVWGAGTTVTVSSTKTTAPSVYPLAP 151

RESULT 5
Q8VCX7 PRELIMINARY; PRT; 613 AA.
AC Q8VCX7;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical 67.9 kDa protein.
GN IGH-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018315; AAH18315.1;
DR MGD; MGI:96448; Igh-6.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 66.7%; Score 544; DB 11; Length 613;
Best Local Similarity 69.5%; Pred. No. 5.1e-43;
Matches 105; Conservative 17; Mismatches 25; Indels 4; Gaps 2;

QY 1 MECSWVFLFLSITTVGHVSQAYLQOQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTP 60
DB 11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MEWTWVFLFLSVTAGVHVSQVQLQOQSGAELMKPGASVKISCKATGYTFSSYIWDWKQRP 60
QY 61 GQGLEWIGNFPNGDYYNQKFKGASLTADTSSSTAYMQISLTSSEDSAVYFCAR--G 118
DB 11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 GHGLEWIGELPGSGRTNYNEKFKGTTFTADTSSNTAYMQLSSLTSSEDSAVYCYARRLG 120
QY 119 WEGALDYWGQGTSTVTVSSAKTTPPPVPLV 149
DB 11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 RW--YFDVWGAGTTVTVSSESQSPNVPPLV 149

RESULT 6
Q91WT1 PRELIMINARY; PRT; 481 AA.
ID Q91WT1
AC Q91WT1;
```

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DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical 52.1 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1;
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 64.5%; Score 526.5; DB 11; Length 481;
Best Local Similarity 70.3%; Pred. No. 1.7e-41;
Matches 102; Conservative 13; Mismatches 27; Indels 3; Gaps 2;

QY 5 WVFLLSITTVGHVSQAYLQOQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTPGQGL 64
DB 11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 5 WIFLLSGTAGVQCQVQLQSGPELVKPGASVKISCKASGYTFTSYIIHWKQRPQGL 64
QY 65 EWIGNFPNGDYYNQKFKGASLTADTSSSTAYMQISLTSSEDSAVYFCAR-GNWEGA 123
DB 11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 65 VWIGWIYPGDNTKYNEKFKGTTFTADTSSSTAYMFLSSLTSSEDSAVYFCARGGW--A 122
QY 124 LDVWGQGTSTVTVSSAKTTPPPVPL 148
DB 11 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 123 FDVWGQGTTLTVSSEPAEPTIYPL 147

RESULT 7
Q8R3H6 PRELIMINARY; PRT; 474 AA.
ID Q8R3H6
AC Q8R3H6;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical 51.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1;
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 64.3%; Score 524.5; DB 11; Length 474;
Best Local Similarity 66.4%; Pred. No. 2.6e-41;
Matches 101; Conservative 20; Mismatches 30; Indels 1; Gaps 1;
```


RESULT 14
Q8VCV5

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ID Q8VCV5 PRELIMINARY; PRT; 481 AA.
AC Q8VCV5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018455; AAH18455.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match 60.6%; Score 494.5; DB 11; Length 481;
Best Local Similarity 63.2%; Pred. No. 1.8e-38;
Matches 98; Conservative 21; Mismatches 33; Indels 3; Gaps 3;

Qy 1 MECSWVFLFLSITGVHISOAYLQOQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTP 60
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MECSWVFLFLSITGVHISOAYLQOQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTP 60
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 GQGLEWIGNIPPGNGDTYYNOKFKGKASLTADTSSSTAYMIOISLTSDESDSAVYFCARGNW 120
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GQGLEWIGNIPPGNGDTYYNOKFKGKASLTADTSSSTAYMIOISLTSDESDSAVYFCARGNW 120
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 EGA-LDYWGQGTSTVSSAKTTPPPVYPL-VPGL 153
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 YGANFAFWGQGTLTVTSAESARNPTIYPLTLPPAL 154

RESULT 15
Q91WR1 PRELIMINARY; PRT; 488 AA.
AC Q91WR1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 53.0 kDa protein.
GN IGH-VJ558 OR A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013539; AAH13539.1; -.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;
```

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Query Match 60.4%; Score 493; DB 11; Length 488;
Best Local Similarity 61.3%; Pred. No. 2.6e-38;
Matches 95; Conservative 24; Mismatches 28; Indels 8; Gaps 2;

Qy 1 MECSWVFLFLSITGVHISOAYLQOQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTP 60
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGWNWIFLLSGTAGIYSEVQLQOQSGPELVKPGASVKLSCKASGYITDYYVWVKQSH 60
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 GQGLEWIGNIPPGNGDTYYNOKFKGKASLTADTSSSTAYMIOISLTSDESDSAVYFCARG-- 118
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GKSLEWIGDINPYNGGTSYNQKFKGKATLTVDKSSSIAYMQLNNLTSDSDSAVYFCARGPV 120
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 119 -----NWEGALDYWGQGTSTVSSAKTTPPPVYPL 148
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 YYSYFSYDRG-DYWGQGTLTVTSAEPAREPTIYPL 154
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: August 30, 2003, 22:06:01
Job time : 38.453 secs
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